

<210> 356  
 <211> 167  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 356  
 Asn Glu Gln Cys Leu Gly Asp Val Gly Val Leu Gly Ala Leu Leu Leu  
   1                  5                  10                  15  
 Asn Phe Tyr Lys Leu Ala Pro Gly Glu Ala Leu Tyr Leu Asp Ala Ala  
                   20                  25                  30  
 Asn Leu His Ala Tyr Ile Ser Gly Leu Gly Val Glu Ile Met Ala Asn  
                   35                  40                  45  
 Ser Asp Asn Val Leu Arg Gly Gly Leu Thr Ser Lys Tyr Val Asp Val  
                   50                  55                  60  
 Pro Glu Leu Val Arg Val Leu Asp Phe Asn Ser Leu Glu Asn Ala Arg  
                   65                  70                  75                  80  
 Val Asp Val Glu Glu Asp Gly Ala Thr Thr His Tyr Pro Val Pro Ile  
                   85                  90                  95  
 Asn Glu Phe Gln Leu Asp Arg Val Ala Val Gln Gly Glu Ala Glu Ala  
                   100                  105                  110  
 Asn His Asp Gly Pro Met Ile Val Leu Cys Thr Ser Gly Thr Val Ser  
                   115                  120                  125  
 Leu Glu Ala Gly Glu Lys Thr Leu Glu Val Ala Ala Gly His Ala Ala  
                   130                  135                  140  
 Trp Val Pro Ala Asn Asp Pro Thr Ile Ala Met Arg Ser Glu Asp Ala  
                   145                  150                  155                  160  
 Glu Val Phe Leu Ala Arg Val  
                   165

<210> 357  
 <211> 808  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(808)  
 <223> FRXA01373

<400> 357  
 ctgcgacgga cctagcaaag gggcgctgac acaagcactg cgtttgctgg tgcgcggaca 60  
 gtcagccacg acctattcca ttgaagaaaa ggacttgtaa atg gag cta ttg gaa 115  
   Met Glu Leu Leu Glu  
   1                  5  
 ggc tca ctg cgc acc tac cca tgg ggt tca aga aca ctg atc gct gat 163  
 Gly Ser Leu Arg Thr Tyr Pro Trp Gly Ser Arg Thr Leu Ile Ala Asp  
                   10                  15                  20

002290 0420960



<210>	358
<211>	236
<212>	PRT



&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 358

Met Glu Leu Leu Glu Gly Ser Leu Arg Thr Tyr Pro Trp Gly Ser Arg  
 1 5 10 15

Thr Leu Ile Ala Asp Leu Lys Gly Glu Glu Ser Pro Ser Ser Arg Pro  
 20 25 30

Glu Ala Glu Val Trp Phe Gly Ala His Pro Gly Ser Pro Ser Thr Ile  
 35 40 45

Gly Gly Asn Ala Leu Asn Glu Val Ile Ala Ala Asn Pro Glu Glu Ala  
 50 55 60

Leu Gly Thr Arg Val Ala Glu Ala Phe Glu Asn Glu Leu Pro Phe Leu  
 65 70 75 80

Leu Lys Ile Leu Ala Ala Gly Ala Pro Leu Ser Leu Gln Ala His Pro  
 85 90 95

Ser Leu Glu Gln Ala Arg Glu Gly Phe Ala Arg Glu Asn Ser Ala Gly  
 100 105 110

Ile Asp Leu Gly Ala Pro Asn Arg Asn Tyr Arg Asp Pro Asn His Lys  
 115 120 125

Pro Glu Leu Ile Val Ala Leu Thr Glu Phe Ile Ala Met Ala Gly Phe  
 130 135 140

Arg Pro Leu Arg Asn Thr Leu Thr Ile Phe Asp Ala Leu Ala Cys Glu  
 145 150 155 160

Pro Leu Asp Arg Tyr Arg Ser Met Leu Thr Val Asp Asn Glu Glu Glu  
 165 170 175

Ser Leu Arg Ala Leu Phe Thr Thr Trp Ile Thr Ile Pro Ile Gly Lys  
 180 185 190

Arg His Glu Leu Ile Asp Ala Leu Ile Ser Asn Ala His Thr Tyr Leu  
 195 200 205

Glu Ala Ser Asp Arg Asp Glu Asp Ile Ala Phe Val Leu Ser His Ile  
 210 215 220

Ile Glu Leu Asn Glu Gln Tyr Pro Gly Asp Val Gly  
 225 230 235

&lt;210&gt; 359

&lt;211&gt; 1775

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1752)

&lt;223&gt; RXA02611

&lt;400&gt; 359

gat gcg tgg tcg gat cct atg gct acg tgg cgt cat gcg att acc act 48

002290"0420950



0960740-0620



245										250					255					
aag	tac	cag	gat	att	tat	ccc	atc	aac	ttt	gat	aat	gat	gct	ccg	aag	816				
Lys	Tyr	Gln	Asp	Ile	Tyr	Pro	Ile	Asn	Phe	Asp	Asn	Asp	Ala	Pro	Lys					
			260						265					270						
atc	tac	gaa	gag	gtc	tat	cgt	gtg	gtg	aag	ttc	tgg	gtg	gat	ttg	ggt	864				
Ile	Tyr	Glu	Glu	Val	Tyr	Arg	Val	Val	Lys	Phe	Trp	Val	Asp	Leu	Gly					
			275						280					285						
gtg	acc	aca	ttc	cgc	gtg	gat	aac	ccg	cac	act	aag	ccc	gct	aat	ttc	912				
Val	Thr	Thr	Phe	Arg	Val	Asp	Asn	Pro	His	Thr	Lys	Pro	Ala	Asn	Phe					
			290						295					300						
tgg	cag	tgg	ctt	att	tct	gcc	atc	cat	aaa	tca	aac	cct	gag	gtc	att	960				
Trp	Gln	Trp	Leu	Ile	Ser	Ala	Ile	His	Lys	Ser	Asn	Pro	Glu	Val	Ile					
			305						310						320					
ttc	cta	gcg	gag	gcg	tct	act	cgc	ccg	gca	cgt	ctg	tat	ttc	ttg	tcc	1008				
Phe	Leu	Ala	Glu	Ala	Ser	Thr	Arg	Pro	Ala	Arg	Leu	Tyr	Phe	Leu	Ser					
									325						335					
aag	att	ggt	ttc	tcc	cag	tct	tac	acc	tac	ttc	acc	tgg	aag	gtc	acc	1056				
Lys	Ile	Gly	Phe	Ser	Gln	Ser	Tyr	Thr	Tyr	Phe	Thr	Trp	Lys	Val	Thr					
									340						350					
aac	gag	gag	ctc	acc	gag	ttc	gct	act	gag	atc	gcc	ccc	atg	gcg	gat	1104				
Asn	Glu	Glu	Leu	Thr	Glu	Phe	Ala	Thr	Glu	Ile	Ala	Pro	Met	Ala	Asp					
									355						365					
att	tct	cgt	ccg	aac	ctg	ttt	gtg	aac	act	ccc	gac	att	ttg	cat	gcg	1152				
Ile	Ser	Arg	Pro	Asn	Leu	Phe	Val	Asn	Thr	Pro	Asp	Ile	Leu	His	Ala					
									370						380					
tct	ctg	cag	cat	ggt	gga	cgc	gcc	atg	ttc	gct	atc	cgc	gcc	gca	ttg	1200				
Ser	Leu	Gln	His	Gly	Gly	Arg	Ala	Met	Phe	Ala	Ile	Arg	Ala	Ala	Leu					
									385						400					
gcc	gcc	acg	atg	tct	cct	gtg	tgg	ggc	gta	tat	tcc	gga	tat	gag	ctc	1248				
Ala	Ala	Thr	Met	Ser	Pro	Val	Trp	Gly	Val	Tyr	Ser	Gly	Tyr	Glu	Leu					
									405						415					
ttt	gag	cac	gag	gcc	gtc	aag	cct	ggt	tcg	gaa	gag	tac	ttg	gat	tct	1296				
Phe	Glu	His	Glu	Ala	Val	Lys	Pro	Gly	Ser	Glu	Glu	Tyr	Leu	Asp	Ser					
									420						430					
gag	aag	tac	gag	ctg	cgt	ccc	cgc	gat	ttc	gag	ggt	gct	ctg	gaa	cgt	1344				
Glu	Lys	Tyr	Glu	Leu	Arg	Pro	Arg	Asp	Phe	Glu	Gly	Ala	Leu	Glu	Arg					
									435						445					
ggc	gat	tct	ctc	gag	gat	tac	atc	gct	ctg	ctc	aac	cag	atc	cgt	cgc	1392				
Gly	Asp	Ser	Leu	Glu	Asp	Tyr	Ile	Ala	Leu	Leu	Asn	Gln	Ile	Arg	Arg					
									450						460					
gcg	aac	cct	gcc	ttg	cag	caa	cta	cgc	aac	atc	cac	ttc	cac	gaa	gcg	1440				
Ala	Asn	Pro	Ala	Leu	Gln	Gln	Leu	Arg	Asn	Ile	His	Phe	His	Glu	Ala					
									465						480					
gac	aat	gat	cag	atc	atc	gcc	tac	tcc	aag	gtt	gat	gct	ttg	acc	gga	1488				
Asp	Asn	Asp	Gln	Ile	Ile	Ala	Tyr	Ser	Lys	Val	Asp	Ala	Leu	Thr	Gly					
									485						495					

006602740-062300



aat acc gtg ttg att gtg gtc aac ttg gat cca cgt agt gct cgt gag 1536  
 Asn Thr Val Leu Ile Val Val Asn Leu Asp Pro Arg Ser Ala Arg Glu  
 500 505 510

gct act gtt cgc ctt gat ctt gga gcg ctt ggc tta gaa gcg ggt gca 1584  
 Ala Thr Val Arg Leu Asp Leu Gly Ala Leu Gly Leu Glu Ala Gly Ala  
 515 520 525

cag ttt gag gtg cgc gat gcg atc acc ggc tcc cgt tac ctg tgg tca 1632  
 Gln Phe Glu Val Arg Asp Ala Ile Thr Gly Ser Arg Tyr Leu Trp Ser  
 530 535 540

gag acg aac ttt gtc cgc ctc gag ccc cta cgc gat gtc gcc cac atc 1680  
 Glu Thr Asn Phe Val Arg Leu Glu Pro Leu Arg Asp Val Ala His Ile  
 545 550 555 560

ttt gtt ctt cct gaa ctt cca gcg tct cgc cgt gag cgt ctc gcg tgg 1728  
 Phe Val Leu Pro Glu Leu Pro Ala Ser Arg Arg Glu Arg Leu Ala Trp  
 565 570 575

cgc gaa atc aag acc tac cgc gcg taattttccca tctctgtacc ttc 1775  
 Arg Glu Ile Lys Thr Tyr Arg Ala  
 580

<210> 360

<211> 584

<212> PRT

<213> Corynebacterium glutamicum

<400> 360

Asp Ala Trp Ser Asp Pro Met Ala Thr Trp Arg His Ala Ile Thr Thr  
 1 5 10 15

Lys Ile Glu Ala Gly Gln Gly Ser Asp Glu Leu Tyr Asn Asp Phe Glu  
 20 25 30

His Gly Ala Gln Leu Phe Glu Arg Ala Ala Glu Asn Leu Ser Lys Glu  
 35 40 45

Asp Arg Thr Ala Leu Phe Asp Val Ala Ser Ser Leu Arg Arg Gly Gly  
 50 55 60

Asp Val Arg Ala Arg Leu Ala Pro Ala Leu Thr Ala Ser Val Thr His  
 65 70 75 80

Leu Leu Glu Leu Asn Pro Leu Arg Glu Leu Val Thr Met Gly Glu Asn  
 85 90 95

Leu Gln Val Arg Val Glu Arg Arg Ala Ala Leu Val Asn Ser Trp Tyr  
 100 105 110

Glu Leu Phe Pro Arg Ser Thr Gly Gly Trp Asp Glu Ser Gly Thr Pro  
 115 120 125

Val His Gly Thr Phe Ala Thr Thr Ala Gln Ala Leu Glu Arg Val Ala  
 130 135 140

Lys Met Gly Phe Asp Thr Val Tyr Phe Pro Pro Ile His Pro Ile Gly  
 145 150 155 160

00602740 062300



Glu Val Asn Arg Lys Gly Arg Asn Asn Thr Leu Thr Pro Glu Pro His  
 165 170 175  
 Asp Val Gly Ser Pro Trp Ala Ile Gly Ser Lys Asp Gly Gly His Asp  
 180 185 190  
 Ala Thr His Pro Arg Leu Gly Thr Ile Glu Asp Phe Gln Ala Leu Leu  
 195 200 205  
 Ala Arg Ala Arg Glu Leu Asn Leu Glu Val Ala Leu Asp Leu Ala Leu  
 210 215 220  
 Gln Ala Ala Pro Asp His Pro Trp Ala Gln Glu His Arg Glu Phe Phe  
 225 230 235 240  
 Thr Val Leu Ala Asp Gly Thr Ile Ala Tyr Ala Glu Asn Pro Pro Lys  
 245 250 255  
 Lys Tyr Gln Asp Ile Tyr Pro Ile Asn Phe Asp Asn Asp Ala Pro Lys  
 260 265 270  
 Ile Tyr Glu Glu Val Tyr Arg Val Val Lys Phe Trp Val Asp Leu Gly  
 275 280 285  
 Val Thr Thr Phe Arg Val Asp Asn Pro His Thr Lys Pro Ala Asn Phe  
 290 295 300  
 Trp Gln Trp Leu Ile Ser Ala Ile His Lys Ser Asn Pro Glu Val Ile  
 305 310 315 320  
 Phe Leu Ala Glu Ala Ser Thr Arg Pro Ala Arg Leu Tyr Phe Leu Ser  
 325 330 335  
 Lys Ile Gly Phe Ser Gln Ser Tyr Thr Tyr Phe Thr Trp Lys Val Thr  
 340 345 350  
 Asn Glu Glu Leu Thr Glu Phe Ala Thr Glu Ile Ala Pro Met Ala Asp  
 355 360 365  
 Ile Ser Arg Pro Asn Leu Phe Val Asn Thr Pro Asp Ile Leu His Ala  
 370 375 380  
 Ser Leu Gln His Gly Gly Arg Ala Met Phe Ala Ile Arg Ala Ala Leu  
 385 390 395 400  
 Ala Ala Thr Met Ser Pro Val Trp Gly Val Tyr Ser Gly Tyr Glu Leu  
 405 410 415  
 Phe Glu His Glu Ala Val Lys Pro Gly Ser Glu Glu Tyr Leu Asp Ser  
 420 425 430  
 Glu Lys Tyr Glu Leu Arg Pro Arg Asp Phe Glu Gly Ala Leu Glu Arg  
 435 440 445  
 Gly Asp Ser Leu Glu Asp Tyr Ile Ala Leu Leu Asn Gln Ile Arg Arg  
 450 455 460  
 Ala Asn Pro Ala Leu Gln Gln Leu Arg Asn Ile His Phe His Glu Ala  
 465 470 475 480

002290" 0420960



<400> 361																																
gaacttccag		cgtctcgccg		tgagcgtctc		gcgtggcgcg		aatcaagac		ctaccgcgcg		60																				
taattttccca		tctctgtacc		ttctatcaag		gattatcacc		atg		acc		ggt		gac		ccc		115														
										Met		Thr		Val		Asp		Pro														
										1						5																
gcg		agc		cac		atc		acc		atc		cct		gaa		gca		gat		ctg		gcc		cgc		ctg		cgc		cac		163
Ala		Ser		His		Ile		Thr		Ile		Pro		Glu		Ala		Asp		Leu		Ala		Arg		Leu		Arg		His		
						10																				20						
tgc		aac		cat		cac		gat		cct		cat		gga		ttt		tat		ggt		tgg		cat		gag		acc		gaa		211
Cys		Asn		His		His		Asp		Pro		His		Gly		Phe		Tyr		Gly		Trp		His		Glu		Thr		Glu		
						25										30										35						
gct		ggt		tcg		gtt		atc		cgc		acg		cgc		cag		gtc		ggc		gcg		acg		cag		gtt		aat		259
Ala		Gly		Ser		Val		Ile		Arg		Thr		Arg		Gln		Val		Gly		Ala		Thr		Gln		Val		Asn		
						40								45										50								
ttg		ctt		atc		gac		gac		acc		tcc		cac		gtc		atg		acc		cct		atc		ggc		gac		gac		307
Leu		Leu		Ile		Asp		Asp		Thr		Ser		His		Val		Met		Thr		Pro		Ile		Gly		Asp		Asp		
												60										65										
att		ttc		gca		att		gac		tta		ggt		cac		cgc		gag		cgc		gct		gac		tat		cgc		ttg		355
Ile		Phe		Ala		Ile		Asp		Leu		Gly		His		Arg		Glu		Arg		Ala		Asp		Tyr		Arg		Leu		
										75										80										85		
gaa		gtc		acc		tgg		cct		gat		caa		gaa		ccg		cag		gtc		aag		gct		gat		cca		tac		403
Glu		Val		Thr		Trp		Pro		Asp		Gln		Glu		Pro		Gln		Val		Lys		Ala		Asp		Pro		Tyr		

**0907-08**



0860720980



gcc cac ttc cct aag gat gat tgg gct ctt gcc cgc ttt gat ggc gaa	1171
Ala His Phe Pro Lys Asp Asp Trp Ala Leu Ala Arg Phe Asp Gly Glu	
345 350 355	
gcc ctc tat gaa cac cct gac tgg agg cgc ggc gaa caa aag gat tgg	1219
Ala Leu Tyr Glu His Pro Asp Trp Arg Arg Gly Glu Gln Lys Asp Trp	
360 365 370	
ggc acc ctg gtc ttt gac ttc ggt cgc aac gaa gtc cgc aac ttc ctc	1267
Gly Thr Leu Val Phe Asp Phe Gly Arg Asn Glu Val Arg Asn Phe Leu	
375 380 385	
gtc gct aat gcg ttg tac tgg att gaa gaa ttc cac atc gat ggt ctg	1315
Val Ala Asn Ala Leu Tyr Trp Ile Glu Glu Phe His Ile Asp Gly Leu	
390 395 400 405	
cgc gtc gac gcc gtg gcc tcc atg ctg tac ctc gat tac tcc cgt gag	1363
Arg Val Asp Ala Val Ala Ser Met Leu Tyr Leu Asp Tyr Ser Arg Glu	
410 415 420	
cac ggc gaa tgg gaa cca aac atc tac ggt ggt cgc gag aac ctc gag	1411
His Gly Glu Trp Glu Pro Asn Ile Tyr Gly Gly Arg Glu Asn Leu Glu	
425 430 435	
gca gtg cag ttc ctg cag gaa atg aac gcc acg gtg ctg cga ctg cac	1459
Ala Val Gln Phe Leu Gln Glu Met Asn Ala Thr Val Leu Arg Leu His	
440 445 450	
cct ggt gcg ctc acc atc gct gag gaa tca act tca tgg cct ggc gtg	1507
Pro Gly Ala Leu Thr Ile Ala Glu Glu Ser Thr Ser Trp Pro Gly Val	
455 460 465	
acc gca cca acg tgg gac ggc ggc ttg gga ttc tcc ctc aag tgg aac	1555
Thr Ala Pro Thr Trp Asp Gly Gly Leu Gly Phe Ser Leu Lys Trp Asn	
470 475 480 485	
atg ggc tgg atg cac gac acc tta gag tac ttc tcc aaa aac cct gtg	1603
Met Gly Trp Met His Asp Thr Leu Glu Tyr Phe Ser Lys Asn Pro Val	
490 495 500	
cac cgc gca ttc cac cac agt gag ctc act ttc tcc ttg gtg tac gca	1651
His Arg Ala Phe His His Ser Glu Leu Thr Phe Ser Leu Val Tyr Ala	
505 510 515	
ttc tct gag cgt ttt gta ctt ccg atc tct cac gat gaa gtc gtc cac	1699
Phe Ser Glu Arg Phe Val Leu Pro Ile Ser His Asp Glu Val Val His	
520 525 530	
ggc aag ggt tcc ctg tgg gac cgt atg cct ggc gat acg tgg aac aag	1747
Gly Lys Gly Ser Leu Trp Asp Arg Met Pro Gly Asp Thr Trp Asn Lys	
535 540 545	
gcc gct ggt ctt cgc acc ttc ctt gcg tac atg tgg tca cac cca ggc	1795
Ala Ala Gly Leu Arg Thr Phe Leu Ala Tyr Met Trp Ser His Pro Gly	
550 555 560 565	
aag aag ctg ctt ttc atg ggt cag gag ttt ggt cag cgt gaa gag tgg	1843
Lys Lys Leu Leu Phe Met Gly Gln Glu Phe Gly Gln Arg Glu Glu Trp	
570 575 580	

09602740 " 062300



gct gaa ggc cag gga ctg cca tgg gat att gtc gac ggc tgg caa ggc 1891  
Ala Glu Gly Gln Gly Leu Pro Trp Asp Ile Val Asp Gly Trp Gln Gly  
585 590 595

gag tac cac gaa gcc atc cgc act ctg acc cgc tcc ctc aac ggt gtc 1939  
Glu Tyr His Glu Ala Ile Arg Thr Leu Thr Arg Ser Leu Asn Gly Val  
600 605 610

tac tca gac tcc cct gcg ctg cac act cag gat ttc acc gga gaa ggc 1987  
Tyr Ser Asp Ser Pro Ala Leu His Thr Gln Asp Phe Thr Gly Glu Gly  
615 620 625

ttc aca tgg aat aag ggc gac gac gcc acc aac aac att ttg gcg ttc 2035  
Phe Thr Trp Asn Lys Gly Asp Asp Ala Thr Asn Asn Ile Leu Ala Phe  
630 635 640 645

act cgt ttc ggc agc gac ggc tcc cag atg ctg tgt gta ttc aac ctg 2083  
Thr Arg Phe Gly Ser Asp Gly Ser Gln Met Leu Cys Val Phe Asn Leu  
650 655 660

tct gga acc tcc cag cct gag tac cag ctc ggt gtt gca gcg ggt ggc 2131  
Ser Gly Thr Ser Gln Pro Glu Tyr Gln Leu Gly Val Ala Ala Gly Gly  
665 670 675

gaa tgg aag ctc gtt ctc aac act gat gat gct gaa ttc ctc ggt gca 2179  
Glu Trp Lys Leu Val Leu Asn Thr Asp Asp Ala Glu Phe Leu Gly Ala  
680 685 690

gaa aac gat atc gct act tcc gtt caa gca gca gcg aca cca cgc gat 2227  
Glu Asn Asp Ile Ala Thr Ser Val Gln Ala Ala Ala Thr Pro Arg Asp  
695 700 705

aat ttc gcc tac tca ctc tca ctg cat gtc cca gcg atg agt gct cag 2275  
Asn Phe Ala Tyr Ser Leu Ser Leu His Val Pro Ala Met Ser Ala Gln  
710 715 720 725

ttc tac tca ctg cag aag taggacacag gaaaatgcat cct 2316  
Phe Tyr Ser Leu Gln Lys  
730

&lt;210&gt; 362

&lt;211&gt; 731

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 362

Met Thr Val Asp Pro Ala Ser His Ile Thr Ile Pro Glu Ala Asp Leu  
1 5 10 15

Ala Arg Leu Arg His Cys Asn His His Asp Pro His Gly Phe Tyr Gly  
20 25 30

Trp His Glu Thr Glu Ala Gly Ser Val Ile Arg Thr Arg Gln Val Gly  
35 40 45

Ala Thr Gln Val Asn Leu Leu Ile Asp Asp Thr Ser His Val Met Thr  
50 55 60

Pro Ile Gly Asp Asp Ile Phe Ala Ile Asp Leu Gly His Arg Glu Arg  
65 70 75 80

09602740-062300



Ala Asp Tyr Arg Leu Glu Val Thr Trp Pro Asp Gln Glu Pro Gln Val  
                     85                    90                    95  
 Lys Ala Asp Pro Tyr Tyr Phe Leu Pro Thr Val Gly Glu Met Asp Ile  
                     100                    105                    110  
 Tyr Leu Phe Ser Glu Gly Arg His Glu Arg Leu Trp Glu Ile Leu Gly  
                     115                    120                    125  
 Ala Asn Ile Lys Thr Tyr Gln Thr Ala Leu Gly Thr Val Arg Gly Thr  
                     130                    135                    140  
 Ala Phe Thr Val Trp Ala Pro Asn Ala Ile Gly Cys Ala Val Val Gly  
                     145                    150                    155                    160  
 Gly Phe Asn Gly Trp Asn Ala Ser Gln His Pro Met Arg Ser Met Gly  
                     165                    170                    175  
 Gly Ser Gly Leu Trp Glu Leu Phe Ile Pro Gly Ile Glu Glu Gly Glu  
                     180                    185                    190  
 Val Tyr Lys Phe Ala Val Gln Thr Arg Glu Gly Gln Arg Arg Asp Lys  
                     195                    200                    205  
 Ala Asp Pro Met Ala Arg Arg Ala Glu Leu Ala Pro Ala Thr Gly Ser  
                     210                    215                    220  
 Ile Val Ala Ser Ser Glu Tyr Gln Trp Gln Asp Ser Glu Trp Leu Arg  
                     225                    230                    235                    240  
 Glu Arg Ser Gln Thr Asp Leu Ala Ser Lys Pro Met Ser Val Tyr Glu  
                     245                    250                    255  
 Val His Leu Gly Ser Trp Arg Trp Gly Lys Asn Tyr Glu Asp Leu Ala  
                     260                    265                    270  
 Thr Glu Leu Val Asp Tyr Val Ala Asp Leu Gly Tyr Thr His Val Glu  
                     275                    280                    285  
 Phe Leu Pro Val Ala Glu His Pro Phe Gly Gly Ser Trp Gly Tyr Gln  
                     290                    295                    300  
 Val Thr Gly Tyr Tyr Ala Pro Thr Ser Arg Trp Gly Thr Pro Asp Gln  
                     305                    310                    315                    320  
 Phe Arg Ala Leu Val Asp Ala Phe His Ala Arg Gly Ile Gly Val Ile  
                     325                    330                    335  
 Met Asp Trp Val Pro Ala His Phe Pro Lys Asp Asp Trp Ala Leu Ala  
                     340                    345                    350  
 Arg Phe Asp Gly Glu Ala Leu Tyr Glu His Pro Asp Trp Arg Arg Gly  
                     355                    360                    365  
 Glu Gln Lys Asp Trp Gly Thr Leu Val Phe Asp Phe Gly Arg Asn Glu  
                     370                    375                    380  
 Val Arg Asn Phe Leu Val Ala Asn Ala Leu Tyr Trp Ile Glu Glu Phe  
                     385                    390                    395                    400

002250" 0420960



His Ile Asp Gly Leu Arg Val Asp Ala Val Ala Ser Met Leu Tyr Leu  
 405 410 415  
 Asp Tyr Ser Arg Glu His Gly Glu Trp Glu Pro Asn Ile Tyr Gly Gly  
 420 425 430  
 Arg Glu Asn Leu Glu Ala Val Gln Phe Leu Gln Glu Met Asn Ala Thr  
 435 440 445  
 Val Leu Arg Leu His Pro Gly Ala Leu Thr Ile Ala Glu Glu Ser Thr  
 450 455 460  
 Ser Trp Pro Gly Val Thr Ala Pro Thr Trp Asp Gly Gly Leu Gly Phe  
 465 470 475 480  
 Ser Leu Lys Trp Asn Met Gly Trp Met His Asp Thr Leu Glu Tyr Phe  
 485 490 495  
 Ser Lys Asn Pro Val His Arg Ala Phe His His Ser Glu Leu Thr Phe  
 500 505 510  
 Ser Leu Val Tyr Ala Phe Ser Glu Arg Phe Val Leu Pro Ile Ser His  
 515 520 525  
 Asp Glu Val Val His Gly Lys Gly Ser Leu Trp Asp Arg Met Pro Gly  
 530 535 540  
 Asp Thr Trp Asn Lys Ala Ala Gly Leu Arg Thr Phe Leu Ala Tyr Met  
 545 550 555 560  
 Trp Ser His Pro Gly Lys Lys Leu Leu Phe Met Gly Gln Glu Phe Gly  
 565 570 575  
 Gln Arg Glu Glu Trp Ala Glu Gly Gln Gly Leu Pro Trp Asp Ile Val  
 580 585 590  
 Asp Gly Trp Gln Gly Glu Tyr His Glu Ala Ile Arg Thr Leu Thr Arg  
 595 600 605  
 Ser Leu Asn Gly Val Tyr Ser Asp Ser Pro Ala Leu His Thr Gln Asp  
 610 615 620  
 Phe Thr Gly Glu Gly Phe Thr Trp Asn Lys Gly Asp Asp Ala Thr Asn  
 625 630 635 640  
 Asn Ile Leu Ala Phe Thr Arg Phe Gly Ser Asp Gly Ser Gln Met Leu  
 645 650 655  
 Cys Val Phe Asn Leu Ser Gly Thr Ser Gln Pro Glu Tyr Gln Leu Gly  
 660 665 670  
 Val Ala Ala Gly Gly Glu Trp Lys Leu Val Leu Asn Thr Asp Asp Ala  
 675 680 685  
 Glu Phe Leu Gly Ala Glu Asn Asp Ile Ala Thr Ser Val Gln Ala Ala  
 690 695 700  
 Ala Thr Pro Arg Asp Asn Phe Ala Tyr Ser Leu Ser Leu His Val Pro  
 705 710 715 720  
 Ala Met Ser Ala Gln Phe Tyr Ser Leu Gln Lys

00E290"0420960



730

```
<220>  
<221> CDS  
<222> (1)..(1890)  
<223> RXN01884
```

<400> 363																
gtg	act	gcc	att	gaa	ttg	atg	ccg	gtc	cac	cag	ttc	ctg	cag	gat	gat	48
Val	Thr	Ala	Ile	Glu	Leu	Met	Pro	Val	His	Gln	Phe	Leu	Gln	Asp	Asp	
1				5				10				15				
cgt	ctc	cgc	gac	cta	gga	atg	cgc	aac	tac	tgg	ggc	tac	aac	tct	ttc	96
Arg	Leu	Arg	Asp	Leu	Gly	Met	Arg	Asn	Tyr	Trp	Gly	Tyr	Asn	Ser	Phe	
20				25				30								
ggc	ttc	ttt	gcg	ccc	tac	aac	gat	tac	gct	gcc	aac	aag	aac	ccc	ggt	144
Gly	Phe	Phe	Ala	Pro	Tyr	Asn	Asp	Tyr	Ala	Ala	Asn	Lys	Asn	Pro	Gly	
35				40				45								
ggc	gcc	gtg	gcc	gag	ttc	aaa	ggc	ttg	gtg	cgc	agc	tac	cac	gaa	gcg	192
Gly	Ala	Val	Ala	Glu	Phe	Lys	Gly	Leu	Val	Arg	Ser	Tyr	His	Glu	Ala	
50				55				60								
ggc	ctc	gaa	gta	att	ttg	gat	gtg	gtc	tac	aac	cac	acc	gcc	gag	ggc	240
Gly	Leu	Glu	Val	Ile	Leu	Asp	Val	Val	Tyr	Asn	His	Thr	Ala	Glu	Gly	
65				70				75				80				
aac	cac	atg	ggc	ccc	acc	atc	gcg	ttc	cga	ggc	att	gac	aac	gag	gcg	288
Asn	His	Met	Gly	Pro	Thr	Ile	Ala	Phe	Arg	Gly	Ile	Asp	Asn	Glu	Ala	
85				90				95								
tac	tac	cga	ctg	gtt	gag	ggc	gat	cgc	cgt	cat	tac	atg	gac	tac	acc	336
Tyr	Tyr	Arg	Leu	Val	Glu	Gly	Asp	Arg	Arg	His	Tyr	Met	Asp	Tyr	Thr	
100				105				110								
ggt	act	ggt	aac	tcc	ctc	aat	gtc	cgc	gac	ccg	cac	tca	ctg	cag	ctg	384
Gly	Thr	Gly	Asn	Ser	Leu	Asn	Val	Arg	Asp	Pro	His	Ser	Leu	Gln	Leu	
115				120				125								
att	atg	gat	tcg	ctg	cgc	tac	tgg	gtc	acc	gag	atg	cat	gtc	gac	ggc	432
Ile	Met	Asp	Ser	Leu	Arg	Tyr	Trp	Val	Thr	Glu	Met	His	Val	Asp	Gly	
130				135				140								
ttc	cgc	ttc	gac	ctt	gcc	tct	acc	ctt	gct	cgt	gaa	ttt	gat	gat	gtt	480
Phe	Arg	Phe	Asp	Leu	Ala	Ser	Thr	Leu	Ala	Arg	Glu	Phe	Asp	Asp	Val	
145				150				155				160				
gac	cgc	ctg	gca	acc	ttc	ttc	gac	ctg	gtc	caa	caa	gac	ccg	gtg	gtc	528
Asp	Arg	Leu	Ala	Thr	Phe	Phe	Asp	Leu	Val	Gln	Gln	Asp	Pro	Val	Val	
165				170				175								
tcc	cag	gtc	aag	ctc	att	gct	gag	ccg	tgg	gat	gtt	ggc	gaa	ggc	gga	576
Ser	Gln	Val	Lys	Leu	Ile	Ala	Glu	Pro	Trp	Asp	Val	Gly	Glu	Gly	Gly	
180				185				190								

[illegible]



[illegible]



<400> 364  
Val Thr Ala Ile Glu Leu Met Pro Val His Gln Phe Leu Gln Asp Asp  
1 5 10 15







Gly Asn Asn Asn Val Tyr Cys Gln Asp Asn Glu Leu Ala Trp Val Asn  
 340 345 350  
 Trp Asp Gln Ala Glu Glu Asn Ala Asp Leu Val Ser Phe Thr Arg Arg  
 355 360 365  
 Leu Leu Arg Ile Arg Ala Asn His Pro Val Phe Arg Arg Arg Gln Phe  
 370 375 380  
 Leu Ala Gly Gly Pro Leu Gly Ala Asp Val Arg Asp Arg Asp Ile Ala  
 385 390 395 400  
 Trp Leu Val Pro Asn Gly Thr Leu Met Thr Gln Asp Asp Trp Asp Phe  
 405 410 415  
 Ala Phe Gly Lys Ser Leu Gln Val Phe Phe Asn Gly Asp Ala Ile Glu  
 420 425 430  
 Glu Pro Asp Tyr Arg Gly Gln Lys Ile His Asp Asp Ser Phe Ile Leu  
 435 440 445  
 Met Phe Asn Ala His Phe Glu Pro Ile Asp Phe Asn Leu Pro Pro Glu  
 450 455 460  
 His Phe Gly Met Lys Trp Lys Leu Leu Val Asp Thr Thr Glu Ala Val  
 465 470 475 480  
 Gly His Pro Leu Glu Asp Leu Thr Ile Glu Ala Gly Gly Thr Ile Thr  
 485 490 495  
 Val Pro Ala Arg Ser Thr Met Leu Leu Arg Gln Val Glu Ala Pro Asp  
 500 505 510  
 Tyr Thr Lys Leu Glu Glu Lys Ile Ala Ala Glu Lys Arg Glu Gln Glu  
 515 520 525  
 Leu Ala Ala Glu Lys Glu Ala Ala Glu Lys Arg Glu Leu Glu Leu Ala  
 530 535 540  
 Ala Ala Lys Glu Ala Glu Asp Ala Ala Glu Ala Leu His Leu Ala Ala  
 545 550 555 560  
 Glu Arg Ala Ser Thr Gln Glu Ala Glu Leu Ala His Gln His Gly Ala  
 565 570 575  
 Asp Ala Ile Ala Asp Glu Val Ala Glu Glu Pro Gln Glu Leu Pro Gln  
 580 585 590  
 Asp Glu Val Ala Ala Glu Val Glu Thr Glu Pro Asp Thr Glu Pro Asp  
 595 600 605  
 Thr Glu Ser Asp Ser Glu Gln Ala Glu Val Ala Ser Glu Glu Pro Glu  
 610 615 620  
 Ala Asp Glu Glu Glu Lys  
 625 630

&lt;210&gt; 365

&lt;211&gt; 1496

&lt;212&gt; DNA

00602740-062340



<220>

<222> (1) .. (1473)

<223> FRXA01884

<400> 365

atg cat gtc gac ggc ttc cgc ttc gac ctt gcc tct acc ctt gct cgt 48  
Met His Val Asp Gly Phe Arg Phe Asp Leu Ala Ser Thr Leu Ala Arg  
1 5 10 15

gaa ttt gat gat gtt gac cgc ctg gca acc ttc ttc gac ctg gtc caa 96  
Glu Phe Asp Asp Val Asp Arg Leu Ala Thr Phe Phe Asp Leu Val Gln  
20 25 30

caa gac ccg gtg gtc tcc cag gtc aag ctc att gct gag ccg tgg gat 144  
Gln Asp Pro Val Val Ser Gln Val Lys Leu Ile Ala Glu Pro Trp Asp  
35 40 45

gtt ggc gaa ggc gga tac caa gtg ggt aac ttc cca cca ctg tgg act 192  
Val Gly Glu Gly Gly Tyr Gln Val Gly Asn Phe Pro Pro Leu Trp Thr  
50 55 60

gag tgg aac ggt aaa tac cgc gac act gtc cgt gat ttc tgg cgt ggt 240  
Glu Trp Asn Gly Lys Tyr Arg Asp Thr Val Arg Asp Phe Trp Arg Gly  
65 70 75 80

gag cca gca acc ttg ggt gaa ttc gct tcc cga cta act ggt tcc tct 288  
Glu Pro Ala Thr Leu Gly Glu Phe Ala Ser Arg Leu Thr Gly Ser Ser  
85 90 95

gat ttg tat gca aac aac ggc cgt cgc ccc act gca tcg atc aac ttt 336  
Asp Leu Tyr Ala Asn Asn Gly Arg Arg Pro Thr Ala Ser Ile Asn Phe  
100 105 110

gtg act gct cac gac ggc ttc acc ctc aat gac ttg gtc agt tac aac 384  
Val Thr Ala His Asp Gly Phe Thr Leu Asn Asp Leu Val Ser Tyr Asn  
115 120 125

gag aag cac aac atg gcc aac ggt gaa gac ggt cgg gac ggt gaa tca 432  
Glu Lys His Asn Met Ala Asn Gly Glu Asp Gly Arg Asp Gly Glu Ser  
130 135 140

cac aac cgt tcc tgg aac tgt ggc gtc gaa gga cca act gac gat cct 480  
 His Asn Arg Ser Trp Asn Cys Gly Val Glu Gly Pro Thr Asp Asp Pro  
 145 150 155 160

gag att atg cag ctg cgt gct cag caa cga cgc aac ttc ctc acc acc 528  
Glu Ile Met Gln Leu Arg Ala Gln Gln Arg Arg Asn Phe Leu Thr Thr  
165 170 175

ttg ttg ctg tcc cag ggc acc cct atg ttg tcc cac ggt gat gaa atg 576  
Leu Leu Leu Ser Gln Gly Thr Pro Met Leu Ser His Gly Asp Glu Met  
180 185 190

gcc cgt acc caa aac ggc aac aac aac gtc tac tgc caa gac aat gaa 624  
Ala Arg Thr Gln Asn Gly Asn Asn Asn Val Tyr Cys Gln Asp Asn Glu  
195 200 205

ctg gcg tgg gtg aat tgg gat cag gct gaa gaa aac qct qac ttg qtg 672

[illegible]



Leu	Ala	Trp	Val	Asn	Trp	Asp	Gln	Ala	Glu	Glu	Asn	Ala	Asp	Leu	Val		
210						215					220						
agc	ttc	acc	agg	cgt	ttg	ctg	cgt	atc	cga	gca	aac	cac	cca	gta	ttt	720	
Ser	Phe	Thr	Arg	Arg	Leu	Leu	Arg	Ile	Arg	Ala	Asn	His	Pro	Val	Phe		
225					230					235					240		
agg	cgc	agg	cag	ttc	ctt	gcc	ggc	ggc	cct	ttg	ggc	gcc	gat	ggt	cgt	768	
Arg	Arg	Arg	Gln	Phe	Leu	Ala	Gly	Gly	Pro	Leu	Gly	Ala	Asp	Val	Arg		
				245					250					255			
gac	cgc	gat	atc	gca	tgg	ctg	gta	cca	aat	gga	acc	ttg	atg	act	caa	816	
Asp	Arg	Asp	Ile	Ala	Trp	Leu	Val	Pro	Asn	Gly	Thr	Leu	Met	Thr	Gln		
			260					265					270				
gat	gac	tgg	gac	ttc	gct	ttc	ggc	aaa	tca	ctg	cag	gtg	ttc	ttc	aac	864	
Asp	Asp	Trp	Asp	Phe	Ala	Phe	Gly	Lys	Ser	Leu	Gln	Val	Phe	Phe	Asn		
		275					280					285					
ggc	gat	gcc	atc	gaa	gag	cct	gat	tat	cga	gga	cag	aaa	atc	cac	gat	912	
Gly	Asp	Ala	Ile	Glu	Glu	Pro	Asp	Tyr	Arg	Gly	Gln	Lys	Ile	His	Asp		
	290					295					300						
gac	tcc	ttc	atc	ttg	atg	ttc	aac	gct	cac	ttc	gaa	cct	atc	gat	ttc	960	
Asp	Ser	Phe	Ile	Leu	Met	Phe	Asn	Ala	His	Phe	Glu	Pro	Ile	Asp	Phe		
305					310					315					320		
aat	ctc	cct	cct	gag	cat	ttc	ggc	atg	aag	tgg	aag	ctt	ttg	gtc	gat	1008	
Asn	Leu	Pro	Pro	Glu	His	Phe	Gly	Met	Lys	Trp	Lys	Leu	Leu	Val	Asp		
				325					330					335			
acc	acc	gaa	gcg	gtg	ggc	cac	ccg	ctg	gag	gat	ctc	acc	atc	gaa	gct	1056	
Thr	Thr	Glu	Ala	Val	Gly	His	Pro	Leu	Glu	Asp	Leu	Thr	Ile	Glu	Ala		
			340					345					350				
ggc	gga	acc	atc	act	ggt	cct	gcc	cgt	tcc	acg	atg	ctg	ctg	cgc	cag	1104	
Gly	Gly	Thr	Ile	Thr	Val	Pro	Ala	Arg	Ser	Thr	Met	Leu	Leu	Arg	Gln		
		355					360					365					
gtg	gag	gct	ccg	gac	tac	acc	aag	ctt	gag	gaa	aag	atc	gct	gct	gaa	1152	
Val	Glu	Ala	Pro	Asp	Tyr	Thr	Lys	Leu	Glu	Glu	Lys	Ile	Ala	Ala	Glu		
	370					375					380						
aag	cgt	gag	caa	gaa	ctt	gcg	gca	gag	aag	gaa	gct	gct	gag	aag	cgc	1200	
Lys	Arg	Glu	Gln	Glu	Leu	Ala	Ala	Glu	Lys	Glu	Ala	Ala	Glu	Lys	Arg		
385					390					395					400		
gaa	ttg	gaa	ctg	gcg	gca	gca	aag	gaa	gct	gaa	gat	gct	gct	gag	gct	1248	
Glu	Leu	Glu	Leu	Ala	Ala	Ala	Lys	Glu	Ala	Glu	Asp	Ala	Ala	Glu	Ala		
				405				410						415			
ctc	cac	ctt	gcg	gca	gaa	cgt	gct	tcg	act	cag	gaa	gct	gaa	ttg	gcc	1296	
Leu	His	Leu	Ala	Ala	Glu	Arg	Ala	Ser	Thr	Gln	Glu	Ala	Glu	Leu	Ala		
			420					425					430				
cat	caa	cac	ggt	gct	gat	gcg	att	gcc	gat	gag	gta	gcg	gaa	gaa	cca	1344	
His	Gln	His	Gly	Ala	Asp	Ala	Ile	Ala	Asp	Glu	Val	Ala	Glu	Glu	Pro		
		435					440					445					
caa	gag	ctg	cca	caa	gat	gaa	gta	gcg	gca	gag	gtc	gag	act	gag	ccc	1392	
Gln	Glu	Leu	Pro	Gln	Asp	Glu	Val	Ala	Ala	Glu	Val	Glu	Thr	Glu	Pro		

002290-0420960



450				455				460									
gac	acc	gag	cct	gac	act	gaa	tct	gac	tcc	gag	cag	gct	gag	gta	gct	1440	
Asp	Thr	Glu	Pro	Asp	Thr	Glu	Ser	Asp	Ser	Glu	Gln	Ala	Glu	Val	Ala		
465				470				475				480					
tca	gag	gag	cct	gaa	gcg	gac	gaa	gaa	gag	aag	tagtacaccg				aaagtggcgt	1493	
Ser	Glu	Glu	Pro	Glu	Ala	Asp	Glu	Glu	Glu	Lys							
				485				490									
cgc																1496	

```
<210> 366
<211> 491
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 366															
Met 1	His	Val	Asp	Gly 5	Phe	Arg	Phe	Asp	Leu 10	Ala	Ser	Thr	Leu	Ala 15	Arg
Glu	Phe	Asp	Asp 20	Val	Asp	Arg	Leu	Ala 25	Thr	Phe	Phe	Asp	Leu 30	Val	Gln
Gln	Asp	Pro 35	Val	Val	Ser	Gln	Val 40	Lys	Leu	Ile	Ala	Glu 45	Pro	Trp	Asp
Val	Gly 50	Glu	Gly	Gly	Tyr	Gln 55	Val	Gly	Asn	Phe	Pro 60	Pro	Leu	Trp	Thr
Glu 65	Trp	Asn	Gly	Lys	Tyr 70	Arg	Asp	Thr	Val	Arg 75	Asp	Phe	Trp	Arg	Gly 80
Glu	Pro	Ala	Thr	Leu 85	Gly	Glu	Phe	Ala	Ser 90	Arg	Leu	Thr	Gly	Ser 95	Ser
Asp	Leu	Tyr	Ala 100	Asn	Asn	Gly	Arg	Arg 105	Pro	Thr	Ala	Ser	Ile 110	Asn	Phe
Val	Thr	Ala 115	His	Asp	Gly	Phe	Thr 120	Leu	Asn	Asp	Leu	Val 125	Ser	Tyr	Asn
Glu	Lys 130	His	Asn	Met	Ala	Asn 135	Gly	Glu	Asp	Gly	Arg 140	Asp	Gly	Glu	Ser
His 145	Asn	Arg	Ser	Trp	Asn 150	Cys	Gly	Val	Glu	Gly 155	Pro	Thr	Asp	Asp	Pro 160
Glu	Ile	Met	Gln	Leu 165	Arg	Ala	Gln	Gln	Arg 170	Arg	Asn	Phe	Leu	Thr 175	Thr
Leu	Leu	Leu	Ser 180	Gln	Gly	Thr	Pro	Met 185	Leu	Ser	His	Gly	Asp 190	Glu	Met
Ala	Arg	Thr 195	Gln	Asn	Gly	Asn	Asn 200	Asn	Val	Tyr	Cys	Gln 205	Asp	Asn	Glu
Leu	Ala 210	Trp	Val	Asn	Trp	Asp 215	Gln	Ala	Glu	Glu	Asn 220	Ala	Asp	Leu	Val

[illegible]



Ser Phe Thr Arg Arg Leu Leu Arg Ile Arg Ala Asn His Pro Val Phe  
 225 230 235 240  
 Arg Arg Arg Gln Phe Leu Ala Gly Gly Pro Leu Gly Ala Asp Val Arg  
 245 250 255  
 Asp Arg Asp Ile Ala Trp Leu Val Pro Asn Gly Thr Leu Met Thr Gln  
 260 265 270  
 Asp Asp Trp Asp Phe Ala Phe Gly Lys Ser Leu Gln Val Phe Phe Asn  
 275 280 285  
 Gly Asp Ala Ile Glu Glu Pro Asp Tyr Arg Gly Gln Lys Ile His Asp  
 290 295 300  
 Asp Ser Phe Ile Leu Met Phe Asn Ala His Phe Glu Pro Ile Asp Phe  
 305 310 315 320  
 Asn Leu Pro Pro Glu His Phe Gly Met Lys Trp Lys Leu Leu Val Asp  
 325 330 335  
 Thr Thr Glu Ala Val Gly His Pro Leu Glu Asp Leu Thr Ile Glu Ala  
 340 345 350  
 Gly Gly Thr Ile Thr Val Pro Ala Arg Ser Thr Met Leu Leu Arg Gln  
 355 360 365  
 Val Glu Ala Pro Asp Tyr Thr Lys Leu Glu Glu Lys Ile Ala Ala Glu  
 370 375 380  
 Lys Arg Glu Gln Glu Leu Ala Ala Glu Lys Glu Ala Ala Glu Lys Arg  
 385 390 395 400  
 Glu Leu Glu Leu Ala Ala Ala Lys Glu Ala Glu Asp Ala Ala Glu Ala  
 405 410 415  
 Leu His Leu Ala Ala Glu Arg Ala Ser Thr Gln Glu Ala Glu Leu Ala  
 420 425 430  
 His Gln His Gly Ala Asp Ala Ile Ala Asp Glu Val Ala Glu Glu Pro  
 435 440 445  
 Gln Glu Leu Pro Gln Asp Glu Val Ala Ala Glu Val Glu Thr Glu Pro  
 450 455 460  
 Asp Thr Glu Pro Asp Thr Glu Ser Asp Ser Glu Gln Ala Glu Val Ala  
 465 470 475 480  
 Ser Glu Glu Pro Glu Ala Asp Glu Glu Glu Lys  
 485 490

&lt;210&gt; 367

&lt;211&gt; 547

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(547)

&lt;223&gt; RXA01111

002290"0420960



<400> 367

agaaaaccct gccgatgcaa actttgagga gagattcaat caaggaatag aaatcattct 60

ggtgggtcta gacgcgcttg ggcatataag atgacgttcc atg aca tca acg att 115  
Met Thr Ser Thr Ile  
1 5

gag cac tcg tac caa gtt tgg cct gga cat gct tat cct ctg ggt tca 163  
Glu His Ser Tyr Gln Val Trp Pro Gly His Ala Tyr Pro Leu Gly Ser  
10 15 20

acc tat gac ggt gct gga acg aac ttc gca ctc ttc tcc gac gtt gca 211  
Thr Tyr Asp Gly Ala Gly Thr Asn Phe Ala Leu Phe Ser Asp Val Ala  
25 30 35

gag cgt gtt gag ctg tgt cta tta gat gca gat aac aac gag act cga 259  
Glu Arg Val Glu Leu Cys Leu Leu Asp Ala Asp Asn Asn Glu Thr Arg  
40 45 50

att cca ctc gaa gag cgc gat gcc cac att tgg cat tgc tac ctt cct 307  
Ile Pro Leu Glu Glu Arg Asp Ala His Ile Trp His Cys Tyr Leu Pro  
55 60 65

ggc gtt caa cct gga cag cgc tac gga ttc cga gtt cat ggc ccg tgg 355  
Gly Val Gln Pro Gly Gln Arg Tyr Gly Phe Arg Val His Gly Pro Trp  
70 75 80 85

aac cca gat gag ggt aag cgg tgc gac gcg aac aaa ctt cta gtt gat 403  
Asn Pro Asp Glu Gly Lys Arg Cys Asp Ala Asn Lys Leu Leu Val Asp  
90 95 100

```

ccc tat gct cgt gct ttc gat gga gat ttt gat gga cat ccg tca cta    451
Pro Tyr Ala Arg Ala Phe Asp Gly Asp Phe Asp Gly His Pro Ser Leu
      105                      110                      115

```

ttt tct tac gac atc acc aat cca aat gac ccc aac ggt cgc aat acc 499  
 Phe Ser Tyr Asp Ile Thr Asn Pro Asn Asp Pro Asn Gly Arg Asn Thr  
 120 125 130

gaa gac agc att gat cac aca atg aag tct gtc gtg gtg aac cca ttc 547  
Glu Asp Ser Ile Asp His Thr Met Lys Ser Val Val Val Asn Pro Phe  
135 140 145

<210> 368

<211> 149

<212> PRT

<213> Corynebacterium glutamicum

<400> 368

Met Thr Ser Thr Ile Glu His Ser Tyr Gln Val Trp Pro Gly His Ala  
1 5 10 15

Tyr Pro Leu Gly Ser Thr Tyr Asp Gly Ala Gly Thr Asn Phe Ala Leu  
20 25 30

Phe Ser Asp Val Ala Glu Arg Val Glu Leu Cys Leu Leu Asp Ala Asp  
35 40 45

Asn Asn Glu Thr Arg Ile Pro Leu Glu Glu Arg Asp Ala His Ile Trp

The figure consists of nine subplots arranged vertically, each labeled with a time step \$t\$ from 0 to 8. Each subplot displays a rectangular domain filled with numerical values representing the stream function. At \$t=0\$, the values are mostly zero with some minor fluctuations. As time progresses, a distinct pattern emerges, characterized by higher values (up to 0.9) concentrated in the upper right quadrant and lower values (down to -0.9) in the lower left quadrant, forming a dipole-like structure. By \$t=8\$, this structure has become more pronounced and stable.



50					55					60					
His 65	Cys	Tyr	Leu	Pro	Gly 70	Val	Gln	Pro	Gly	Gln 75	Arg	Tyr	Gly	Phe	Arg 80
Val	His	Gly	Pro	Trp 85	Asn	Pro	Asp	Glu	Gly 90	Lys	Arg	Cys	Asp	Ala 95	Asn
Lys	Leu	Leu	Val 100	Asp	Pro	Tyr	Ala 105	Arg	Ala	Phe	Asp	Gly	Asp 110	Phe	Asp
Gly	His	Pro 115	Ser	Leu	Phe	Ser	Tyr 120	Asp	Ile	Thr	Asn	Pro 125	Asn	Asp	Pro
Asn	Gly 130	Arg	Asn	Thr	Glu	Asp 135	Ser	Ile	Asp	His	Thr 140	Met	Lys	Ser	Val
Val 145	Val	Asn	Pro	Phe											

```
<210> 369
<211> 1635
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(1612)
<223> RXN01550
```

<400> 369  
ttcgccagca gtactttcttc acctctgctt ccctgcaggc catgattcag ggccacctgg 60

cgaccacaa ggacctcagc aactttgccg agttcactcc gtg cag ctc aat gac 115  
Val Gln Leu Asn Asp  
1 5

act cac cca gtg ttg gct atc cct gag ctt atg cgt ctg ctc atg gac 163  
Thr His Pro Val Leu Ala Ile Pro Glu Leu Met Arg Leu Leu Met Asp  
10 15 20

gag cat gac atg ggc tgg gaa gaa tcc tgg gca atc gtg ttc aag acc 211  
Glu His Asp Met Gly Trp Glu Glu Ser Trp Ala Ile Val Phe Lys Thr  
25 30 35

ttc gca tac acc aac cac acc gtg ctc acc gaa gct ctt gag cag tgg 259  
 Phe Ala Tyr Thr Asn His Thr Val Leu Thr Glu Ala Leu Glu Gln Trp  
 40 45 50

gat cag cag atc ttc caa cag ctg ttc tgg cgc gtg tgg gaa atc atc 307  
Asp Gln Gln Ile Phe Gln Gln Leu Phe Trp Arg Val Trp Glu Ile Ile  
55 60 65

aca gag atc gat cgc cgc ttc cgt ttg gag cgc gca gcc gat gga ctg 355  
Thr Glu Ile Asp Arg Arg Phe Arg Leu Glu Arg Ala Ala Asp Gly Leu  
70 75 80 85

gat gaa gag acc atc gac cgc atg gct cca atc cag cac ggc act gtt 403  
Asp Glu Glu Thr Ile Asp Arg Met Ala Pro Ile Gln His Gly Thr Val  
90 95 100

[illegible]



cat atg gca tgg att gcc tgt tac gcg gca tat tcc atc aat ggc gtg	451
His Met Ala Trp Ile Ala Cys Tyr Ala Ala Tyr Ser Ile Asn Gly Val	
105 110 115	
gca gcg ctg cac acc gag atc atc aag gcc gag acc ttg gct gac tgg	499
Ala Ala Leu His Thr Glu Ile Ile Lys Ala Glu Thr Leu Ala Asp Trp	
120 125 130	
tac gca ctg tgg cca gag aag ttc aac aac aag act aac ggt gtt acc	547
Tyr Ala Leu Trp Pro Glu Lys Phe Asn Asn Lys Thr Asn Gly Val Thr	
135 140 145	
cca cgc cgt tgg ctg cgc atg atc aac cca ggt ctg tct gac ctg ctc	595
Pro Arg Arg Trp Leu Arg Met Ile Asn Pro Gly Leu Ser Asp Leu Leu	
150 155 160 165	
act cga ctt tcc ggt tcc gat gat tgg gta acc gat ctg gat gag ctg	643
Thr Arg Leu Ser Gly Ser Asp Asp Trp Val Thr Asp Leu Asp Glu Leu	
170 175 180	
aag aag ctg cgc tcc tat gcc gac gat aag tcc gtg ctt gaa gaa ctc	691
Lys Lys Leu Arg Ser Tyr Ala Asp Asp Lys Ser Val Leu Glu Glu Leu	
185 190 195	
cgc gct atc aag gct gct aat aag caa gac ttc gcc gag tgg atc ctc	739
Arg Ala Ile Lys Ala Ala Asn Lys Gln Asp Phe Ala Glu Trp Ile Leu	
200 205 210	
gag cgc cag ggc att gag att gat cca gaa tcc atc ttt gac gtg cag	787
Glu Arg Gln Gly Ile Glu Ile Asp Pro Glu Ser Ile Phe Asp Val Gln	
215 220 225	
att aag cgc ctc cac gag tac aag cgc cag ctc atg aac gcg ctc tac	835
Ile Lys Arg Leu His Glu Tyr Lys Arg Gln Leu Met Asn Ala Leu Tyr	
230 235 240 245	
gta cta gac ctt tac ttc cgt att aag gaa gat ggc ctc acc gac atc	883
Val Leu Asp Leu Tyr Phe Arg Ile Lys Glu Asp Gly Leu Thr Asp Ile	
250 255 260	
cca gca cgc act gtc atc ttt ggc gcc aag gcc gcg ccg ggt tat gtc	931
Pro Ala Arg Thr Val Ile Phe Gly Ala Lys Ala Ala Pro Gly Tyr Val	
265 270 275	
cgc gcc aag gcg att atc aag ctc atc aac tct att gct gac ttg gta	979
Arg Ala Lys Ala Ile Ile Lys Leu Ile Asn Ser Ile Ala Asp Leu Val	
280 285 290	
aac aac gat cct gag gtc tcc ccg ctg ctc aag gtg gtc ttt gta gag	1027
Asn Asn Asp Pro Glu Val Ser Pro Leu Leu Lys Val Val Phe Val Glu	
295 300 305	
aac tac aac gtc tcc cct gct gag cac atc ttg cct gcg tct gat gtc	1075
Asn Tyr Asn Val Ser Pro Ala Glu His Ile Leu Pro Ala Ser Asp Val	
310 315 320 325	
tcc gaa cag att tcc acc gcc ggc aag gaa gcc agc ggt acc tcc aac	1123
Ser Glu Gln Ile Ser Thr Ala Gly Lys Glu Ala Ser Gly Thr Ser Asn	
330 335 340	

0062740-062300







50					55					60					
Val	Trp	Glu	Ile	Ile	Thr	Glu	Ile	Asp	Arg	Arg	Phe	Arg	Leu	Glu	Arg
65					70					75					80
Ala	Ala	Asp	Gly	Leu	Asp	Glu	Glu	Thr	Ile	Asp	Arg	Met	Ala	Pro	Ile
				85					90					95	
Gln	His	Gly	Thr	Val	His	Met	Ala	Trp	Ile	Ala	Cys	Tyr	Ala	Ala	Tyr
			100					105					110		
Ser	Ile	Asn	Gly	Val	Ala	Ala	Leu	His	Thr	Glu	Ile	Ile	Lys	Ala	Glu
		115					120					125			
Thr	Leu	Ala	Asp	Trp	Tyr	Ala	Leu	Trp	Pro	Glu	Lys	Phe	Asn	Asn	Lys
	130					135					140				
Thr	Asn	Gly	Val	Thr	Pro	Arg	Arg	Trp	Leu	Arg	Met	Ile	Asn	Pro	Gly
145					150					155					160
Leu	Ser	Asp	Leu	Leu	Thr	Arg	Leu	Ser	Gly	Ser	Asp	Asp	Trp	Val	Thr
				165					170					175	
Asp	Leu	Asp	Glu	Leu	Lys	Lys	Leu	Arg	Ser	Tyr	Ala	Asp	Asp	Lys	Ser
			180					185					190		
Val	Leu	Glu	Glu	Leu	Arg	Ala	Ile	Lys	Ala	Ala	Asn	Lys	Gln	Asp	Phe
		195					200					205			
Ala	Glu	Trp	Ile	Leu	Glu	Arg	Gln	Gly	Ile	Glu	Ile	Asp	Pro	Glu	Ser
	210					215					220				
Ile	Phe	Asp	Val	Gln	Ile	Lys	Arg	Leu	His	Glu	Tyr	Lys	Arg	Gln	Leu
225					230					235					240
Met	Asn	Ala	Leu	Tyr	Val	Leu	Asp	Leu	Tyr	Phe	Arg	Ile	Lys	Glu	Asp
				245					250					255	
Gly	Leu	Thr	Asp	Ile	Pro	Ala	Arg	Thr	Val	Ile	Phe	Gly	Ala	Lys	Ala
			260					265					270		
Ala	Pro	Gly	Tyr	Val	Arg	Ala	Lys	Ala	Ile	Ile	Lys	Leu	Ile	Asn	Ser
		275					280					285			
Ile	Ala	Asp	Leu	Val	Asn	Asn	Asp	Pro	Glu	Val	Ser	Pro	Leu	Leu	Lys
	290					295					300				
Val	Val	Phe	Val	Glu	Asn	Tyr	Asn	Val	Ser	Pro	Ala	Glu	His	Ile	Leu
305					310					315					320
Pro	Ala	Ser	Asp	Val	Ser	Glu	Gln	Ile	Ser	Thr	Ala	Gly	Lys	Glu	Ala
				325					330					335	
Ser	Gly	Thr	Ser	Asn	Met	Lys	Phe	Met	Met	Asn	Gly	Ala	Leu	Thr	Leu
			340					345					350		
Gly	Thr	Met	Asp	Gly	Ala	Asn	Val	Glu	Ile	Val	Asp	Ser	Val	Gly	Glu
		355					360					365			
Glu	Asn	Ala	Tyr	Ile	Phe	Gly	Ala	Arg	Val	Glu	Glu	Leu	Pro	Ala	Leu
	370					375					380				

002290" 04220950







Variable	Mean	SD	Min	Max
Age	34.5	10.2	21	55
Gender	0.5	0.5	0	1
Marital Status	0.6	0.5	0	1
Education	12.5	1.5	9	16
Income	3500	1500	1000	8000
Health	0.8	0.2	0	1
Smoking	0.3	0.5	0	1
Alcohol	0.2	0.4	0	1
Exercise	0.4	0.5	0	1
Stress	0.6	0.5	0	1
Sleep	0.7	0.3	0	1
Diet	0.5	0.5	0	1
Work	0.8	0.2	0	1
Family	0.6	0.5	0	1
Friends	0.7	0.4	0	1
Hobbies	0.5	0.5	0	1
Travel	0.4	0.5	0	1
Religion	0.5	0.5	0	1
Politics	0.5	0.5	0	1
Environment	0.6	0.4	0	1
Technology	0.7	0.3	0	1
Art	0.4	0.5	0	1
Music	0.5	0.5	0	1
Sports	0.6	0.4	0	1
Gardening	0.3	0.5	0	1
Reading	0.7	0.3	0	1
Writing	0.4	0.5	0	1
Cooking	0.5	0.5	0	1
Cleaning	0.6	0.4	0	1
Shopping	0.7	0.3	0	1
Driving	0.8	0.2	0	1
Volunteering	0.3	0.5	0	1
Charity	0.4	0.5	0	1
Philanthropy	0.5	0.5	0	1
Activism	0.6	0.4	0	1
Leadership	0.7	0.3	0	1
Entrepreneurship	0.8	0.2	0	1
Investment	0.9	0.1	0	1
Real Estate	0.7	0.3	0	1
Stocks	0.6	0.4	0	1
Bonds	0.5	0.5	0	1
Commodities	0.4	0.5	0	1
Cryptocurrency	0.3	0.5	0	1
Art Collection	0.2	0.4	0	1
Real Estate Collection	0.1	0.3	0	1
Stock Collection	0.2	0.4	0	1
Bond Collection	0.1	0.3	0	1
Commodity Collection	0.1	0.3	0	1
Cryptocurrency Collection	0.1	0.3	0	1
Art Collection Value	100000	50000	0	500000
Real Estate Collection Value	200000	100000	0	1000000
Stock Collection Value	50000	25000	0	250000
Bond Collection Value	30000	15000	0	150000
Commodity Collection Value	20000	10000	0	100000
Cryptocurrency Collection Value	10000	5000	0	50000



Leu Tyr Glu Thr Val Pro Gly Leu Lys Arg Ala Leu Asp Ala Leu Asp  
 340 345 350

aac ggc acc ctc aac gac aac aac agt ggt ttg ttc tac gac ctc aag 1104  
 Asn Gly Thr Leu Asn Asp Asn Asn Ser Gly Leu Phe Tyr Asp Leu Lys  
 355 360 365

cat tcc ttg atc cac ggt tat gga aaa gac gcc agc gac acc tac tac 1152  
 His Ser Leu Ile His Gly Tyr Gly Lys Asp Ala Ser Asp Thr Tyr Tyr  
 370 375 380

gtg ctt ggc gat ttc gca gat tac cgc gag acc cgc gac cgt atg gcc 1200  
 Val Leu Gly Asp Phe Ala Asp Tyr Arg Glu Thr Arg Asp Arg Met Ala  
 385 390 395 400

gcc gac tac gcc tcc gat ccc ctg ggt tgg gca cgc atg gcc tgg atc 1248  
 Ala Asp Tyr Ala Ser Asp Pro Leu Gly Trp Ala Arg Met Ala Trp Ile  
 405 410 415

aac att tgc gag tcc ggc cgt ttc tcc tcc gac cgc acc atc cgc gat 1296  
 Asn Ile Cys Glu Ser Gly Arg Phe Ser Ser Asp Arg Thr Ile Arg Asp  
 420 425 430

tat gcc acc gag atc tgg aag ctc gag cca act cct gct gtt aag aag 1344  
 Tyr Ala Thr Glu Ile Trp Lys Leu Glu Pro Thr Pro Ala Val Lys Lys  
 435 440 445

taggttttaa cctccgcttc taa 1367

<210> 372  
 <211> 448  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 372  
 Ile Phe Gln Gln Leu Phe Trp Arg Val Trp Glu Ile Ile Thr Glu Ile  
 1 5 10 15

Asp Arg Arg Phe Arg Leu Glu Arg Ala Ala Asp Gly Leu Asp Glu Glu  
 20 25 30

Thr Ile Asp Arg Met Ala Pro Ile Gln Arg Gly Thr Val His Met Ala  
 35 40 45

Trp Ile Ala Cys Tyr Ala Ala Tyr Ser Ile Asn Gly Val Ala Ala Leu  
 50 55 60

His Thr Glu Ile Ile Lys Ala Glu Thr Leu Ala Asp Trp Tyr Ala Leu  
 65 70 75 80

Trp Pro Glu Lys Phe Asn Asn Lys Thr Asn Gly Val Thr Pro Arg Arg  
 85 90 95

Trp Leu Arg Met Ile Asn Pro Gly Leu Ser Asp Leu Leu Thr Arg Leu  
 100 105 110

Ser Gly Ser Asp Asp Trp Val Thr Asp Leu Asp Glu Leu Lys Lys Leu  
 115 120 125

Arg Ser Tyr Ala Asp Asp Lys Ser Val Leu Glu Glu Leu Arg Ala Ile

09602740.062300



0960270-06300



```
<220>  
<221> CDS  
<222> (1) .. (2325)  
<223> RXN02100
```

Figure 1 illustrates the construction of a 3D rectangular prism from a 2D net. The sequence shows the net being folded step-by-step, with labels 1 through 10 indicating the progression. The final result is a 3D rectangular prism.



gca ttc tgc gaa gct cgt ggt ctg aag cgc tca tct gtt gca cac ctc	624
Ala Phe Cys Glu Ala Arg Gly Leu Lys Arg Ser Ser Val Ala His Leu	
195 200 205	
aac gaa ggc cac gca ggt ttc ctg acc ctg gag cgt atc cgc gag cgc	672
Asn Glu Gly His Ala Gly Phe Leu Thr Leu Glu Arg Ile Arg Glu Arg	
210 215 220	
atc gca gag ggc atg gag tac cca gca gca ttc gag cag gtt cgt gcg	720
Ile Ala Glu Gly Met Glu Tyr Pro Ala Ala Phe Glu Gln Val Arg Ala	
225 230 235 240	
tcc aac atc ttc acc acc cac acc cca gtc cca gca ggc atc gac cgc	768
Ser Asn Ile Phe Thr Thr His Thr Pro Val Pro Ala Gly Ile Asp Arg	
245 250 255	
ttc gac atg gag atg gtg cgt cgt tat ctc ggt ggc ggt cag cca gaa	816
Phe Asp Met Glu Met Val Arg Arg Tyr Leu Gly Gly Gly Gln Pro Glu	
260 265 270	
gat cag cag ctg tgc gtt ggt gtt cca att gag aag gca ctt gag ctt	864
Asp Gln Gln Leu Cys Val Gly Val Pro Ile Glu Lys Ala Leu Glu Leu	
275 280 285	
ggt caa gag tcc gat cca cac cgc ttc aac atg gct cat atg ggc ctt	912
Gly Gln Glu Ser Asp Pro His Arg Phe Asn Met Ala His Met Gly Leu	
290 295 300	
cgc gcg agc caa cat gct aat ggc gtc gca aag ctt cat ggt gaa gta	960
Arg Ala Ser Gln His Ala Asn Gly Val Ala Lys Leu His Gly Glu Val	
305 310 315 320	
agc cgt gac atg ttc gcc ggc ctg tac ccc gga tat gag cct cgt gaa	1008
Ser Arg Asp Met Phe Ala Gly Leu Tyr Pro Gly Tyr Glu Pro Arg Glu	
325 330 335	
gtg ccc atc ggg cac gtc acc aac ggt gtt cac ctg ccg acg tgg gtc	1056
Val Pro Ile Gly His Val Thr Asn Gly Val His Leu Pro Thr Trp Val	
340 345 350	
aag cca gag atg aag gaa ctc atc gat cgc gtc act ggc ggc gct gat	1104
Lys Pro Glu Met Lys Glu Leu Ile Asp Arg Val Thr Gly Gly Ala Asp	
355 360 365	
ctt gcg gtt gct gat tct tgg tca aac cca cag gct gtc gag tct gag	1152
Leu Ala Val Ala Asp Ser Trp Ser Asn Pro Gln Ala Val Glu Ser Glu	
370 375 380	
aag atc tgg aag gtg cgc aac aag ttc cgt gct gac cta gtg gag gtt	1200
Lys Ile Trp Lys Val Arg Asn Lys Phe Arg Ala Asp Leu Val Glu Val	
385 390 395 400	
gct cgc gct gca act gca aag tcc tgg tct cac cgt gga cac acc gaa	1248
Ala Arg Ala Ala Thr Ala Lys Ser Trp Ser His Arg Gly His Thr Glu	
405 410 415	
gca gaa ctt gcg tgg acc tcc cgc gtt ctg gat cca aac gtg ctg acc	1296
Ala Glu Leu Ala Trp Thr Ser Arg Val Leu Asp Pro Asn Val Leu Thr	
420 425 430	
att ggt ttc gca cgt cgc gta tcc acc tac aag cgc ttg acc ttg atg	1344

09602740-062300



Ile	Gly	Phe	Ala	Arg	Arg	Val	Ser	Thr	Tyr	Lys	Arg	Leu	Thr	Leu	Met	
		435					440					445				
ctg	cgc	aac	cct	gaa	cgc	ctg	cgt	tcc	atc	ttg	ctt	aat	gag	gaa	cgc	1392
Leu	Arg	Asn	Pro	Glu	Arg	Leu	Arg	Ser	Ile	Leu	Leu	Asn	Glu	Glu	Arg	
		450				455					460					
cca	gtt	cag	ttc	gtt	att	gct	ggg	aag	gca	cac	cca	cat	gac	atg	ggg	1440
Pro	Val	Gln	Phe	Val	Ile	Ala	Gly	Lys	Ala	His	Pro	His	Asp	Met	Gly	
					470					475					480	
ggc	aag	aag	ctc	atg	cag	gaa	atc	gtc	cac	ttc	gct	gat	caa	gct	ggg	1488
Gly	Lys	Lys	Leu	Met	Gln	Glu	Ile	Val	His	Phe	Ala	Asp	Gln	Ala	Gly	
				485					490					495		
gtc	cgt	gac	cgt	ttc	ctc	ttc	ctg	cct	gat	tac	gac	atc	aac	ctg	gcc	1536
Val	Arg	Asp	Arg	Phe	Leu	Phe	Leu	Pro	Asp	Tyr	Asp	Ile	Asn	Leu	Ala	
			500					505					510			
agc	tac	ctg	atc	tct	ggg	gct	gac	gtg	tgg	ctg	aac	aac	cca	gtg	cgc	1584
Ser	Tyr	Leu	Ile	Ser	Gly	Ala	Asp	Val	Trp	Leu	Asn	Asn	Pro	Val	Arg	
		515					520					525				
cct	cag	gaa	gca	tcg	gga	acc	tcc	ggg	atg	aag	gcc	gtc	atg	aat	ggg	1632
Pro	Gln	Glu	Ala	Ser	Gly	Thr	Ser	Gly	Met	Lys	Ala	Val	Met	Asn	Gly	
		530				535					540					
ggc	ctg	acc	ctg	tcc	atc	tct	gat	ggg	tgg	tgg	gat	gaa	atg	cct	aag	1680
Gly	Leu	Thr	Leu	Ser	Ile	Ser	Asp	Gly	Trp	Trp	Asp	Glu	Met	Pro	Lys	
				550					555						560	
gag	acc	acc	ggc	tgg	acc	atc	cca	acc	gtt	gag	tcc	cag	gac	ttg	gaa	1728
Glu	Thr	Thr	Gly	Trp	Thr	Ile	Pro	Thr	Val	Glu	Ser	Gln	Asp	Leu	Glu	
				565					570					575		
tgc	cgc	gac	cac	ctg	gaa	tcc	cag	gcg	ctg	tac	gac	ctg	ctg	gaa	aac	1776
Cys	Arg	Asp	His	Leu	Glu	Ser	Gln	Ala	Leu	Tyr	Asp	Leu	Leu	Glu	Asn	
			580					585					590			
gaa	gtt	gca	ccg	ctg	ttt	tac	aag	cgc	gac	aag	aac	ggc	atc	cca	cag	1824
Glu	Val	Ala	Pro	Leu	Phe	Tyr	Lys	Arg	Asp	Lys	Asn	Gly	Ile	Pro	Gln	
		595					600					605				
gac	tgg	ctg	gac	ctg	gtt	cgc	gaa	tcc	tgg	acc	acc	ctg	tca	cca	atg	1872
Asp	Trp	Leu	Asp	Leu	Val	Arg	Glu	Ser	Trp	Thr	Thr	Leu	Ser	Pro	Met	
		610				615					620					
gtc	acc	tcc	acc	cgc	atg	gtg	cgc	gac	tac	acc	acc	cag	tac	tac	cgc	1920
Val	Thr	Ser	Thr	Arg	Met	Val	Arg	Asp	Tyr	Thr	Thr	Gln	Tyr	Tyr	Arg	
					630				635						640	
cca	acc	aaa	cac	cag	gca	gag	ctc	att	gcg	cag	cct	gca	gaa	gca	gcg	1968
Pro	Thr	Lys	His	Gln	Ala	Glu	Leu	Ile	Ala	Gln	Pro	Ala	Glu	Ala	Ala	
				645					650					655		
gat	tac	gcg	gca	tgg	ctt	gag	cac	atc	aaa	gca	gag	tgg	gct	ggc	gtc	2016
Asp	Tyr	Ala	Ala	Trp	Leu	Glu	His	Ile	Lys	Ala	Glu	Trp	Ala	Gly	Val	
			660					665					670			
aag	gtc	tca	gac	ctg	aag	atc	agc	gag	agc	gcc	atc	acg	gcg	cag	gag	2064
Lys	Val	Ser	Asp	Leu	Lys	Ile	Ser	Glu	Ser	Ala	Ile	Thr	Ala	Gln	Glu	

09602740-062300



[illegible]



145                      150                      155                      160  
 Leu Arg Asn Val Thr Asp Arg Leu Tyr Gly Gly Asp Asn Glu His Arg  
                                  165                                   170                                   175  
 Ile Lys Gln Glu Leu Val Leu Gly Val Gly Gly Val Arg Ala Val Asn  
                                  180                                   185                                   190  
 Ala Phe Cys Glu Ala Arg Gly Leu Lys Arg Ser Ser Val Ala His Leu  
                                  195                                   200                                   205  
 Asn Glu Gly His Ala Gly Phe Leu Thr Leu Glu Arg Ile Arg Glu Arg  
                                  210                                   215                                   220  
 Ile Ala Glu Gly Met Glu Tyr Pro Ala Ala Phe Glu Gln Val Arg Ala  
 225                                   230                                   235                                   240  
 Ser Asn Ile Phe Thr Thr His Thr Pro Val Pro Ala Gly Ile Asp Arg  
                                  245                                   250                                   255  
 Phe Asp Met Glu Met Val Arg Arg Tyr Leu Gly Gly Gly Gln Pro Glu  
                                  260                                   265                                   270  
 Asp Gln Gln Leu Cys Val Gly Val Pro Ile Glu Lys Ala Leu Glu Leu  
                                  275                                   280                                   285  
 Gly Gln Glu Ser Asp Pro His Arg Phe Asn Met Ala His Met Gly Leu  
                                  290                                   295                                   300  
 Arg Ala Ser Gln His Ala Asn Gly Val Ala Lys Leu His Gly Glu Val  
 305                                   310                                   315                                   320  
 Ser Arg Asp Met Phe Ala Gly Leu Tyr Pro Gly Tyr Glu Pro Arg Glu  
                                  325                                   330                                   335  
 Val Pro Ile Gly His Val Thr Asn Gly Val His Leu Pro Thr Trp Val  
                                  340                                   345                                   350  
 Lys Pro Glu Met Lys Glu Leu Ile Asp Arg Val Thr Gly Gly Ala Asp  
                                  355                                   360                                   365  
 Leu Ala Val Ala Asp Ser Trp Ser Asn Pro Gln Ala Val Glu Ser Glu  
                                  370                                   375                                   380  
 Lys Ile Trp Lys Val Arg Asn Lys Phe Arg Ala Asp Leu Val Glu Val  
 385                                   390                                   395                                   400  
 Ala Arg Ala Ala Thr Ala Lys Ser Trp Ser His Arg Gly His Thr Glu  
                                  405                                   410                                   415  
 Ala Glu Leu Ala Trp Thr Ser Arg Val Leu Asp Pro Asn Val Leu Thr  
                                  420                                   425                                   430  
 Ile Gly Phe Ala Arg Arg Val Ser Thr Tyr Lys Arg Leu Thr Leu Met  
                                  435                                   440                                   445  
 Leu Arg Asn Pro Glu Arg Leu Arg Ser Ile Leu Leu Asn Glu Glu Arg  
                                  450                                   455                                   460  
 Pro Val Gln Phe Val Ile Ala Gly Lys Ala His Pro His Asp Met Gly  
 465                                   470                                   475                                   480

09602740-062300



<211> 941



&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(918)

&lt;223&gt; FRXA02100

&lt;400&gt; 375

att gct ggt aag gca cac cca cat gac atg ggt ggc aag aag ctc atg	48
Ile Ala Gly Lys Ala His Pro His Asp Met Gly Gly Lys Lys Leu Met	
1 5 10 15	
cag gaa atc gtc cac ttc gct gat caa gct ggt gtc cgt gac cgt ttc	96
Gln Glu Ile Val His Phe Ala Asp Gln Ala Gly Val Arg Asp Arg Phe	
20 25 30	
ctc ttc ctg cct gat tac gac atc aac ctg gcc agc tac ctg atc tct	144
Leu Phe Leu Pro Asp Tyr Asp Ile Asn Leu Ala Ser Tyr Leu Ile Ser	
35 40 45	
ggt gct gac gtg tgg ctg aac aac cca gtg cgc cct cag gaa gca tcg	192
Gly Ala Asp Val Trp Leu Asn Asn Pro Val Arg Pro Gln Glu Ala Ser	
50 55 60	
gga acc tcc ggt atg aag gcc gtc atg aat ggt ggc ctg acc ctg tcc	240
Gly Thr Ser Gly Met Lys Ala Val Met Asn Gly Gly Leu Thr Leu Ser	
65 70 75 80	
atc tct gat ggt tgg tgg gat gaa atg cct aag gag acc acc ggc tgg	288
Ile Ser Asp Gly Trp Trp Asp Glu Met Pro Lys Glu Thr Thr Gly Trp	
85 90 95	
acc atc cca acc gtt gag tcc cag gac ttg gaa tgc cgc gac cac ctg	336
Thr Ile Pro Thr Val Glu Ser Gln Asp Leu Glu Cys Arg Asp His Leu	
100 105 110	
gaa tcc cag gcg ctg tac gac ctg ctg gaa aac gaa gtt gca ccg ctg	384
Glu Ser Gln Ala Leu Tyr Asp Leu Leu Glu Asn Glu Val Ala Pro Leu	
115 120 125	
ttt tac aag cgc gac aag aac ggc atc cca cag gac tgg ctg gac ctg	432
Phe Tyr Lys Arg Asp Lys Asn Gly Ile Pro Gln Asp Trp Leu Asp Leu	
130 135 140	
gtt cgc gaa tcc tgg acc acc ctg tca cca atg gtc acc tcc acc cgc	480
Val Arg Glu Ser Trp Thr Thr Leu Ser Pro Met Val Thr Ser Thr Arg	
145 150 155 160	
atg gtg cgc gac tac acc acc cag tac tac cgc cca acc aaa cac cag	528
Met Val Arg Asp Tyr Thr Thr Gln Tyr Tyr Arg Pro Thr Lys His Gln	
165 170 175	
gca gag ctc att gcg cag cct gca gaa gca gcg gat tac gcg gca tgg	576
Ala Glu Leu Ile Ala Gln Pro Ala Glu Ala Ala Asp Tyr Ala Ala Trp	
180 185 190	
ctt gag cac atc aaa gca gag tgg gct ggc gtc aag gtc tca gac ctg	624
Leu Glu His Ile Lys Ala Glu Trp Ala Gly Val Lys Val Ser Asp Leu	
195 200 205	

09602740-062300



**SECRET**



0960240-06200

0960240-06200

0960240-06200

0960240-06200



0960240 06300



cgc gcg agc caa cat gct aat ggc gtc gca aag ctt cat ggt gaa gta 960  
 Arg Ala Ser Gln His Ala Asn Gly Val Ala Lys Leu His Gly Glu Val  
 305 310 315 320  
 agc cgt gac atg ttc gcc ggc ctg tac ccc gga tat gag cct cgt gaa 1008  
 Ser Arg Asp Met Phe Ala Gly Leu Tyr Pro Gly Tyr Glu Pro Arg Glu  
 325 330 335  
 gtg ccc atc ggg cac gtc acc aac ggt gtt cac ctg ccg acg tgg gtc 1056  
 Val Pro Ile Gly His Val Thr Asn Gly Val His Leu Pro Thr Trp Val  
 340 345 350  
 aag cca gag atg aag gaa ctc atc gat cgc gtc act ggc ggc gct gat 1104  
 Lys Pro Glu Met Lys Glu Leu Ile Asp Arg Val Thr Gly Gly Ala Asp  
 355 360 365  
 ctt gcg gtt gct gat tct tgg tca aac cca cag gct gtc gag tct gag 1152  
 Leu Ala Val Ala Asp Ser Trp Ser Asn Pro Gln Ala Val Glu Ser Glu  
 370 375 380  
 aag atc tgg aag gtg cgc aac aag ttc cgt gct gac cta gtg gag gtt 1200  
 Lys Ile Trp Lys Val Arg Asn Lys Phe Arg Ala Asp Leu Val Glu Val  
 385 390 395 400  
 gct cgc 1206  
 Ala Arg

&lt;210&gt; 378

&lt;211&gt; 402

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 378

Leu Gly Arg Ile Asn Ala Glu Glu Gln Asn Leu Ser Glu Tyr Leu Ser  
 1 5 10 15

Asp Lys Leu Trp Tyr Gln Asp Thr Ala Asp Ala Thr Asp Ala Val Gly  
 20 25 30

Asp Pro Leu Val Ala Tyr Phe Ser Met Glu Phe Gly Ile His Pro Ser  
 35 40 45

Leu Pro Ile Tyr Ser Gly Gly Leu Gly Val Leu Ala Gly Glu Asn Met  
 50 55 60

Lys Ser Ala Ser Asp Leu Gly Val Pro Leu Ile Gly Val Gly Leu Leu  
 65 70 75 80

Tyr Thr His Gly Tyr Phe Thr Gln Ser Leu Ser Gly Asp Gly Trp Gln  
 85 90 95

Gln Glu Glu Tyr Lys Tyr His Asp Pro Ala Glu Leu Pro Ile Glu Ala  
 100 105 110

Val Lys Asp Lys Asn Gly Glu Gln Val Thr Val Ser Val Thr Tyr Pro  
 115 120 125

Gly Ala Gln Glu Val Lys Ile Ala Leu Trp Val Ala Asn Val Gly Arg  
 130 135 140

09602740-062300



```

Ile Pro Leu Leu Leu Leu Asp Thr Asn Ile Glu Ala Asn Pro Glu Glu
145                      150                      155                      160

Leu Arg Asn Val Thr Asp Arg Leu Tyr Gly Gly Asp Asn Glu His Arg
                      165                      170                      175

Ile Lys Gln Glu Leu Val Leu Gly Val Gly Gly Val Arg Ala Val Asn
                      180                      185                      190

Ala Phe Cys Glu Ala Arg Gly Leu Lys Arg Ser Ser Val Ala His Leu
                      195                      200                      205

Asn Glu Gly His Ala Gly Phe Leu Thr Leu Glu Arg Ile Arg Glu Arg
210                      215                      220

Ile Ala Glu Gly Met Glu Tyr Pro Ala Ala Phe Glu Gln Val Arg Ala
225                      230                      235                      240

Ser Asn Ile Phe Thr Thr His Thr Pro Val Pro Ala Gly Ile Asp Arg
                      245                      250                      255

Phe Asp Met Glu Met Val Arg Arg Tyr Leu Gly Gly Gly Gln Pro Glu
260                      265                      270

Asp Gln Gln Leu Cys Val Gly Val Pro Ile Glu Lys Ala Leu Glu Leu
275                      280                      285

Gly Gln Glu Ser Asp Pro His Arg Phe Asn Met Ala His Met Gly Leu
290                      295                      300

Arg Ala Ser Gln His Ala Asn Gly Val Ala Lys Leu His Gly Glu Val
305                      310                      315                      320

Ser Arg Asp Met Phe Ala Gly Leu Tyr Pro Gly Tyr Glu Pro Arg Glu
325                      330                      335

Val Pro Ile Gly His Val Thr Asn Gly Val His Leu Pro Thr Trp Val
340                      345                      350

Lys Pro Glu Met Lys Glu Leu Ile Asp Arg Val Thr Gly Gly Ala Asp
355                      360                      365

Leu Ala Val Ala Asp Ser Trp Ser Asn Pro Gln Ala Val Glu Ser Glu
370                      375                      380

Lys Ile Trp Lys Val Arg Asn Lys Phe Arg Ala Asp Leu Val Glu Val
385                      390                      395                      400

Ala Arg

```

```

<210> 379
<211> 1140
<212> DNA
<213> Corynebacterium glutamicum

```

```

<220>
<221> CDS
<222> (101)..(1117)

```

09602740.062300



<400> 379

gtggagttgc ttgaatgagg ttgatagggg atttttgaag atg ttt ggt cgc cgt 115  
Met Phe Gly Arg Arg  
1 5

tg	gt	ag	gt	gt	gc	tc	tg	gt	at	gc	ag	ac	ct	at	ct	163
Trp	Val	Ser	Val	Val	Ala	Ser	Cys	Val	Ile	Ala	Ser	Thr	Leu	Ile	Leu	
				10					15					20		

gtg cct tcg cat tcc ggt gcg gag gaa gtc gat caa ctg att gct gat 211  
Val Pro Ser His Ser Gly Ala Glu Glu Val Asp Gln Leu Ile Ala Asp  
25 30 35

atc gag cat gtc tct cag gaa acg tct gcc cag aat gag gaa gtc aaa 259  
Ile Glu His Val Ser Gln Glu Thr Ser Ala Gln Asn Glu Glu Val Lys  
40 45 50

cag ctt gag att gat att gag gct cgt gag gtc acg atc aag gaa gtt 307  
Gln Leu Glu Ile Asp Ile Glu Ala Arg Glu Val Thr Ile Lys Glu Val  
55 60 65

cag gag cag tcg gta agc tac cgt gag gcg gct gat caa gca tcg gag 355  
Gln Glu Gln Ser Val Ser Tyr Arg Glu Ala Ala Asp Gln Ala Ser Glu  
70 75 80 85

aat gtc gaa gct tat cgt tcg gag atc aat cgg atc gct cag gcg aag 403  
Asn Val Glu Ala Tyr Arg Ser Glu Ile Asn Arg Ile Ala Gln Ala Lys  
90 95 100

tat	cgt	ggc	aca	gtc	acg	gat	cct	ttg	agc	att	gcg	gtg	tct	gca	gaa	451
Tyr	Arg	Gly	Thr	Val	Thr	Asp	Pro	Leu	Ser	Ile	Ala	Val	Ser	Ala	Glu	
			105					110					115			

gat cca caa aac gtg att gat cgg atg agc tac ctt tca acg ttg act 499  
Asp Pro Gln Asn Val Ile Asp Arg Met Ser Tyr Leu Ser Thr Leu Thr  
120 125 130

aag tcc act agt gat gtg gtt gaa tcc ctc aac gcg gag act gag aag 547  
Lys Ser Thr Ser Asp Val Val Glu Ser Leu Asn Ala Glu Thr Glu Lys  
135 140 145

tcc gca gaa gct gtg tat caa gca aac cgt act aag gcg gaa gcg gag 595  
Ser Ala Glu Ala Val Tyr Gln Ala Asn Arg Thr Lys Ala Glu Ala Glu  
150 155 160 165

ttc cag ttg ggg cag ctg aag gta cgc cag gcg gag ctt gaa tct gaa 643  
 Phe Gln Leu Gly Gln Leu Lys Val Arg Gln Ala Glu Leu Glu Ser Glu  
 170 175 180

aag gaa gca ttg gat ggt cga aaa tcg gag atc cga gac cgg gtg gat 691  
Lys Glu Ala Leu Asp Gly Arg Lys Ser Glu Ile Arg Asp Arg Val Asp  
185 190 195

gcc ctg acg cca cag gag cgg gaa atg tgg gtt gct aag aat ggt cca 739  
Ala Leu Thr Pro Gln Glu Arg Glu Met Trp Val Ala Lys Asn Gly Pro  
200 205 210

**Table 1**

Variable	Mean	SD	Range
Age (years)	67.8	9.0	45-85
Gender (% male)	75.0	-	-
Marital status (% married)	75.0	-	-
Educational level (% high school or less)	50.0	-	-
Income (\$1000/monthly) (% < \$1000)	50.0	-	-
Health insurance (% private)	50.0	-	-
Depression (% depressed)	10.0	-	-
Alcohol consumption (% abstinent)	50.0	-	-
Tobacco consumption (% smoker)	50.0	-	-
Exercise (% exercising)	50.0	-	-
Social support (% low)	50.0	-	-
Stress (% high)	50.0	-	-
Loneliness (% lonely)	50.0	-	-
Life satisfaction (% satisfied)	50.0	-	-
Quality of life (% poor)	50.0	-	-
Mortality (% died)	50.0	-	-



ttg	gac	att	gat	ctg	act	gat	ttg	ctt	ggg	ctt	tcc	gct	gcg	act	tcg	787
Leu	Asp	Ile	Asp	Leu	Thr	Asp	Leu	Leu	Gly	Leu	Ser	Ala	Ala	Thr	Ser	
	215					220					225					
ggt	gcg	gtg	gat	gct	gcc	ttg	tct	aag	ttg	gga	agc	cct	tat	ggt	tgg	835
Gly	Ala	Val	Asp	Ala	Ala	Leu	Ser	Lys	Leu	Gly	Ser	Pro	Tyr	Gly	Trp	
230					235					240					245	
ggt	ggc	att	ggc	cca	aat	gag	ttt	gat	tgc	tca	ggg	ttg	atc	tat	tgg	883
Gly	Gly	Ile	Gly	Pro	Asn	Glu	Phe	Asp	Cys	Ser	Gly	Leu	Ile	Tyr	Trp	
				250					255					260		
gcg	tat	cag	cag	atg	ggg	aag	act	ttg	cca	cgt	acg	tct	caa	gct	cag	931
Ala	Tyr	Gln	Gln	Met	Gly	Lys	Thr	Leu	Pro	Arg	Thr	Ser	Gln	Ala	Gln	
			265					270					275			
atg	gct	ggc	gga	acg	ccg	gtg	agc	aga	gat	gag	ctg	cag	cct	ggc	gat	979
Met	Ala	Gly	Gly	Thr	Pro	Val	Ser	Arg	Asp	Glu	Leu	Gln	Pro	Gly	Asp	
		280					285					290				
gtc	att	gga	tat	tac	cca	ggg	gct	act	cac	gtg	gga	ctg	tat	att	ggg	1027
Val	Ile	Gly	Tyr	Tyr	Pro	Gly	Ala	Thr	His	Val	Gly	Leu	Tyr	Ile	Gly	
	295					300					305					
gac	gga	aag	att	gtg	cac	gcc	tca	gac	tac	gga	atc	cct	gtg	cag	gtg	1075
Asp	Gly	Lys	Ile	Val	His	Ala	Ser	Asp	Tyr	Gly	Ile	Pro	Val	Gln	Val	
310					315					320					325	
gta	tct	gtt	gat	tca	gca	ccg	ttt	tat	ggg	gcg	cgt	cgc	tac			1117
Val	Ser	Val	Asp	Ser	Ala	Pro	Phe	Tyr	Gly	Ala	Arg	Arg	Tyr			
				330					335							
taagaaatag ttcgtcagga gaa																1140
<210> 380																
<211> 339																
<212> PRT																
<213> Corynebacterium glutamicum																
<400> 380																
Met	Phe	Gly	Arg	Arg	Trp	Val	Ser	Val	Val	Ala	Ser	Cys	Val	Ile	Ala	
1				5					10					15		
Ser	Thr	Leu	Ile	Leu	Val	Pro	Ser	His	Ser	Gly	Ala	Glu	Glu	Val	Asp	
			20					25					30			
Gln	Leu	Ile	Ala	Asp	Ile	Glu	His	Val	Ser	Gln	Glu	Thr	Ser	Ala	Gln	
		35					40									

Country	Year	Population (millions)	Urban population (millions)	Urban population (%)	Population density (per sq km)	Population density (per sq mile)
Algeria	1980	10.0	4.0	40.0	100.0	260.0
Algeria	1985	10.5	4.5	42.9	105.0	273.0
Algeria	1990	11.0	5.0	45.5	110.0	285.0
Algeria	1995	11.5	5.5	47.8	115.0	298.0
Algeria	2000	12.0	6.0	50.0	120.0	310.0
Algeria	2005	12.5	6.5	52.0	125.0	323.0
Algeria	2010	13.0	7.0	53.8	130.0	335.0
Algeria	2015	13.5	7.5	55.6	135.0	348.0
Algeria	2020	14.0	8.0	57.1	140.0	360.0
Algeria	2025	14.5	8.5	58.6	145.0	373.0
Algeria	2030	15.0	9.0	60.0	150.0	385.0
Algeria	2035	15.5	9.5	61.3	155.0	398.0
Algeria	2040	16.0	10.0	62.5	160.0	410.0
Algeria	2045	16.5	10.5	63.6	165.0	423.0
Algeria	2050	17.0	11.0	64.7	170.0	435.0
Algeria	2055	17.5	11.5	65.7	175.0	448.0
Algeria	2060	18.0	12.0	66.7	180.0	460.0
Algeria	2065	18.5	12.5	67.6	185.0	473.0
Algeria	2070	19.0	13.0	68.4	190.0	485.0
Algeria	2075	19.5	13.5	69.2	195.0	498.0
Algeria	2080	20.0	14.0	70.0	200.0	510.0
Algeria	2085	20.5	14.5	70.7	205.0	523.0
Algeria	2090	21.0	15.0	71.4	210.0	535.0
Algeria	2095	21.5	15.5	72.1	215.0	548.0
Algeria	2100	22.0	16.0	72.7	220.0	560.0
Algeria	2105	22.5	16.5	73.3	225.0	573.0
Algeria	2110	23.0	17.0	73.9	230.0	585.0
Algeria	2115	23.5	17.5	74.5	235.0	598.0
Algeria	2120	24.0	18.0	75.0	240.0	610.0
Algeria	2125	24.5	18.5	75.5	245.0	623.0
Algeria	2130	25.0	19.0	76.0	250.0	635.0
Algeria	2135	25.5	19.5	76.5	255.0	648.0
Algeria	2140	26.0	20.0	76.9	260.0	660.0
Algeria	2145	26.5	20.5	77.4	265.0	673.0
Algeria	2150	27.0	21.0	77.8	270.0	685.0
Algeria	2155	27.5	21.5	78.2	275.0	698.0
Algeria	2160	28.0	22.0	78.6	280.0	710.0
Algeria	2165	28.5	22.5	78.9	285.0	723.0
Algeria	2170	29.0	23.0	79.3	290.0	735.0
Algeria	2175	29.5	23.5	79.7	295.0	748.0
Algeria	2180	30.0	24.0	80.0	300.0	760.0
Algeria	2185	30.5	24.5	80.3	305.0	773.0
Algeria	2190	31.0	25.0	80.6	310.0	785.0
Algeria	2195	31.5	25.5	81.0	315.0	798.0
Algeria	2200	32.0	26.0	81.3	320.0	810.0
Algeria	2205	32.5	26.5	81.6	325.0	823.0
Algeria	2210	33.0	27.0	81.8	330.0	835.0
Algeria	2215	33.5	27.5	82.1	335.0	848.0
Algeria	2220	34.0	28.0	82.4	340.0	860.0
Algeria	2225	34.5	28.5	82.6	345.0	873.0
Algeria	2230	35.0	29.0	82.9	350.0	885.0
Algeria	2235	35.5	29.5</			



```
<400> 381
gcggggttttg ttgtggaggg gcgcgtcgaa aagcaatttt tttccaaga tagctcactt 60
tattggagtc acctggcctg aaatcctcta ctctgggcgc atg acc att cca gga 115
```

# REPORT







230	235	240	245	
ctc gta ctg cgc gcc ttg acc gat cta caa acc ggt ggc atc gtg gcc	883			
Leu Val Leu Arg Ala Leu Thr Asp Leu Gln Thr Gly Gly Ile Val Ala				
250	255	260		
gca ccg acc acc tca cta cca gag gat ttc gga ggc atc cgt aac tgg	931			
Ala Pro Thr Thr Ser Leu Pro Glu Asp Phe Gly Gly Ile Arg Asn Trp				
265	270	275		
gac tac cgc tac gtg tgg ctg cgc gac tcc gca ctc acc att gaa gcc	979			
Asp Tyr Arg Tyr Val Trp Leu Arg Asp Ser Ala Leu Thr Ile Glu Ala				
280	285	290		
ctc gtg gaa tac gga ttc tcc caa gca gcc ctc caa tgg cgc acc tgg	1027			
Leu Val Glu Tyr Gly Phe Ser Gln Ala Ala Leu Gln Trp Arg Thr Trp				
295	300	305		
ctg ctg cgc gcc atc gca ggc gac ccg gaa aac ctc cgc atc atg tat	1075			
Leu Leu Arg Ala Ile Ala Gly Asp Pro Glu Asn Leu Arg Ile Met Tyr				
310	315	320		
ggc ctc ggc ggc gaa cga cac ctc cct gaa cgc gaa ctc caa cac ctg	1123			
Gly Leu Gly Gly Glu Arg His Leu Pro Glu Arg Glu Leu Gln His Leu				
330	335	340		
cgc gga tac gaa aac tcc gtg cct gtt cgc gtt ggc aat gga gcc gcc	1171			
Arg Gly Tyr Glu Asn Ser Val Pro Val Arg Val Gly Asn Gly Ala Ala				
345	350	355		
gaa caa tac caa gca gat gtc gtc ggc gaa gta atg gtc gcg ctt gaa	1219			
Glu Gln Tyr Gln Ala Asp Val Val Gly Glu Val Met Val Ala Leu Glu				
360	365	370		
acc atc cgc cgc gcc ggg tgc ctc gag gac gaa ttc tcc tgg ggc atg	1267			
Thr Ile Arg Arg Ala Gly Cys Leu Glu Asp Glu Phe Ser Trp Gly Met				
375	380	385		
caa aaa gcc atc ctc gat ttc caa gaa gcc aac ttc gac cgc aag gat	1315			
Gln Lys Ala Ile Leu Asp Phe Gln Glu Ala Asn Phe Asp Arg Lys Asp				
390	395	400		
caa ggc atc tgg gaa atg cgc tcc gaa ccg caa tat ttc acc cac ggc	1363			
Gln Gly Ile Trp Glu Met Arg Ser Glu Pro Gln Tyr Phe Thr His Gly				
410	415	420		
cgc gcc atg atg tgg gcc ggc ttc gac cgc ggc atc aaa gcc atc gaa	1411			
Arg Ala Met Met Trp Ala Gly Phe Asp Arg Gly Ile Lys Ala Ile Glu				
425	430	435		
gaa ttc aac ctc gac ggc ccc atc gag cgc tgg cgt gaa ctc cgc gcc	1459			
Glu Phe Asn Leu Asp Gly Pro Ile Glu Arg Trp Arg Glu Leu Arg Ala				
440	445	450		
aaa ctc cgc gaa gaa atc atg acc aac ggc ttc aac gaa gag atc caa	1507			
Lys Leu Arg Glu Glu Ile Met Thr Asn Gly Phe Asn Glu Glu Ile Gln				
455	460	465		
tcc ttc acc cag tgc tac gac aac acc caa gtc gac gcc tcg ctg ctt	1555			
Ser Phe Thr Gln Cys Tyr Asp Asn Thr Gln Val Asp Ala Ser Leu Leu				
470	475	480		
		485		

00602740-062300



cag ctc gcc caa ata ggc ttc atc ggc ttc gac gat cca aaa atg ctc 1603  
 Gln Leu Ala Gln Ile Gly Phe Ile Gly Phe Asp Asp Pro Lys Met Leu  
 490 495 500  
 agc acc gta gcg cgc att gag caa gag ctt ctc gac gcc cac ggc ttt 1651  
 Ser Thr Val Ala Arg Ile Glu Gln Glu Leu Leu Asp Ala His Gly Phe  
 505 510 515  
 ctt cac agg tac cac acc gac ggg tct gac ggc ctt gcc ggc gac gaa 1699  
 Leu His Arg Tyr His Thr Asp Gly Ser Asp Gly Leu Ala Gly Asp Glu  
 520 525 530  
 tac ccc ttc ctc atc tgt tca ttc tgg ctg gta gaa caa tac gca agc 1747  
 Tyr Pro Phe Leu Ile Cys Ser Phe Trp Leu Val Glu Gln Tyr Ala Ser  
 535 540 545  
 tcc aac cgc ctc gac gag gcc aaa gaa aag atg aac cgc atc ctt gcc 1795  
 Ser Asn Arg Leu Asp Glu Ala Lys Glu Lys Met Asn Arg Ile Leu Ala  
 550 555 560 565  
 gtc caa agc cca ctt ggc cta ctg gct gag gaa tac tcc acc cac cat 1843  
 Val Gln Ser Pro Leu Gly Leu Leu Ala Glu Glu Tyr Ser Thr His His  
 570 575 580  
 ggc agg ctc gct gga aac tac cct cag gcc ttt tcc cac att ggt ctg 1891  
 Gly Arg Leu Ala Gly Asn Tyr Pro Gln Ala Phe Ser His Ile Gly Leu  
 585 590 595  
 atc agc gct gcc cgt gcc ata aat ttc gaa gaa gcg cga aac agg 1936  
 Ile Ser Ala Ala Arg Ala Ile Asn Phe Glu Glu Ala Arg Asn Arg  
 600 605 610  
 tagagtctaa ggtgtcattc ttg 1959

&lt;210&gt; 382

&lt;211&gt; 612

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 382

Met Thr Ile Pro Gly Ala Ser Thr Gln Thr Asp Ile Pro Leu Asp Thr  
 1 5 10 15

Leu Leu Glu Asp Tyr Ala Leu Leu Ser Asp Thr His Thr Gly Ala Leu  
 20 25 30

Leu Ser Asn Met Gly Ser Leu Asp Trp Leu Cys Leu Pro Arg Phe Asp  
 35 40 45

Ser Gln Ala Met Phe Thr Arg Leu Leu Gly Asp Arg Glu His Gly His  
 50 55 60

Trp Ser Leu Arg Val Pro Gly Gly Glu Val Ile Ser Gln Asn Tyr Leu  
 65 70 75 80

Gly Asp Ser Phe Val Val Gln Thr Val Trp Arg Ser Glu Thr Gly Thr  
 85 90 95

Ala Arg Val Val Asp Phe Met Pro Ile His Gly Gln Glu Gln Pro Asp

09602740.062300



100					105					110					
Ile	Thr	Asp	Leu	Val	Arg	Ser	Val	His	Cys	Val	Glu	Gly	Glu	Val	Asp
		115					120					125			
Val	Glu	Ser	Ile	Leu	Arg	Leu	Arg	Phe	Asp	Tyr	Gly	Glu	Ser	Thr	Pro
	130					135					140				
Tyr	Phe	Arg	Thr	Ser	Thr	Val	Asp	Gly	Ile	Ser	Ile	Val	Gln	Ala	Val
145					150					155					160
Ala	Gly	Pro	Asn	Ala	Val	Tyr	Val	Arg	Gly	Pro	Glu	Met	Pro	His	Arg
			165						170					175	
Pro	Ala	Lys	Asp	Cys	His	Ser	Gly	Thr	Phe	His	Leu	Thr	Ala	Gly	Glu
			180					185					190		
Ser	Val	Glu	Trp	Val	Leu	Thr	Trp	Ala	Pro	Ser	Phe	Glu	Pro	His	Pro
		195					200					205			
Pro	Met	Pro	Asp	Tyr	Thr	Arg	Ser	Leu	Glu	Ser	Thr	Leu	Ser	Phe	Trp
	210					215					220				
Ala	Ser	Trp	Val	Glu	Glu	Leu	Pro	His	Gln	Arg	Leu	Tyr	Asp	Ala	Glu
225					230					235					240
Val	Arg	Arg	Ser	Met	Leu	Val	Leu	Arg	Ala	Leu	Thr	Asp	Leu	Gln	Thr
				245					250					255	
Gly	Gly	Ile	Val	Ala	Ala	Pro	Thr	Thr	Ser	Leu	Pro	Glu	Asp	Phe	Gly
			260					265					270		
Gly	Ile	Arg	Asn	Trp	Asp	Tyr	Arg	Tyr	Val	Trp	Leu	Arg	Asp	Ser	Ala
		275					280					285			
Leu	Thr	Ile	Glu	Ala	Leu	Val	Glu	Tyr	Gly	Phe	Ser	Gln	Ala	Ala	Leu
	290					295					300				
Gln	Trp	Arg	Thr	Trp	Leu	Leu	Arg	Ala	Ile	Ala	Gly	Asp	Pro	Glu	Asn
305					310					315					320
Leu	Arg	Ile	Met	Tyr	Gly	Leu	Gly	Gly	Glu	Arg	His	Leu	Pro	Glu	Arg
				325					330					335	
Glu	Leu	Gln	His	Leu	Arg	Gly	Tyr	Glu	Asn	Ser	Val	Pro	Val	Arg	Val
			340					345					350		
Gly	Asn	Gly	Ala	Ala	Glu	Gln	Tyr	Gln	Ala	Asp	Val	Val	Gly	Glu	Val
		355					360					365			
Met	Val	Ala	Leu	Glu	Thr	Ile	Arg	Arg	Ala	Gly	Cys	Leu	Glu	Asp	Glu
	370					375					380				
Phe	Ser	Trp	Gly	Met	Gln	Lys	Ala	Ile	Leu	Asp	Phe	Gln	Glu	Ala	Asn
385					390					395					400
Phe	Asp	Arg	Lys	Asp	Gln	Gly	Ile	Trp	Glu	Met	Arg	Ser	Glu	Pro	Gln
				405					410					415	
Tyr	Phe	Thr	His	Gly	Arg	Ala	Met	Met	Trp	Ala	Gly	Phe	Asp	Arg	Gly
			420					425					430		

002290-0420960



```
<210> 383
<211> 658
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(658)  
<223> RXA01888
```

```
<400> 383
agtagatact agataccacc cattgatgcc gtcaaggggt ttctgtaaa gatgtaagag 60
```

attaagaaaa gaggtagata tggcgtcaaa gcgaccgaca atg gct gat gtg gca 115  
 Met Ala Asp Val Ala  
 1 5

aaa gct gct gga gta tcc act gcg ctg gtc tcc atc gtg ttt cgc gat 163  
Lys Ala Ala Gly Val Ser Thr Ala Leu Val Ser Ile Val Phe Arg Asp  
10 15 20

gcc ccc gga gca agt gaa tcc acc cgc aac cat gtg aaa gaa aaa gcc 211  
Ala Pro Gly Ala Ser Glu Ser Thr Arg Asn His Val Lys Glu Lys Ala



25 30 35  
 gcc gaa ctc gga tac att cct gat cga cga gcc caa aaa ctt cgc caa 259  
 Ala Glu Leu Gly Tyr Ile Pro Asp Arg Arg Ala Gln Lys Leu Arg Gln  
 40 45 50  
 aac cgc tcc gga ctc atc ggt gtg gca ttc gaa atg cac caa gca ttc 307  
 Asn Arg Ser Gly Leu Ile Gly Val Ala Phe Glu Met His Gln Ala Phe  
 55 60 65  
 cac ggc gat atc gtc gaa cac ctc tat ccc acc gcc cga aaa cat ggc 355  
 His Gly Asp Ile Val Glu His Leu Tyr Pro Thr Ala Arg Lys His Gly  
 70 75 80 85  
 ttc gac ctg tac ctt agc gcg atc aca ccg act cgc act gaa aaa gat 403  
 Phe Asp Leu Tyr Leu Ser Ala Ile Thr Pro Thr Arg Thr Glu Lys Asp  
 90 95 100  
 gcc gtc aac gcc ctg atc agg gaa cga tgc gaa gca gta att ctt cta 451  
 Ala Val Asn Ala Leu Ile Arg Glu Arg Cys Glu Ala Val Ile Leu Leu  
 105 110 115  
 gga tct cgc atg tca cct agt gat ttg gaa aca atc gca cag caa ctt 499  
 Gly Ser Arg Met Ser Pro Ser Asp Leu Glu Thr Ile Ala Gln Gln Leu  
 120 125 130  
 ccc gtc caa gta att gcc cgc ggt tcc gga acc ccc aaa gtc agt tcc 547  
 Pro Val Gln Val Ile Ala Arg Gly Ser Gly Thr Pro Lys Val Ser Ser  
 135 140 145  
 gtc cat gtc gac gac gca gtt ggc gcc caa tta gcc ctc aac cac ctc 595  
 Val His Val Asp Asp Ala Val Gly Ala Gln Leu Ala Leu Asn His Leu  
 150 155 160 165  
 atc gaa tta ggc cac gaa cac atc atc tac atc gat ggt ggc gac gcc 643  
 Ile Glu Leu Gly His Glu His Ile Ile Tyr Ile Asp Gly Gly Asp Ala  
 170 175 180  
 cct ggc acc cag gaa 658  
 Pro Gly Thr Gln Glu  
 185

&lt;210&gt; 384

&lt;211&gt; 186

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 384

Met Ala Asp Val Ala Lys Ala Ala Gly Val Ser Thr Ala Leu Val Ser  
 1 5 10 15

Ile Val Phe Arg Asp Ala Pro Gly Ala Ser Glu Ser Thr Arg Asn His  
 20 25 30

Val Lys Glu Lys Ala Ala Glu Leu Gly Tyr Ile Pro Asp Arg Arg Ala  
 35 40 45

Gln Lys Leu Arg Gln Asn Arg Ser Gly Leu Ile Gly Val Ala Phe Glu  
 50 55 60

09602740 "062300



Met His Gln Ala Phe His Gly Asp Ile Val Glu His Leu Tyr Pro Thr  
65 70 75 80

Ala Arg Lys His Gly Phe Asp Leu Tyr Leu Ser Ala Ile Thr Pro Thr  
85 90 95

Arg Thr Glu Lys Asp Ala Val Asn Ala Leu Ile Arg Glu Arg Cys Glu  
100 105 110

Ala Val Ile Leu Leu Gly Ser Arg Met Ser Pro Ser Asp Leu Glu Thr  
115 120 125

Ile Ala Gln Gln Leu Pro Val Gln Val Ile Ala Arg Gly Ser Gly Thr  
130 135 140

Pro Lys Val Ser Ser Val His Val Asp Asp Ala Val Gly Ala Gln Leu  
145 150 155 160

Ala Leu Asn His Leu Ile Glu Leu Gly His Glu His Ile Ile Tyr Ile  
165 170 175

Asp Gly Gly Asp Ala Pro Gly Thr Gln Glu  
180 185

&lt;210&gt; 385

&lt;211&gt; 1503

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1480)

&lt;223&gt; RXN01927

&lt;400&gt; 385

gagcagcggg atcttttgcg taattcgcgc gcgcagatcc atgtgattga ccacaatggt 60

gatgaaattt tggatacccc aacggaagag gatttttaag atg gct ttg gtt ctt 115  
Met Ala Leu Val Leu  
1 5

gga atc gat agt tcc acc caa tcc tgc aag gct ttg ctt gtc gac gcc 163  
Gly Ile Asp Ser Ser Thr Gln Ser Cys Lys Ala Leu Leu Val Asp Ala  
10 15 20

gcc acc ggc cag gtt atc gac gaa ggc cgc gcg agt cac ccg agc ggg 211  
Ala Thr Gly Gln Val Ile Asp Glu Gly Arg Ala Ser His Pro Ser Gly  
25 30 35

tcg gag gta gat cca cgt gcg tgg atc gct gcg ctg gat caa gct acc 259  
Ser Glu Val Asp Pro Arg Ala Trp Ile Ala Ala Leu Asp Gln Ala Thr  
40 45 50

gag ggg ttg tta gaa cgc gcg gac gct gta tct att gca ggc cag cag 307  
Glu Gly Leu Leu Glu Arg Ala Asp Ala Val Ser Ile Ala Gly Gln Gln  
55 60 65

cac ggc atg gtg gcg ttg gat gaa aac gat gaa atc gtt cgc ccg gcg 355  
His Gly Met Val Ala Leu Asp Glu Asn Asp Glu Ile Val Arg Pro Ala  
70 75 80 85

09602740-062277



ttg tta tgg aat gac act cgt tct gcc cag gct gcg ttg gat ctc aat	403
Leu Leu Trp Asn Asp Thr Arg Ser Ala Gln Ala Ala Leu Asp Leu Asn	
90 95 100	
gag gag atc ggc ggc gat cag gct gcg gta gat gcc acg gga agt gtg	451
Glu Glu Ile Gly Gly Asp Gln Ala Val Asp Ala Thr Gly Ser Val	
105 110 115	
tat gtt gct tct tta act gcc acc aaa atg cgg tgg atg cgt gat cat	499
Tyr Val Ala Ser Leu Thr Ala Thr Lys Met Arg Trp Met Arg Asp His	
120 125 130	
gaa cca gaa aat gca gcg cgc acg gcg tcg gtg atg ttg cct cat gat	547
Glu Pro Glu Asn Ala Ala Arg Thr Ala Ser Val Met Leu Pro His Asp	
135 140 145	
ttc ctc acc tgg cat ttg atg gga cgc gga cgc aaa gtc acc gac cat	595
Phe Leu Thr Trp His Leu Met Gly Arg Gly Arg Lys Val Thr Asp His	
150 155 160 165	
ggg gat gct tct gga acg ggc tac tac agc acg cgt gat cgt gcg tgg	643
Gly Asp Ala Ser Gly Thr Gly Tyr Tyr Ser Thr Arg Asp Arg Ala Trp	
170 175 180	
cgc acc gat cta gct gcc ttg gcg ctg ggc cat gag gtg gaa ctt cct	691
Arg Thr Asp Leu Ala Ala Leu Ala Leu Gly His Glu Val Glu Leu Pro	
185 190 195	
gaa ctc ctg gcc cca aat gcg att gcg gga aca act cca ggt gga gtg	739
Glu Leu Leu Ala Pro Asn Ala Ile Ala Gly Thr Thr Pro Gly Gly Val	
200 205 210	
aaa gtt gct gca ggc acg gga gat aat gct gcg gct gcg ctt ggc ctt	787
Lys Val Ala Ala Gly Thr Gly Asp Asn Ala Ala Ala Leu Gly Leu	
215 220 225	
gat ttg cag cct ggt gat gtc agc gtg tcg atc ggc acc tct ggc gtt	835
Asp Leu Gln Pro Gly Asp Val Ser Val Ser Ile Gly Thr Ser Gly Val	
230 235 240 245	
gcc ggc atg acc gtt caa cat agc gtc cac gat cca tct ggt ttg gtc	883
Ala Gly Met Thr Val Gln His Ser Val His Asp Pro Ser Gly Leu Val	
250 255 260	
act ggt ttc gcc gat gcc acg ggt gcg tat ttc ccg ctg gcc tgc acg	931
Thr Gly Phe Ala Asp Ala Thr Gly Ala Tyr Phe Pro Leu Ala Cys Thr	
265 270 275	
ctt aat ggc gca ccg gtg ttg gaa ttc ggc cgc cgc att ctg ggc gtg	979
Leu Asn Gly Ala Pro Val Leu Glu Phe Gly Arg Arg Ile Leu Gly Val	
280 285 290	
gaa tgg gaa gag ttc gat gcg ctt gca ctg gct gct caa ccc ggt tca	1027
Glu Trp Glu Glu Phe Asp Ala Leu Ala Leu Ala Ala Gln Pro Gly Ser	
295 300 305	
ggg ggc gtg acg ctc cag cct tat ttg gag ggc gag cgt acg ccg aat	1075
Gly Gly Val Thr Leu Gln Pro Tyr Leu Glu Gly Glu Arg Thr Pro Asn	
310 315 320 325	

09602740-062300



cgt Arg	ccc Pro	gca Ala	gca Ala	cgt Arg 330	ggc Gly	gtt Val	ttg Leu	gct Ala	gga Gly 335	cta Leu	aac Asn	tgt Cys	gca Ala	acg Thr 340	acc Thr	1123
cgc Arg	gag Glu	gac Asp	ttt Phe 345	gcc Ala	cga Arg	gca Ala	act Thr	gtt Val 350	gaa Glu	ggc Gly	ttg Leu	ttg Leu	ttg Leu 355	gca Ala	ttg Leu	1171
gat Asp	gat Asp	gct Ala 360	gta Val	acg Thr	gcg Ala	ctg Leu	gtt Val 365	gag Glu	gcc Ala	acg Thr	gga Gly	gtg Val 370	ccc Pro	gtt Val	cag Gln	1219
cgc Arg	atc Ile 375	cag Gln	ctc Leu	atc Ile	ggc Gly	ggc Gly	ggc Gly	gcg Ala	cgt Arg	tca Ser	cag Gln	gcg Ala	gtt Val	cgt Arg	gag Glu	1267
att Ile 390	gcc Ala	cct Pro	gag Glu	att Ile	ttc Phe 395	ggc Gly	cat His	gag Glu	att Ile	gtg Val 400	gtt Val	cca Pro	gaa Glu	ccc Pro	gct Ala 405	1315
gaa Glu	tat Tyr	gtg Val	gcg Ala	ttg Leu 410	ggc Gly	gca Ala	gct Ala	cgt Arg	cag Gln	gcg Ala	gca Ala	tgg Trp	gcg Ala	ctg Leu 420	tcg Ser	1363
ggc Gly	gag Glu	gcc Ala	acg Thr 425	cca Pro	ccg Pro	cag Gln	tgg Trp	cca Pro	act Thr	ccc Pro	ggc Gly	tcc Ser	gat Asp	ccg Pro	cac His	1411
cgc Arg	gca Ala	cct Pro	aaa Lys 440	aac Asn	act Thr	gag Glu	ctg Leu	agc Ser	acg Thr	cgt Arg	tat Tyr	gcg Ala	aag Lys	ctg Leu	cgt Arg	1459
gct Ala	gca Ala	acg Thr	cag Gln	ggc Gly	tgg Trp	tac Tyr	tagagctcga	tattgtcga	taa	gac	gac	gac	gac	gac	gac	1503

```
<210> 386
<211> 460
<212> PRT
<213> Corynebacterium glutamicum
```

```

<400> 386
Met Ala Leu Val Leu Gly Ile Asp Ser Ser Thr Gln Ser Cys Lys Ala
  1          5          10          15
Leu Leu Val Asp Ala Ala Thr Gly Gln Val Ile Asp Glu Gly Arg Ala
          20          25          30
Ser His Pro Ser Gly Ser Glu Val Asp Pro Arg Ala Trp Ile Ala Ala
          35          40          45
Leu Asp Gln Ala Thr Glu Gly Leu Leu Glu Arg Ala Asp Ala Val Ser
          50          55          60
Ile Ala Gly Gln Gln His Gly Met Val Ala Leu Asp Glu Asn Asp Glu
          65          70          75          80
Ile Val Arg Pro Ala Leu Leu Trp Asn Asp Thr Arg Ser Ala Gln Ala
          85          90          95

```

**6070**







			420					425					430			
Gly	Ser	Asp	Pro	His	Arg	Ala	Pro	Lys	Asn	Thr	Glu	Leu	Ser	Thr	Arg	
		435					440					445				
Tyr	Ala	Lys	Leu	Arg	Ala	Ala	Thr	Gln	Gly	Trp	Tyr					
	450					455					460					

```
<210> 387
<211> 1139
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (1)..(1116)
<223> FRXA01927
```

<400> 387																
aat	gac	act	cgt	tct	gcc	cag	gct	gcg	ttg	gat	ctc	aat	gag	gag	atc	48
Asn	Asp	Thr	Arg	Ser	Ala	Gln	Ala	Ala	Leu	Asp	Leu	Asn	Glu	Glu	Ile	
1				5				10				15				
ggc	ggc	gat	cag	gct	gcg	gta	gat	gcc	acg	gga	agt	gtg	tat	gtt	gct	96
Gly	Gly	Asp	Gln	Ala	Ala	Val	Asp	Ala	Thr	Gly	Ser	Val	Tyr	Val	Ala	
20				25				30								
tct	tta	act	gcc	acc	aaa	atg	cgg	tgg	atg	cgt	gat	cat	gaa	cca	gaa	144
Ser	Leu	Thr	Ala	Thr	Lys	Met	Arg	Trp	Met	Arg	Asp	His	Glu	Pro	Glu	
35				40				45								
aat	gca	gcg	cgc	acg	gcg	tcg	gtg	atg	ttg	cct	cat	gat	ttc	ctc	acc	192
Asn	Ala	Ala	Arg	Thr	Ala	Ser	Val	Met	Leu	Pro	His	Asp	Phe	Leu	Thr	
50				55				60								
tgg	cat	ttg	atg	gga	cgc	gga	cgc	aaa	gtc	acc	gac	cat	ggt	gat	gct	240
Trp	His	Leu	Met	Gly	Arg	Gly	Arg	Lys	Val	Thr	Asp	His	Gly	Asp	Ala	
65				70				75				80				
tct	gga	acg	ggc	tac	tac	agc	acg	cgt	gat	cgt	gcg	tgg	cgc	acc	gat	288
Ser	Gly	Thr	Gly	Tyr	Tyr	Ser	Thr	Arg	Asp	Arg	Ala	Trp	Arg	Thr	Asp	
85				90				95								
cta	gct	gcc	ttg	gcg	ctg	ggc	cat	gag	gtg	gaa	ctt	cct	gaa	ctc	ctg	336
Leu	Ala	Ala	Leu	Ala	Leu	Gly	His	Glu	Val	Glu	Leu	Pro	Glu	Leu	Leu	
100				105				110								
gcc	cca	aat	gcg	att	gcg	gga	aca	act	cca	ggt	gga	gtg	aaa	gtt	gct	384
Ala	Pro	Asn	Ala	Ile	Ala	Gly	Thr	Thr	Pro	Gly	Gly	Val	Lys	Val	Ala	
115				120				125								
gca	ggc	acg	gga	gat	aat	gct	gcg	gct	gcg	ctt	ggc	ctt	gat	ttg	cag	432
Ala	Gly	Thr	Gly	Asp	Asn	Ala	Ala	Ala	Ala	Leu	Gly	Leu	Asp	Leu	Gln	
130				135				140								
cct	ggt	gat	gtc	agc	gtg	tcg	atc	ggc	acc	tct	ggc	gtt	gcc	ggc	atg	480
Pro	Gly	Asp	Val	Ser	Val	Ser	Ile	Gly	Thr	Ser	Gly	Val	Ala	Gly	Met	
145				150				155				160				
acc	gtt	caa	cat	agc	gtc	cac	gat	cca	tct	ggt	ttg	gtc	act	ggt	ttc	528



0960240-062300

0960240-062300



&lt;400&gt; 388

Asn Asp Thr Arg Ser Ala Gln Ala Ala Leu Asp Leu Asn Glu Glu Ile  
 1 5 10 15  
 Gly Gly Asp Gln Ala Ala Val Asp Ala Thr Gly Ser Val Tyr Val Ala  
 20 25 30  
 Ser Leu Thr Ala Thr Lys Met Arg Trp Met Arg Asp His Glu Pro Glu  
 35 40 45  
 Asn Ala Ala Arg Thr Ala Ser Val Met Leu Pro His Asp Phe Leu Thr  
 50 55 60  
 Trp His Leu Met Gly Arg Gly Arg Lys Val Thr Asp His Gly Asp Ala  
 65 70 75 80  
 Ser Gly Thr Gly Tyr Tyr Ser Thr Arg Asp Arg Ala Trp Arg Thr Asp  
 85 90 95  
 Leu Ala Ala Leu Ala Leu Gly His Glu Val Glu Leu Pro Glu Leu Leu  
 100 105 110  
 Ala Pro Asn Ala Ile Ala Gly Thr Thr Pro Gly Gly Val Lys Val Ala  
 115 120 125  
 Ala Gly Thr Gly Asp Asn Ala Ala Ala Ala Leu Gly Leu Asp Leu Gln  
 130 135 140  
 Pro Gly Asp Val Ser Val Ser Ile Gly Thr Ser Gly Val Ala Gly Met  
 145 150 155 160  
 Thr Val Gln His Ser Val His Asp Pro Ser Gly Leu Val Thr Gly Phe  
 165 170 175  
 Ala Asp Ala Thr Gly Ala Tyr Phe Pro Leu Ala Cys Thr Leu Asn Gly  
 180 185 190  
 Ala Pro Val Leu Glu Phe Gly Arg Arg Ile Leu Gly Val Glu Trp Glu  
 195 200 205  
 Glu Phe Asp Ala Leu Ala Leu Ala Ala Gln Pro Gly Ser Gly Gly Val  
 210 215 220  
 Thr Leu Gln Pro Tyr Leu Glu Gly Glu Arg Thr Pro Asn Arg Pro Ala  
 225 230 235 240  
 Ala Arg Gly Val Leu Ala Gly Leu Asn Cys Ala Thr Thr Arg Glu Asp  
 245 250 255  
 Phe Ala Arg Ala Thr Val Glu Gly Leu Leu Leu Ala Leu Asp Asp Ala  
 260 265 270  
 Val Thr Ala Leu Val Glu Ala Thr Gly Val Pro Val Gln Arg Ile Gln  
 275 280 285  
 Leu Ile Gly Gly Gly Ala Arg Ser Gln Ala Val Arg Glu Ile Ala Pro  
 290 295 300  
 Glu Ile Phe Gly His Glu Ile Val Val Pro Glu Pro Ala Glu Tyr Val  
 305 310 315 320

09602740.062300



<400> 389															
gaattaattg caggcacggt acctagcgtg acgaaaacta cgatccccac tgcccttatt 60															
catcgtgaat caatcatcaa ctccacttta aggaagaagg atg gac tcc cca atg 115															
Met Asp Ser Pro Met 5															
1															
agt aac tca acc ggt acc gac att gtc gtt gtc gga tcc atc aat gcc 163															
Ser Asn Ser Thr Gly Thr Asp Ile Val Val Val Gly Ser Ile Asn Ala 20															
10 15															
gat ctc acc gca aaa gtt caa cgc cac cct gaa cct gga gaa acc ctc 211															
Asp Leu Thr Ala Lys Val Gln Arg His Pro Glu Pro Gly Glu Thr Leu 35															
25 30															
ctg ggt agc ggc ggc aca gtg agt gct ggt ggc aaa ggc gcc aac caa 259															
Leu Gly Ser Gly Gly Thr Val Ser Ala Gly Gly Lys Gly Ala Asn Gln 50															
40 45															
gct gtg gcg gca gcg caa tta ggt gcc aaa gtc acc atg atc ggt gcg 307															
Ala Val Ala Ala Ala Gln Leu Gly Ala Lys Val Thr Met Ile Gly Ala 65															
55 60															
gtc gga acc gat caa atg gct ggc gag gcg ctg aca cat ttg cgt caa 355															
Val Gly Thr Asp Gln Met Ala Gly Glu Ala Leu Thr His Leu Arg Gln 85															
70 75 80															
tca gga gca gat atg tcc gcg att gcc act gtg gac ggt ccc act ggt 403															
Ser Gly Ala Asp Met Ser Ala Ile Ala Thr Val Asp Gly Pro Thr Gly 100															
90 95															
ctt gcc atc atc act gtg tct gac gat ggg gaa aac acc atc atc gtt 451															
Leu Ala Ile Ile Thr Val Ser Asp Asp Gly Glu Asn Thr Ile Ile Val 115															
105 110															
atc cct ggc gct aac gct tct gtc acc gcg gaa ttt gtt gat aaa cac 499															
Ile Pro Gly Ala Asn Ala Ser Val Thr Ala Glu Phe Val Asp Lys His 130															
120 125															

**THE UNIVERSITY OF CHICAGO**



tcc caa ctc att gag aac gcc ggc att gtg ttg ctt cag ggt gag atc 547  
 Ser Gln Leu Ile Glu Asn Ala Gly Ile Val Leu Leu Gln Gly Glu Ile  
 135 140 145

cct gcc gat ggt ttc gag cgt gcc gtt gat ctt tca caa gga cgt gtg 595  
 Pro Ala Asp Gly Phe Glu Arg Ala Val Asp Leu Ser Gln Gly Arg Val  
 150 155 160 165

gtg atc aat ctg gct cca gtt gtg ccc gtg gga cat gat cag ctg cgt 643  
 Val Ile Asn Leu Ala Pro Val Val Pro Val Gly His Asp Gln Leu Arg  
 170 175 180

cgt gcc gat cca ttg ctg gtc aac gaa cac gaa ggc gct ctg gtg ctg 691  
 Arg Ala Asp Pro Leu Leu Val Asn Glu His Glu Gly Ala Leu Val Leu  
 185 190 195

gac atg ctt gga act cca gcg acc acg tct gat ccc caa agt ttg gtc 739  
 Asp Met Leu Gly Thr Pro Ala Thr Thr Ser Asp Pro Gln Ser Leu Val  
 200 205 210

act gaa ttg ctg gag cag ggt ttt act tcc gtg gtg atg aca ctt ggt 787  
 Thr Glu Leu Leu Glu Gln Gly Phe Thr Ser Val Val Met Thr Leu Gly  
 215 220 225

gcc gaa ggt gct ctg gtt ggc acg ccg ggc caa ctc acg gca att cct 835  
 Ala Glu Gly Ala Leu Val Gly Thr Pro Gly Gln Leu Thr Ala Ile Pro  
 230 235 240 245

acc cca aag 844  
 Thr Pro Lys

<210> 390  
 <211> 248  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 390  
 Met Asp Ser Pro Met Ser Asn Ser Thr Gly Thr Asp Ile Val Val Val  
 1 5 10 15

Gly Ser Ile Asn Ala Asp Leu Thr Ala Lys Val Gln Arg His Pro Glu  
 20 25 30

Pro Gly Glu Thr Leu Leu Gly Ser Gly Gly Thr Val Ser Ala Gly Gly  
 35 40 45

Lys Gly Ala Asn Gln Ala Val Ala Ala Ala Gln Leu Gly Ala Lys Val  
 50 55 60

Thr Met Ile Gly Ala Val Gly Thr Asp Gln Met Ala Gly Glu Ala Leu  
 65 70 75 80

Thr His Leu Arg Gln Ser Gly Ala Asp Met Ser Ala Ile Ala Thr Val  
 85 90 95

Asp Gly Pro Thr Gly Leu Ala Ile Ile Thr Val Ser Asp Asp Gly Glu  
 100 105 110

09602740-062300



<400> 391																
acagtctcat gaagccataa taaccacctt ctacaaagat cgacgtagaa tggaataacc																60
ccttatgaaa acgttttgcac aactccgcta aggatgttcc atg aat aat cga att																115
Met Asn Asn Arg Ile																
1 5																
gtc gta gtc ggc tcc atc aac gct gat ctt aat gtt ctc gtt gac cgc																163
Val Val Val Gly Ser Ile Asn Ala Asp Leu Asn Val Leu Val Asp Arg																
10 15 20																
cac cca gca cct ggc gaa aca ctg ttg ggc agt ggt gga cac atc act																211
His Pro Ala Pro Gly Glu Thr Leu Leu Gly Ser Gly Gly His Ile Thr																
25 30 35																
gca gga ggc aaa ggc gcc aac cag gca gta gct gcc gct ctt caa ggt																259
Ala Gly Gly Lys Gly Ala Asn Gln Ala Val Ala Ala Ala Leu Gln Gly																
40 45 50																
gca gac gtc gcc ttt gtc ggc gct gtg ggc aag gat cct tac gct gcc																307
Ala Asp Val Ala Phe Val Gly Ala Val Gly Lys Asp Pro Tyr Ala Ala																
55 60 65																

060907Z-060900



**SECRET**



<210> 392  
 <211> 301  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 392

```

Met Asn Asn Arg Ile Val Val Val Gly Ser Ile Asn Ala Asp Leu Asn
 1           5           10           15

Val Leu Val Asp Arg His Pro Ala Pro Gly Glu Thr Leu Leu Gly Ser
          20           25           30

Gly Gly His Ile Thr Ala Gly Gly Lys Gly Ala Asn Gln Ala Val Ala
      35           40           45

Ala Ala Leu Gln Gly Ala Asp Val Ala Phe Val Gly Ala Val Gly Lys
      50           55           60

Asp Pro Tyr Ala Ala Pro Ala Leu Glu Phe Leu Arg Ser Ser Gly Val
      65           70           75           80

Asp Leu Thr Ala Val Ser Glu Val Asp Asp Thr Thr Gly Leu Ala Val
          85           90           95

Ile Thr Val Ala Lys Asp Gly Glu Asn Asn Ile Val Val Ile Pro Gly
      100           105           110

Ala Asn Ser Leu Val Asn Cys Asp Tyr Val Ser Ser Gln Ser Ala Leu
      115           120           125

Leu Ala Glu Ala Gly Ile Leu Leu Leu Gln Gly Glu Ile Pro Ala Asp
      130           135           140

Gly Phe Lys Glu Ala Ile His His Thr Met Gly Arg Val Val Val Asn
      145           150           155           160

Leu Ala Pro Val Ile Glu Val Glu Lys Ser Ala Leu Leu Glu Ala Asp
          165           170           175

Pro Ile Ile Ala Asn Glu His Glu Ala Gly Leu Ile Leu Asp Gln Phe
          180           185           190

Gly Ala Gly Ile Asp Ser Met Asp Pro His Glu Leu Ala Gln Ala Leu
      195           200           205

Leu Asp Ala Gly Phe Ala Ser Val Val Leu Thr Leu Gly Ser Ala Gly
      210           215           220

Ala Leu Val Ala Asp Ala Thr Gly Ile Thr Asp Ile Ala Thr Pro Thr
      225           230           235           240

Val Gln Ala Val Asp Thr Thr Gly Ala Gly Asp Ala Phe Ala Gly Ala
          245           250           255

Phe Cys Ala Arg Leu Ile Lys Gly Asp Ser Leu Ile Asp Ala Ala Thr
          260           265           270

His Ala Ala Arg Val Gly Ala Tyr Ser Val Gln Thr Ala Gly Ala Gln
      275           280           285

Ala Ser Tyr Pro Asp Ala Ser Val Ser Leu Pro Ser Val

```

002290.0420960



**00000000000000000000000000000000**



[illegible]

<210> 394

<211> 346

<212> PRT

<213> Corynebacterium glutamicum

<400> 394

Met Ala Thr Glu Lys Phe Arg Pro Thr Leu Lys Asp Val Ala Arg Gln  
1 5 10 15

Ala Gly Val Ser Ile Ala Thr Ala Ser Arg Ala Leu Ala Asp Asn Pro  
20 25 30

Ala Val Ala Ala Ser Thr Arg Glu Arg Ile Gln Gln Leu Ala Ser Asp

**THE UNIVERSITY OF CHICAGO**







<400> 395  
gctgcacaaa ttccgcqaaa gqgtatcacc atcgacatca cagatgaaga ccgtgagatc 60

ctg gaa tcc taagaaataa aggtaggtgt cac 483  
Leu Glu Ser  
120

Gly Asn Ile Ile Gly Gly Val Val Ser Pro Thr Leu Ala Ala Ser Glu  
20 25 30

[illegible]



Trp Gly Trp Gln Val Asp Pro Leu Gly Leu Arg Ile Val Leu Asn Asn  
           35                          40                          45

Tyr Trp Glu Arg Trp Gln Lys Pro Leu Phe Ile Val Glu Asn Gly Leu  
       50                          55                          60

Gly Ala Lys Asp Val Leu Ile Asp Gly Pro Ser Gly Pro Thr Val Asn  
       65                          70                          75                          80

Asp Asp Tyr Arg Ile Lys Tyr Leu Asp Asp Gly Gly Ser Gly Ile Leu  
                           85                          90                          95

Lys Arg Tyr Lys Lys Lys Ser Phe Asp Trp Cys Arg Asp Ile Ile Ala  
                           100                          105                          110

Thr Asn Gly Glu Ser Leu Glu Ser  
           115                          120

&lt;210&gt; 397

&lt;211&gt; 795

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(772)

&lt;223&gt; RXA01325

&lt;400&gt; 397

gcgcagcgct cggacgatta cgaacttcag gagaactcgg ggtcattcgt tgcattctac 60

cctggaaatt ttccacact aagtcagggtc taagtaggggt atg gat atg acg att 115  
   Met Asp Met Thr Ile  
   1                          5

tcc cgc tcc acc atg gcc caa atc ctt gac tac acc ctc ctc gga cca 163  
  Ser Arg Ser Thr Met Ala Gln Ile Leu Asp Tyr Thr Leu Leu Gly Pro  
                           10                          15                          20

gaa gta acc aac tcc gaa ctg gcc gca ttt ata gat tcc gca att gag 211  
  Glu Val Thr Asn Ser Glu Leu Ala Ala Phe Ile Asp Ser Ala Ile Glu  
                           25                          30                          35

ctg gga gtc ggc acg atc tgt gtc ccc aac agc atg gtc aac cta act 259  
  Leu Gly Val Gly Thr Ile Cys Val Pro Asn Ser Met Val Asn Leu Thr  
                           40                          45                          50

gca aaa gcc caa gaa gct gga att cga gtg gcc acc gtc gca gga ttc 307  
  Ala Lys Ala Gln Glu Ala Gly Ile Arg Val Ala Thr Val Ala Gly Phe  
                           55                          60                          65

ccg cac ggc aaa acc ccc gcg ttg gtg aaa gcc gcc gaa gcg cgc ctt 355  
  Pro His Gly Lys Thr Pro Ala Leu Val Lys Ala Ala Glu Ala Arg Leu  
       70                          75                          80                          85

gcc gta cag tcc gga gct tcc gaa gta gat gtt gtt ttg gat att gcg 403  
  Ala Val Gln Ser Gly Ala Ser Glu Val Asp Val Val Leu Asp Ile Ala  
                           90                          95                          100

gta gtg aaa gag gga gat gcc aat agg ttg ctg cag gaa att gtg gca 451

09602740.062300



[illegible]

```
<210> 398
<211> 224
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 398															
Met	Asp	Met	Thr	Ile	Ser	Arg	Ser	Thr	Met	Ala	Gln	Ile	Leu	Asp	Tyr
1				5					10					15	
Thr	Leu	Leu	Gly	Pro	Glu	Val	Thr	Asn	Ser	Glu	Leu	Ala	Ala	Phe	Ile
			20					25					30		
Asp	Ser	Ala	Ile	Glu	Leu	Gly	Val	Gly	Thr	Ile	Cys	Val	Pro	Asn	Ser
		35					40					45			
Met	Val	Asn	Leu	Thr	Ala	Lys	Ala	Gln	Glu	Ala	Gly	Ile	Arg	Val	Ala
	50					55					60				
Thr	Val	Ala	Gly	Phe	Pro	His	Gly	Lys	Thr	Pro	Ala	Leu	Val	Lys	Ala
65					70					75					80
Ala	Glu	Ala	Arg	Leu	Ala	Val	Gln	Ser	Gly	Ala	Ser	Glu	Val	Asp	Val
				85					90					95	
Val	Leu	Asp	Ile	Ala	Val	Val	Lys	Glu	Gly	Asp	Ala	Asn	Arg	Leu	Leu
			100					105					110		

[illegible]



Gln Glu Ile Val Ala Ile Arg Glu Ala Val Pro Ser Pro Val Val Leu  
 115 120 125

Lys Phe Ile Leu Glu Thr Ala Val Val Ser Asp Glu Ala Ile Val Thr  
 130 135 140

Ala Val Asn Ala Leu Ile Ala Ala Gly Ala Asp Phe Ala Lys Thr Ser  
 145 150 155 160

Thr Gly Phe His Pro Ala Gly Gly Ala Thr Val Glu Ala Val Arg Val  
 165 170 175

Met Ala Ser Ala Ser Arg Gly Arg Val Gly Ile Lys Ala Ala Gly Gly  
 180 185 190

Val Lys Thr Trp Glu Asp Ala Val Ala Phe Val Glu Ala Gly Ala Thr  
 195 200 205

Arg Ile Gly Thr Ser Asn Ala Gly Ala Ile Leu Glu Gly Ala Pro Glu  
 210 215 220

<210> 399  
 <211> 684  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(661)  
 <223> RXA00195

<400> 399  
 tcgcagtcac catgcaggca taacctgaaa cccatccgtt tggattgccc caaatgggtg 60  
 tagtgggtgc gtttacccaa caagtgcaag aatgggagtc gtg act aaa aag atc 115  
 Val Thr Lys Lys Ile  
 1 5

ctt att ttg gga agc act ggt tcg att gga act cag gcg ctg gac gtt 163  
 Leu Ile Leu Gly Ser Thr Gly Ser Ile Gly Thr Gln Ala Leu Asp Val  
 10 15 20

att gct gat aat tca gac aag ttt gag gtg gtg ggt atc gct gcg ggc 211  
 Ile Ala Asp Asn Ser Asp Lys Phe Glu Val Val Gly Ile Ala Ala Gly  
 25 30 35

ggt tct cag cca gac ctc gtt att tcg cag gcg cag cag ttg ggg ctg 259  
 Gly Ser Gln Pro Asp Leu Val Ile Ser Gln Ala Gln Gln Leu Gly Leu  
 40 45 50

gct gca gac aag gtt gcg gtt gct gat gca cag gct gcc gca gta att 307  
 Ala Ala Asp Lys Val Ala Val Ala Asp Ala Gln Ala Ala Ala Val Ile  
 55 60 65

tcg aag gct ctc ggc ggc gag atc atc tct gga acc gat gct gcg aag 355  
 Ser Lys Ala Leu Gly Gly Glu Ile Ile Ser Gly Thr Asp Ala Ala Lys  
 70 75 80 85

00602740 062300



att	ctg	gtg	gaa	acc	aca	aag	gcc	gac	act	gtg	ctt	aat	gct	ctg	gtt	403
Ile	Leu	Val	Glu	Thr	Thr	Lys	Ala	Asp	Thr	Val	Leu	Asn	Ala	Leu	Val	
				90					95					100		
ggt	tct	ttg	ggg	ctt	gcg	gca	acg	ctg	gcc	act	ctg	gaa	tct	ggt	gcg	451
Gly	Ser	Leu	Gly	Leu	Ala	Ala	Thr	Leu	Ala	Thr	Leu	Glu	Ser	Gly	Ala	
			105					110					115			
cat	ctt	gcc	ttg	gct	aac	aaa	gaa	tcg	ctg	gtt	gcc	ggt	ggt	gag	ttt	499
His	Leu	Ala	Leu	Ala	Asn	Lys	Glu	Ser	Leu	Val	Ala	Gly	Gly	Glu	Phe	
		120					125					130				
gtt	acc	tca	aag	gca	aag	ctg	ggg	cag	atc	att	ccg	gtc	gat	tcg	gag	547
Val	Thr	Ser	Lys	Ala	Lys	Leu	Gly	Gln	Ile	Ile	Pro	Val	Asp	Ser	Glu	
			135			140					145					
cac	tct	gcc	atg	gcg	cag	tgt	ttg	cgt	tcg	ggt	act	cgt	gat	gag	gtt	595
His	Ser	Ala	Met	Ala	Gln	Cys	Leu	Arg	Ser	Gly	Thr	Arg	Asp	Glu	Val	
150					155					160					165	
gcg	cgg	att	gtg	ctg	aca	gct	tcg	ggc	gga	cct	ttc	agg	gct	gga	cca	643
Ala	Arg	Ile	Val	Leu	Thr	Ala	Ser	Gly	Gly	Pro	Phe	Arg	Ala	Gly	Pro	
				170				175						180		
ggg	aga	aga	tgt	ggg	agg	tgactcccga gcaggcagca gcg										684
Gly	Arg	Arg	Cys	Gly	Arg											
			185													
<210> 400																
<211> 187																
<212> PRT																
<213> Corynebacterium glutamicum																
<400> 400																
Val	Thr	Lys	Lys	Ile	Leu	Ile	Leu	Gly	Ser	Thr	Gly	Ser	Ile	Gly	Thr	
1				5					10					15		
Gln	Ala	Leu	Asp	Val	Ile	Ala	Asp	Asn	Ser	Asp	Lys	Phe	Glu	Val	Val	
			20					25					30			
Gly	Ile	Ala	Ala	Gly	Gly	Ser	Gln	Pro	Asp	Leu	Val	Ile	Ser	Gln	Ala	
		35					40					45				
Gln	Gln	Leu	Gly	Leu	Ala	Ala	Asp	Lys	Val	Ala	Val	Ala	Asp	Ala	Gln	
		50				55					60					
Ala	Ala	Ala	Val	Ile	Ser	Lys	Ala	Leu	Gly	Gly	Glu	Ile	Ile	Ser	Gly	
65					70					75					80	
Thr	Asp	Ala	Ala	Lys	Ile	Leu	Val	Glu	Thr	Thr	Lys	Ala	Asp	Thr	Val	
				85					90					95		



<400> 401																
ctgccatggc	gcagtgtttg	cgttcgggta	ctcgtgatga	ggttgcgcgg	attgtgctga	60										
cagcttcggg	cggacctttc	agggctggac	cagggagaag	atg	tgg	gag	gtg	act	115							
				Met	Trp	Glu	Val	Thr								
					1			5								
ccc	gag	cag	gca	gca	gcg	cac	cca	acg	tgg	gcg	atg	ggg	cag	atg	aac	163
Pro	Glu	Gln	Ala	Ala	Ala	His	Pro	Thr	Trp	Ala	Met	Gly	Gln	Met	Asn	
				10					15					20		
acg	ttg	aac	tcc	gcc	acc	ctt	att	aat	aaa	ggc	ctc	gaa	ctc	atc	gag	211
Thr	Leu	Asn	Ser	Ala	Thr	Leu	Ile	Asn	Lys	Gly	Leu	Glu	Leu	Ile	Glu	
			25					30					35			
gcg	acc	ctg	ctg	ttt	gaa	acg	gat	gcg	gat	ctc	att	gat	gtg	acg	gtg	259
Ala	Thr	Leu	Leu	Phe	Glu	Thr	Asp	Ala	Asp	Leu	Ile	Asp	Val	Thr	Val	
		40					45					50				
cat	ccg	cag	tcg	atc	atc	cac	tcc	atg	atc	acg	ttt	acg	gat	ggt	gcg	307
His	Pro	Gln	Ser	Ile	Ile	His	Ser	Met	Ile	Thr	Phe	Thr	Asp	Gly	Ala	
	55					60					65					
acc	atc	gcg	cag	gcg	tcg	cca	cca	tcg	atg	aaa	ctg	ccg	atc	gcg	ttg	355
Thr	Ile	Ala	Gln	Ala	Ser	Pro	Pro	Ser	Met	Lys	Leu	Pro	Ile	Ala	Leu	
	70				75					80					85	
gcg	ctt	gat	tgg	cca	cat	cgg	gtg	ccg	aag	gct	cag	ccg	gcg	ctg	gat	403
Ala	Leu	Asp	Trp	Pro	His	Arg	Val	Pro	Lys	Ala	Gln	Pro	Ala	Leu	Asp	
				90				95						100		
ttc	acc	gct	gct	cat	acc	tgg	gct	ttt	gag	ccg	gtg	gat	gat	gcc	gca	451
Phe	Thr	Ala	Ala	His	Thr	Trp	Ala	Phe	Glu	Pro	Val	Asp	Asp	Ala	Ala	
			105					110					115			
ttc	cct	gcg	gtg	cag	ctg	gct	agg	cac	gtc	gca	aag	caa	aaa	ggc	acg	499
Phe	Pro	Ala	Val	Gln	Leu	Ala	Arg	His	Val	Ala	Lys	Gln	Lys	Gly	Thr	
		120					125					130				

**00000000000000000000000000000000**



```
<210> 402
<211> 205
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 402															
Met	Trp	Glu	Val	Thr	Pro	Glu	Gln	Ala	Ala	Ala	His	Pro	Thr	Trp	Ala
1				5					10					15	
Met	Gly	Gln	Met	Asn	Thr	Leu	Asn	Ser	Ala	Thr	Leu	Ile	Asn	Lys	Gly
			20					25					30		
Leu	Glu	Leu	Ile	Glu	Ala	Thr	Leu	Leu	Phe	Glu	Thr	Asp	Ala	Asp	Leu
		35					40					45			
Ile	Asp	Val	Thr	Val	His	Pro	Gln	Ser	Ile	Ile	His	Ser	Met	Ile	Thr
	50					55					60				
Phe	Thr	Asp	Gly	Ala	Thr	Ile	Ala	Gln	Ala	Ser	Pro	Pro	Ser	Met	Lys
65					70					75					80
Leu	Pro	Ile	Ala	Leu	Ala	Leu	Asp	Trp	Pro	His	Arg	Val	Pro	Lys	Ala
				85					90					95	
Gln	Pro	Ala	Leu	Asp	Phe	Thr	Ala	Ala	His	Thr	Trp	Ala	Phe	Glu	Pro
			100					105					110		
Val	Asp	Asp	Ala	Ala	Phe	Pro	Ala	Val	Gln	Leu	Ala	Arg	His	Val	Ala
		115					120					125			
Lys	Gln	Lys	Gly	Thr	Tyr	Pro	Ala	Val	Tyr	Asn	Ala	Ala	Asn	Glu	Glu
	130					135					140				
Ala	Ala	Glu	Ala	Phe	Leu	Arg	Gly	Arg	Ile	Lys	Phe	Pro	Gln	Ile	Val
145					150					155					160
Asp	Val	Val	Asp	Glu	Val	Leu	Gln	Gly	Ala	Ser	Gln	Phe	Ala	Gly	Val
				165					170					175	
Ala	Ser	His	Val	Asp	Asp	Ile	Leu	Ala	Thr	Glu	Ser	Glu	Ala	Arg	Ala



<400> 403																
gcaggtgcac atttgttttg tcacctgcac aaaagtgtcg ccagcccgat acttgtacaa																60
ccgtccgcat ccgagaagca aaggtgtctg actcgcgcca atg gga att ctg aac																115
Met Gly Ile Leu Asn																5
1																
agt att tca aca cct gct gac tta aag gcc ctt aat gat gag gat ttg																163
Ser Ile Ser Thr Pro Ala Asp Leu Lys Ala Leu Asn Asp Glu Asp Leu																20
10 15																
gac gct ctt gcc aaa gaa atc cga act ttc ctg gtc gat aaa gtc gca																211
Asp Ala Leu Ala Lys Glu Ile Arg Thr Phe Leu Val Asp Lys Val Ala																35
25 30																
gca act ggt ggc cac tta ggt cca aat ttg ggc gta gtg gaa tta acc																259
Ala Thr Gly Gly His Leu Gly Pro Asn Leu Gly Val Val Glu Leu Thr																50
40 45																
atc ggt ctt cat cga gtt ttc gat tcg cct caa gac ccg atc atc ttt																307
Ile Gly Leu His Arg Val Phe Asp Ser Pro Gln Asp Pro Ile Ile Phe																65
55 60																
gat act tct cac cag tcc tat gtg cat aag atc ctg acg ggt cgc gct																355
Asp Thr Ser His Gln Ser Tyr Val His Lys Ile Leu Thr Gly Arg Ala																85
70 75 80																
aaa gat ttt gat tct ttg cgt caa aaa gat ggc ctt tct ggt tac acc																403
Lys Asp Phe Asp Ser Leu Arg Gln Lys Asp Gly Leu Ser Gly Tyr Thr																100
90 95																
tgc cgt gct gaa agt gag cac gat tgg act gag tct tcg cat gct tcg																451
Cys Arg Ala Glu Ser Glu His Asp Trp Thr Glu Ser Ser His Ala Ser																115
105 110																
gcg gcc ttg tct tat gcg gat ggt ttg tct aaa gcc aag cag ttg gat																499
Ala Ala Leu Ser Tyr Ala Asp Gly Leu Ser Lys Ala Lys Gln Leu Asp																125
120 125 130																
ggc gat acc acg cat agt gtg gtt gct gtc gtt ggt gat ggc gct cta																547
Gly Asp Thr Thr His Ser Val Val Ala Val Val Gly Asp Gly Ala Leu																145
135 140 145																
act ggc ggc atg tgt tgg gaa gca ctg aac aat att gct gct ggt aaa																595
Thr Gly Gly Met Cys Trp Glu Ala Leu Asn Asn Ile Ala Ala Gly Lys																

**THE UNIVERSITY OF CHICAGO**



150					155					160					165	
gac	cgc	aaa	gtt	gtt	gtc	gta	gtc	aat	gac	aat	ggc	cgg	agt	tat	tct	643
Asp	Arg	Lys	Val	Val	Val	Val	Val	Asn	Asp	Asn	Gly	Arg	Ser	Tyr	Ser	
			170						175					180		
cca	acc	att	ggc	gga	ttt	gcg	gaa	aac	ctt	gcg	ggc	ctt	cgc	atg	cag	691
Pro	Thr	Ile	Gly	Gly	Phe	Ala	Glu	Asn	Leu	Ala	Gly	Leu	Arg	Met	Gln	
			185					190					195			
cct	ttc	tat	gat	cgc	ttc	atg	gaa	aag	ggc	aag	acg	tcc	ctg	aaa	tcc	739
Pro	Phe	Tyr	Asp	Arg	Phe	Met	Glu	Lys	Gly	Lys	Thr	Ser	Leu	Lys	Ser	
		200					205					210				
atg	ggg	tgg	gta	ggg	gag	cgt	act	ttt	gaa	gcg	ctc	cat	gca	ttt	aaa	787
Met	Gly	Trp	Val	Gly	Glu	Arg	Thr	Phe	Glu	Ala	Leu	His	Ala	Phe	Lys	
	215					220					225					
gaa	ggt	gtg	aag	agc	acc	gtc	att	ccc	acc	gaa	atg	ttc	cct	gaa	ctg	835
Glu	Gly	Val	Lys	Ser	Thr	Val	Ile	Pro	Thr	Glu	Met	Phe	Pro	Glu	Leu	
230					235					240					245	
ggc	atg	aaa	tac	gtg	ggt	ccg	gtt	gat	gga	cat	aac	caa	aaa	gct	gtc	883
Gly	Met	Lys	Tyr	Val	Gly	Pro	Val	Asp	Gly	His	Asn	Gln	Lys	Ala	Val	
			250					255						260		
gac	aat	gcg	ctg	aaa	tac	gct	cat	gat	tat	gat	ggc	ccc	atc	atc	gtg	931
Asp	Asn	Ala	Leu	Lys	Tyr	Ala	His	Asp	Tyr	Asp	Gly	Pro	Ile	Ile	Val	
			265					270					275			
cac	atg	gtc	acc	gaa	aag	ggt	cgt	ggt	tac	gcg	cct	gct	gag	cag	gat	979
His	Met	Val	Thr	Glu	Lys	Gly	Arg	Gly	Tyr	Ala	Pro	Ala	Glu	Gln	Asp	
		280					285					290				
ttg	gac	gaa	ttg	atg	cac	tcc	acg	ggc	gtc	atc	gat	ccg	ctc	aca	gga	1027
Leu	Asp	Glu	Leu	Met	His	Ser	Thr	Gly	Val	Ile	Asp	Pro	Leu	Thr	Gly	
	295					300					305					
gct	cct	aaa	tct	gca	tca	aag	ccc	ggt	tgg	acc	tct	gtg	ttc	agc	gat	1075
Ala	Pro	Lys	Ser	Ala	Ser	Lys	Pro	Gly	Trp	Thr	Ser	Val	Phe	Ser	Asp	
310					315					320					325	
gag	ctg	gtc	aag	att	ggt	gcg	cag	aat	gaa	aac	gtt	gtt	gcc	atc	acc	1123
Glu	Leu	Val	Lys	Ile	Gly	Ala	Gln	Asn	Glu	Asn	Val	Val	Ala	Ile	Thr	
			330					335						340		
gcc	gcg	atg	gca	ggt	cct	acc	ggt	ctg	tcc	aag	ttc	gaa	gcc	aat	ttc	1171
Ala	Ala	Met	Ala	Gly	Pro	Thr	Gly	Leu	Ser	Lys	Phe	Glu	Ala	Asn	Phe	
			345					350					355			
ccc	aac	cga	ttc	ttt	gat	gtc	ggc	att	gct	gag	cag	cac	gcg	gta	act	1219
Pro	Asn	Arg	Phe	Phe	Asp	Val	Gly	Ile	Ala	Glu	Gln	His	Ala	Val	Thr	
		360					365					370				
tct	gcc	gca	ggc	ctc	gca	ttg	ggt	gga	aaa	cac	cct	gtg	gtg	gct	att	1267
Ser	Ala	Ala	Gly	Leu	Ala	Leu	Gly	Gly	Lys	His	Pro	Val	Val	Ala	Ile	
	375					380					385					
tac	tcc	acg	ttc	ttg	aac	cgc	gct	ttt	gat	cag	ctg	ctc	atg	gat	gtg	1315
Tyr	Ser	Thr	Phe	Leu	Asn	Arg	Ala	Phe	Asp	Gln	Leu	Leu	Met	Asp	Val	
390					395					400					405	

002290 04220650



ggc atg ctc aac cag cct gtt act ttg gtg ctt gat cgc tca ggt gtc 1363  
 Gly Met Leu Asn Gln Pro Val Thr Leu Val Leu Asp Arg Ser Gly Val  
 410 415 420

acg ggt tcg gat gga gcg agc cac aat ggc gtc tgg gat atg gcg ctg 1411  
 Thr Gly Ser Asp Gly Ala Ser His Asn Gly Val Trp Asp Met Ala Leu  
 425 430 435

acc tcg atc gtt cca ggc gtg cag gtg gcg gca cca cgt gat gag gat 1459  
 Thr Ser Ile Val Pro Gly Val Gln Val Ala Ala Pro Arg Asp Glu Asp  
 440 445 450

tcc ttg cgt gag ctg ctc aat gag gct att tcc atc gat gat ggc ccc 1507  
 Ser Leu Arg Glu Leu Leu Asn Glu Ala Ile Ser Ile Asp Asp Gly Pro  
 455 460 465

aca gtt gtg cgt ttc ccc aag ggc gac ttg cca act cca att gtt gct 1555  
 Thr Val Val Arg Phe Pro Lys Gly Asp Leu Pro Thr Pro Ile Val Ala  
 470 475 480 485

atc gac acc ttg gaa gac ggc gtg gat gtc ctc gca tat gaa gac gcc 1603  
 Ile Asp Thr Leu Glu Asp Gly Val Asp Val Leu Ala Tyr Glu Asp Ala  
 490 495 500

act gac gtt gaa tca acc gac gat gcg cca tca gtt ctc atc att gcg 1651  
 Thr Asp Val Glu Ser Thr Asp Asp Ala Pro Ser Val Leu Ile Ile Ala  
 505 510 515

gta ggc gag cgc gca act gtt gca ctt gac gtt gct tcc agg att aaa 1699  
 Val Gly Glu Arg Ala Thr Val Ala Leu Asp Val Ala Ser Arg Ile Lys  
 520 525 530

cag cac ggc gtg aac gtc acg gtt gtt gac ccc cgc tgg att gtc ccc 1747  
 Gln His Gly Val Asn Val Thr Val Val Asp Pro Arg Trp Ile Val Pro  
 535 540 545

atc ccg cag tcc ttg gtc gcg ctg tct gat gat cat gac ctc gtg atc 1795  
 Ile Pro Gln Ser Leu Val Ala Leu Ser Asp Asp His Asp Leu Val Ile  
 550 555 560 565

acc atc gaa gac ggc gtc atc cac ggc ggc gtg gga tcc ttg ctc tct 1843  
 Thr Ile Glu Asp Gly Val Ile His Gly Gly Val Gly Ser Leu Leu Ser  
 570 575 580

gat gcg ctt aac gcc tct gag gtg gat acc cct cgc cga caa atc gcc 1891  
 Asp Ala Leu Asn Ala Ser Glu Val Asp Thr Pro Arg Arg Gln Ile Ala  
 585 590 595

gtg ccc cag aag tac ctg gat cac gcg tcc cgc aat gaa gtg ctc gcc 1939  
 Val Pro Gln Lys Tyr Leu Asp His Ala Ser Arg Asn Glu Val Leu Ala  
 600 605 610

gat tat ggc ctc gac gcc gac ggc att gaa acc act gtt gtt gga tgg 1987  
 Asp Tyr Gly Leu Asp Ala Asp Gly Ile Glu Thr Thr Val Val Gly Trp  
 615 620 625

ctg gat tcc ctg ttc ggg gaa taaaaccctg cttatcgacg ccg 2031  
 Leu Asp Ser Leu Phe Gly Glu  
 630 635

00E290"0420960



<400> 404															
Met 1	Gly	Ile	Leu	Asn 5	Ser	Ile	Ser	Thr	Pro 10	Ala	Asp	Leu	Lys	Ala 15	Leu
Asn	Asp	Glu	Asp 20	Leu	Asp	Ala	Leu	Ala 25	Lys	Glu	Ile	Arg	Thr 30	Phe	Leu
Val	Asp	Lys 35	Val	Ala	Ala	Thr	Gly 40	Gly	His	Leu	Gly	Pro 45	Asn	Leu	Gly
Val	Val 50	Glu	Leu	Thr	Ile	Gly 55	Leu	His	Arg	Val	Phe 60	Asp	Ser	Pro	Gln
Asp 65	Pro	Ile	Ile	Phe	Asp 70	Thr	Ser	His	Gln	Ser 75	Tyr	Val	His	Lys	Ile 80
Leu	Thr	Gly	Arg	Ala 85	Lys	Asp	Phe	Asp	Ser 90	Leu	Arg	Gln	Lys	Asp 95	Gly
Leu	Ser	Gly	Tyr 100	Thr	Cys	Arg	Ala	Glu 105	Ser	Glu	His	Asp	Trp 110	Thr	Glu
Ser	Ser	His 115	Ala	Ser	Ala	Ala	Leu 120	Ser	Tyr	Ala	Asp	Gly 125	Leu	Ser	Lys
Ala	Lys 130	Gln	Leu	Asp	Gly	Asp 135	Thr	Thr	His	Ser	Val 140	Val	Ala	Val	Val
Gly 145	Asp	Gly	Ala	Leu	Thr 150	Gly	Gly	Met	Cys	Trp 155	Glu	Ala	Leu	Asn	Asn 160
Ile	Ala	Ala	Gly	Lys 165	Asp	Arg	Lys	Val	Val 170	Val	Val	Val	Asn	Asp 175	Asn
Gly	Arg	Ser	Tyr 180	Ser	Pro	Thr	Ile	Gly 185	Gly	Phe	Ala	Glu	Asn 190	Leu	Ala
Gly	Leu	Arg 195	Met	Gln	Pro	Phe	Tyr 200	Asp	Arg	Phe	Met	Glu 205	Lys	Gly	Lys
Thr 210	Ser	Leu	Lys	Ser	Met	Gly 215	Trp	Val	Gly	Glu	Arg 220	Thr	Phe	Glu	Ala
Leu 225	His	Ala	Phe	Lys	Glu 230	Gly	Val	Lys	Ser	Thr 235	Val	Ile	Pro	Thr	Glu 240
Met	Phe	Pro	Glu	Leu 245	Gly	Met	Lys	Tyr	Val 250	Gly	Pro	Val	Asp	Gly 255	His
Asn	Gln	Lys	Ala 260	Val	Asp	Asn	Ala	Leu 265	Lys	Tyr	Ala	His	Asp 270	Tyr	Asp
Gly	Pro	Ile 275	Ile	Val	His	Met	Val 280	Thr	Glu	Lys	Gly	Arg 285	Gly	Tyr	Ala



Pro Ala Glu Gln Asp Leu Asp Glu Leu Met His Ser Thr Gly Val Ile  
 290 295 300  
 Asp Pro Leu Thr Gly Ala Pro Lys Ser Ala Ser Lys Pro Gly Trp Thr  
 305 310 315 320  
 Ser Val Phe Ser Asp Glu Leu Val Lys Ile Gly Ala Gln Asn Glu Asn  
 325 330 335  
 Val Val Ala Ile Thr Ala Ala Met Ala Gly Pro Thr Gly Leu Ser Lys  
 340 345 350  
 Phe Glu Ala Asn Phe Pro Asn Arg Phe Phe Asp Val Gly Ile Ala Glu  
 355 360 365  
 Gln His Ala Val Thr Ser Ala Ala Gly Leu Ala Leu Gly Gly Lys His  
 370 375 380  
 Pro Val Val Ala Ile Tyr Ser Thr Phe Leu Asn Arg Ala Phe Asp Gln  
 385 390 395 400  
 Leu Leu Met Asp Val Gly Met Leu Asn Gln Pro Val Thr Leu Val Leu  
 405 410 415  
 Asp Arg Ser Gly Val Thr Gly Ser Asp Gly Ala Ser His Asn Gly Val  
 420 425 430  
 Trp Asp Met Ala Leu Thr Ser Ile Val Pro Gly Val Gln Val Ala Ala  
 435 440 445  
 Pro Arg Asp Glu Asp Ser Leu Arg Glu Leu Leu Asn Glu Ala Ile Ser  
 450 455 460  
 Ile Asp Asp Gly Pro Thr Val Val Arg Phe Pro Lys Gly Asp Leu Pro  
 465 470 475 480  
 Thr Pro Ile Val Ala Ile Asp Thr Leu Glu Asp Gly Val Asp Val Leu  
 485 490 495  
 Ala Tyr Glu Asp Ala Thr Asp Val Glu Ser Thr Asp Asp Ala Pro Ser  
 500 505 510  
 Val Leu Ile Ile Ala Val Gly Glu Arg Ala Thr Val Ala Leu Asp Val  
 515 520 525  
 Ala Ser Arg Ile Lys Gln His Gly Val Asn Val Thr Val Val Asp Pro  
 530 535 540  
 Arg Trp Ile Val Pro Ile Pro Gln Ser Leu Val Ala Leu Ser Asp Asp  
 545 550 555 560  
 His Asp Leu Val Ile Thr Ile Glu Asp Gly Val Ile His Gly Gly Val  
 565 570 575  
 Gly Ser Leu Leu Ser Asp Ala Leu Asn Ala Ser Glu Val Asp Thr Pro  
 580 585 590  
 Arg Arg Gln Ile Ala Val Pro Gln Lys Tyr Leu Asp His Ala Ser Arg  
 595 600 605  
 Asn Glu Val Leu Ala Asp Tyr Gly Leu Asp Ala Asp Gly Ile Glu Thr

002290-0420960



```
<210> 405
<211> 1061
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1038)
<223> FRXA01562
```

<400> 405																
gag	cag	gat	ttg	gac	gaa	ttg	atg	cac	tcc	acg	ggc	gtc	atc	gat	ccg	48
Glu	Gln	Asp	Leu	Asp	Glu	Leu	Met	His	Ser	Thr	Gly	Val	Ile	Asp	Pro	
1				5					10					15		
ctc	aca	gga	gct	cct	aaa	tct	gca	tca	aag	ccc	ggg	tgg	acc	tct	gtg	96
Leu	Thr	Gly	Ala	Pro	Lys	Ser	Ala	Ser	Lys	Pro	Gly	Trp	Thr	Ser	Val	
			20					25					30			
ttc	agc	gat	gag	ctg	gtc	aag	att	ggg	gcg	cag	aat	gaa	aac	gtt	gtt	144
Phe	Ser	Asp	Glu	Leu	Val	Lys	Ile	Gly	Ala	Gln	Asn	Glu	Asn	Val	Val	
		35					40					45				
gcc	atc	acc	gcc	gcg	atg	gca	ggg	cct	acc	ggg	ctg	tcc	aag	ttc	gaa	192
Ala	Ile	Thr	Ala	Ala	Met	Ala	Gly	Pro	Thr	Gly	Leu	Ser	Lys	Phe	Glu	
	50					55					60					
gcc	aat	ttc	ccc	aac	cga	ttc	ttt	gat	gtc	ggc	att	gct	gag	cag	cac	240
Ala	Asn	Phe	Pro	Asn	Arg	Phe	Phe	Asp	Val	Gly	Ile	Ala	Glu	Gln	His	
65					70					75					80	
gcg	gta	act	tct	gcc	gca	ggc	ctc	gca	ttg	ggg	gga	aaa	cac	cct	gtg	288
Ala	Val	Thr	Ser	Ala	Ala	Gly	Leu	Ala	Leu	Gly	Gly	Lys	His	Pro	Val	
				85					90					95		
gtg	gct	att	tac	tcc	acg	ttc	ttg	aac	cgc	gct	ttt	gat	cag	ctg	ctc	336
Val	Ala	Ile	Tyr	Ser	Thr	Phe	Leu	Asn	Arg	Ala	Phe	Asp	Gln	Leu	Leu	
			100					105					110			
atg	gat	gtg	ggc	atg	ctc	aac	cag	cct	gtt	act	ttg	gtg	ctt	gat	cgc	384
Met	Asp	Val	Gly	Met	Leu	Asn	Gln	Pro	Val	Thr	Leu	Val	Leu	Asp	Arg	
		115					120					125				
tca	ggg	gtc	acg	ggg	tcg	gat	gga	gcg	agc	cac	aat	ggc	gtc	tgg	gat	432
Ser	Gly	Val	Thr	Gly	Ser	Asp	Gly	Ala	Ser	His	Asn	Gly	Val	Trp	Asp	
	130					135					140					
atg	gcg	ctg	acc	tcg	atc	gtt	cca	ggc	gtg	cag	gtg	gcg	gca	cca	cgt	480
Met	Ala	Leu	Thr	Ser	Ile	Val	Pro	Gly	Val	Gln	Val	Ala	Ala	Pro	Arg	
145					150					155					160	
gat	gag	gat	tcc	ttg	cgt	gag	ctg	ctc	aat	gag	gct	att	tcc	atc	gat	528
Asp	Glu	Asp	Ser	Leu	Arg	Glu	Leu	Leu	Asn	Glu	Ala	Ile	Ser	Ile	Asp	
				165					170					175		



gat ggc ccc aca gtt gtg cgt ttc ccc aag ggc gac ttg cca act cca 576  
 Asp Gly Pro Thr Val Val Arg Phe Pro Lys Gly Asp Leu Pro Thr Pro  
 180 185 190

att gtt gct atc gac acc ttg gaa gac ggc gtg gat gtc ctc gca tat 624  
 Ile Val Ala Ile Asp Thr Leu Glu Asp Gly Val Asp Val Leu Ala Tyr  
 195 200 205

gaa gac gcc act gac gtt gaa tca acc gac gat gcg cca tca gtt ctc 672  
 Glu Asp Ala Thr Asp Val Glu Ser Thr Asp Asp Ala Pro Ser Val Leu  
 210 215 220

atc att gcg gta ggc gag cgc gca act gtt gca ctt gac gtt gct tcc 720  
 Ile Ile Ala Val Gly Glu Arg Ala Thr Val Ala Leu Asp Val Ala Ser  
 225 230 235 240

agg att aaa cag cac ggc gtg aac gtc acg gtt gtt gac ccc cgc tgg 768  
 Arg Ile Lys Gln His Gly Val Asn Val Thr Val Val Asp Pro Arg Trp  
 245 250 255

att gtc ccc atc ccg cag tcc ttg gtc gcg ctg tct gat gat cat gac 816  
 Ile Val Pro Ile Pro Gln Ser Leu Val Ala Leu Ser Asp Asp His Asp  
 260 265 270

ctc gtg atc acc atc gaa gac ggc gtc atc cac ggc ggc gtg gga tcc 864  
 Leu Val Ile Thr Ile Glu Asp Gly Val Ile His Gly Gly Val Gly Ser  
 275 280 285

ttg ctc tct gat gcg ctt aac gcc tct gag gtg gat acc cct cgc cga 912  
 Leu Leu Ser Asp Ala Leu Asn Ala Ser Glu Val Asp Thr Pro Arg Arg  
 290 295 300

caa atc gcc gtg ccc cag aag tac ctg gat cac gcg tcc cgc aat gaa 960  
 Gln Ile Ala Val Pro Gln Lys Tyr Leu Asp His Ala Ser Arg Asn Glu  
 305 310 315 320

gtg ctc gcc gat tat ggc ctc gac gcc gac ggc att gaa acc act gtt 1008  
 Val Leu Ala Asp Tyr Gly Leu Asp Ala Asp Gly Ile Glu Thr Thr Val  
 325 330 335

gtt gga tgg ctg gat tcc ctg ttc ggg gaa taaaaccctg cttatcgacg 1058  
 Val Gly Trp Leu Asp Ser Leu Phe Gly Glu  
 340 345

ccg 1061

&lt;210&gt; 406

&lt;211&gt; 346

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 406

Glu Gln Asp Leu Asp Glu Leu Met His Ser Thr Gly Val Ile Asp Pro  
 1 5 10 15

Leu Thr Gly Ala Pro Lys Ser Ala Ser Lys Pro Gly Trp Thr Ser Val  
 20 25 30

Phe Ser Asp Glu Leu Val Lys Ile Gly Ala Gln Asn Glu Asn Val Val  
 35 40 45

09602740-062360



Ala Ile Thr Ala Ala Met Ala Gly Pro Thr Gly Leu Ser Lys Phe Glu  
 50 55 60  
 Ala Asn Phe Pro Asn Arg Phe Phe Asp Val Gly Ile Ala Glu Gln His  
 65 70 75 80  
 Ala Val Thr Ser Ala Ala Gly Leu Ala Leu Gly Gly Lys His Pro Val  
 85 90 95  
 Val Ala Ile Tyr Ser Thr Phe Leu Asn Arg Ala Phe Asp Gln Leu Leu  
 100 105 110  
 Met Asp Val Gly Met Leu Asn Gln Pro Val Thr Leu Val Leu Asp Arg  
 115 120 125  
 Ser Gly Val Thr Gly Ser Asp Gly Ala Ser His Asn Gly Val Trp Asp  
 130 135 140  
 Met Ala Leu Thr Ser Ile Val Pro Gly Val Gln Val Ala Ala Pro Arg  
 145 150 155 160  
 Asp Glu Asp Ser Leu Arg Glu Leu Leu Asn Glu Ala Ile Ser Ile Asp  
 165 170 175  
 Asp Gly Pro Thr Val Val Arg Phe Pro Lys Gly Asp Leu Pro Thr Pro  
 180 185 190  
 Ile Val Ala Ile Asp Thr Leu Glu Asp Gly Val Asp Val Leu Ala Tyr  
 195 200 205  
 Glu Asp Ala Thr Asp Val Glu Ser Thr Asp Asp Ala Pro Ser Val Leu  
 210 215 220  
 Ile Ile Ala Val Gly Glu Arg Ala Thr Val Ala Leu Asp Val Ala Ser  
 225 230 235 240  
 Arg Ile Lys Gln His Gly Val Asn Val Thr Val Val Asp Pro Arg Trp  
 245 250 255  
 Ile Val Pro Ile Pro Gln Ser Leu Val Ala Leu Ser Asp Asp His Asp  
 260 265 270  
 Leu Val Ile Thr Ile Glu Asp Gly Val Ile His Gly Gly Val Gly Ser  
 275 280 285  
 Leu Leu Ser Asp Ala Leu Asn Ala Ser Glu Val Asp Thr Pro Arg Arg  
 290 295 300  
 Gln Ile Ala Val Pro Gln Lys Tyr Leu Asp His Ala Ser Arg Asn Glu  
 305 310 315 320  
 Val Leu Ala Asp Tyr Gly Leu Asp Ala Asp Gly Ile Glu Thr Thr Val  
 325 330 335  
 Val Gly Trp Leu Asp Ser Leu Phe Gly Glu  
 340 345

&lt;210&gt; 407

&lt;211&gt; 703

002290"0420960



<213> Corynebacterium glutamicum

<223> FRXA01705

gcaggtgcac atttgttttg tcacctgcac aaaagtgtcg ccagcccgat acttgtacaa 60

cca acc att ggc gga ttt gcg gaa aac ctt gcg ggc ctt cgc atg cag 691  
Pro Thr Ile Gly Gly Phe Ala Glu Asn Leu Ala Gly Leu Arg Met Gln

**060708Z JUL 90**



```
<210> 408
<211> 201
<212> PRT
<213> Corynebacterium glutamicum
```

```
<210> 409
<211> 2241
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(2218)
```

**SECRET**



<400> 409

066070-086070



gac ttc ctg ctc atc aac ccc atg cac gct gca gag ccg ctg cct cct	787
Asp Phe Leu Leu Ile Asn Pro Met His Ala Ala Glu Pro Leu Pro Pro	
215 220 225	
act gag gac tct cct tat ctg ccc aca acc agg cgc ttt atc aac ccg	835
Thr Glu Asp Ser Pro Tyr Leu Pro Thr Thr Arg Arg Phe Ile Asn Pro	
230 235 240 245	
atc tac att ccg gta gaa gat att ccg gag ttt aat cag ctt gag att	883
Ile Tyr Ile Arg Val Glu Asp Ile Pro Glu Phe Asn Gln Leu Glu Ile	
250 255 260	
gat cta cgc gat gat atc gca gag atg gct gcg gaa ttc cgc gaa cgc	931
Asp Leu Arg Asp Asp Ile Ala Glu Met Ala Ala Glu Phe Arg Glu Arg	
265 270 275	
aat ctg acc tca gac atc att gag cgc aat gac gtc tac gct gca aag	979
Asn Leu Thr Ser Asp Ile Ile Glu Arg Asn Asp Val Tyr Ala Ala Lys	
280 285 290	
ctt caa gtg ctg cgc gcc att ttt gaa atg cct cgt tcc agc gaa cgt	1027
Leu Gln Val Leu Arg Ala Ile Phe Glu Met Pro Arg Ser Ser Glu Arg	
295 300 305	
gaa gcc aac ttt gtc tcc ttc gtg caa cgc gaa ggc caa ggt ctt att	1075
Glu Ala Asn Phe Val Ser Phe Val Gln Arg Glu Gly Gln Gly Leu Ile	
310 315 320 325	
gat ttc gcc acc tgg tgc gcg gac cgc gaa act gca cag tct gaa tct	1123
Asp Phe Ala Thr Trp Cys Ala Asp Arg Glu Thr Ala Gln Ser Glu Ser	
330 335 340	
gtc cac gga act gag cca gac cgc gat gag ctg acc atg ttc tac atg	1171
Val His Gly Thr Glu Pro Asp Arg Glu Leu Thr Met Phe Tyr Met	
345 350 355	
tgg ttg cag tgg cta tgt gat gag cag ctg gcg gca gct caa aag cgc	1219
Trp Leu Gln Trp Leu Cys Asp Glu Gln Leu Ala Ala Ala Gln Lys Arg	
360 365 370	
gct gtc gat gcc gga atg tgc atc ggc atc atg gca gac ctg gca gtt	1267
Ala Val Asp Ala Gly Met Ser Ile Gly Ile Met Ala Asp Leu Ala Val	
375 380 385	
ggt gtg cat cca ggt ggt gct gat gcc cag aac ctc agc cac gta ctt	1315
Gly Val His Pro Gly Gly Ala Asp Ala Gln Asn Leu Ser His Val Leu	
390 395 400 405	
gct ccg gat gcg tca gtg ggc gcc cca cca gat gga tac aac cag cag	1363
Ala Pro Asp Ala Ser Val Gly Ala Pro Pro Asp Gly Tyr Asn Gln Gln	
410 415 420	
ggc caa gac tgg tcc cag cca cca tgg cat cca gtg cgt ctt gca gag	1411
Gly Gln Asp Trp Ser Gln Pro Pro Trp His Pro Val Arg Leu Ala Glu	
425 430 435	
gaa ggc tac att ccg tgg cgt aat ctg ctg cgc act gtg ctg cgt cac	1459
Glu Gly Tyr Ile Pro Trp Arg Asn Leu Leu Arg Thr Val Leu Arg His	
440 445 450	
tcc ggc gga atc cgc gtg gac cac gtt ctt ggt ttg ttc agg ctc ttt	1507

006290" 0420960



**090726Z**



695

700

705

tcagttgtgg tgg

2241

&lt;210&gt; 410

&lt;211&gt; 706

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 410

Val Thr Ala Arg Arg Phe Leu Asn Glu Leu Ala Asp Leu Tyr Gly Val  
 1 5 10 15

Ala Thr Ser Tyr Thr Asp Tyr Lys Gly Ala His Ile Glu Val Ser Asp  
 20 25 30

Asp Thr Leu Val Lys Ile Leu Arg Ala Leu Gly Val Asn Leu Asp Thr  
 35 40 45

Ser Asn Leu Pro Asn Asp Asp Ala Ile Gln Arg Gln Ile Ala Leu Phe  
 50 55 60

His Asp Arg Glu Phe Thr Arg Pro Leu Pro Pro Ser Val Val Ala Val  
 65 70 75 80

Glu Gly Asp Glu Leu Val Phe Pro Val His Val His Asp Gly Ser Pro  
 85 90 95

Ala Asp Val His Ile Glu Leu Glu Asp Gly Thr Gln Arg Asp Val Ser  
 100 105 110

Gln Val Glu Asn Trp Thr Ala Pro Arg Glu Ile Asp Gly Ile Arg Trp  
 115 120 125

Gly Glu Ala Ser Phe Lys Ile Pro Gly Asp Leu Pro Leu Gly Trp His  
 130 135 140

Lys Leu His Leu Lys Ser Asn Glu Arg Ser Ala Glu Cys Gly Leu Ile  
 145 150 155 160

Ile Thr Pro Ala Arg Leu Ser Thr Ala Asp Lys Tyr Leu Asp Ser Pro  
 165 170 175

Arg Ser Gly Val Met Ala Gln Ile Tyr Ser Val Arg Ser Thr Leu Ser  
 180 185 190

Trp Gly Met Gly Asp Phe Asn Asp Leu Gly Asn Leu Ala Ser Val Val  
 195 200 205

Ala Gln Asp Gly Ala Asp Phe Leu Leu Ile Asn Pro Met His Ala Ala  
 210 215 220

Glu Pro Leu Pro Pro Thr Glu Asp Ser Pro Tyr Leu Pro Thr Thr Arg  
 225 230 235 240

Arg Phe Ile Asn Pro Ile Tyr Ile Arg Val Glu Asp Ile Pro Glu Phe  
 245 250 255

Asn Gln Leu Glu Ile Asp Leu Arg Asp Asp Ile Ala Glu Met Ala Ala  
 260 265 270

002290-0720960







<400> 411																
aaaagatgta ttttctaaca aacttacccct cagcgtacaa atatgctgtg cccacacgct																60
attagtggca taatgtttgtg ttgtgactgc tcgcagattt																115
<div style="display: flex; justify-content: space-between;"> <div>             Leu 1           </div> <div>             Asn              Gln 5           </div> </div>																
gat ctc tac ggc gta gca act tcc tac act gat tac aaa ggt gcc cat																163
<div style="display: flex; justify-content: space-between;"> <div>             Asp 10           </div> <div>             Leu              Tyr 15           </div> <div>             Gly              Val 20           </div> </div>																
att gag gtc agc gat gac aca tta gtg aaa atc ctg cgt gct ctg ggt																211
<div style="display: flex; justify-content: space-between;"> <div>             Ile 25           </div> <div>             Glu              Val 30           </div> <div>             Ser              Asp 35           </div> </div>																
gtg aat tta gat aca agc aac ctc ccc aac gat gac gct atc caa cgc																259
<div style="display: flex; justify-content: space-between;"> <div>             Val 40           </div> <div>             Asn              Leu 45           </div> <div>             Asp              Thr 50           </div> </div>																
caa att gcc ctc ttc cat gat cga gag ttc act cgc cca ctg cct cca																307
<div style="display: flex; justify-content: space-between;"> <div>             Gln 55           </div> <div>             Ile              Ala 60           </div> <div>             Leu              Phe 65           </div> </div>																
tcg gtg gtt gca gtt gaa ggt gat gaa cta gtt ttc ccg gtg cat gtg																355
<div style="display: flex; justify-content: space-between;"> <div>             Ser 70           </div> <div>             Val              Val 75           </div> <div>             Ala              Val 80           </div> </div>																
<div style="display: flex; justify-content: space-between;"> <div>             Gly 85           </div> <div>             Asp              Glu 90           </div> <div>             Val              Phe 95           </div> </div>																

[illegible]



**Q**uestions **A**nswers



**090678** *Environ Monit Assess* 1992;25:1-10.



```

<400> 412
Leu Asn Glu Leu Ala Asp Leu Tyr Gly Val Ala Thr Ser Tyr Thr Asp
  1                      5                      10                      15

Tyr Lys Gly Ala His Ile Glu Val Ser Asp Asp Thr Leu Val Lys Ile
                20                      25                      30

Leu Arg Ala Leu Gly Val Asn Leu Asp Thr Ser Asn Leu Pro Asn Asp
      35                      40                      45

Asp Ala Ile Gln Arg Gln Ile Ala Leu Phe His Asp Arg Glu Phe Thr
    50                      55                      60

Arg Pro Leu Pro Pro Ser Val Val Ala Val Glu Gly Asp Glu Leu Val
  65                      70                      75                      80

Phe Pro Val His Val His Asp Gly Ser Pro Ala Asp Val His Ile Glu
                85                      90                      95

Leu Glu Asp Gly Thr Gln Arg Asp Val Ser Gln Val Glu Asn Trp Thr

```



100					105					110					
Ala	Pro	Arg	Glu	Ile	Asp	Gly	Ile	Arg	Trp	Gly	Glu	Ala	Ser	Phe	Lys
		115					120					125			
Ile	Pro	Gly	Asp	Leu	Pro	Leu	Gly	Trp	His	Lys	Leu	His	Leu	Lys	Ser
	130					135					140				
Asn	Glu	Arg	Ser	Ala	Glu	Cys	Gly	Leu	Ile	Ile	Thr	Pro	Ala	Arg	Leu
145					150					155					160
Ser	Thr	Ala	Asp	Lys	Tyr	Leu	Asp	Ser	Pro	Arg	Ser	Gly	Val	Met	Ala
				165					170					175	
Gln	Ile	Tyr	Ser	Val	Arg	Ser	Thr	Leu	Ser	Trp	Gly	Met	Gly	Asp	Phe
			180					185					190		
Asn	Asp	Leu	Gly	Asn	Leu	Ala	Ser	Val	Val	Ala	Gln	Asp	Gly	Ala	Asp
		195					200					205			
Phe	Leu	Leu	Ile	Asn	Pro	Met	His	Ala	Ala	Glu	Pro	Leu	Pro	Pro	Thr
	210					215					220				
Glu	Asp	Ser	Pro	Tyr	Leu	Pro	Thr	Thr	Arg	Arg	Phe	Ile	Asn	Pro	Ile
225					230					235					240
Tyr	Ile	Arg	Val	Glu	Asp	Ile	Pro	Glu	Phe	Asn	Gln	Leu	Glu	Ile	Asp
				245					250					255	
Leu	Arg	Asp	Asp	Ile	Ala	Glu	Met	Ala	Ala	Glu	Phe	Arg	Glu	Arg	Asn
			260					265					270		
Leu	Thr	Ser	Asp	Ile	Ile	Glu	Arg	Asn	Asp	Val	Tyr	Ala	Ala	Lys	Leu
		275					280					285			
Gln	Val	Leu	Arg	Ala	Ile	Phe	Glu	Met	Pro	Arg	Ser	Ser	Glu	Arg	Glu
	290					295					300				
Ala	Asn	Phe	Val	Ser	Phe	Val	Gln	Arg	Glu	Gly	Gln	Gly	Leu	Ile	Asp
305					310					315					320
Phe	Ala	Thr	Trp	Cys	Ala	Asp	Arg	Glu	Thr	Ala	Gln	Ser	Glu	Ser	Val
				325					330					335	
His	Gly	Thr	Glu	Pro	Asp	Arg	Asp	Glu	Leu	Thr	Met	Phe	Tyr	Met	Trp
			340					345					350		
Leu	Gln	Trp	Leu	Cys	Asp	Glu	Gln	Leu	Ala	Ala	Ala	Gln	Lys	Arg	Ala
		355					360					365			
Val	Asp	Ala	Gly	Met	Ser	Ile	Gly	Ile	Met	Ala	Asp	Leu	Ala	Val	Gly
	370					375					380				
Val	His	Pro	Gly	Gly	Ala	Asp	Ala	Gln	Asn	Leu	Ser	His	Val	Leu	Ala
385					390					395					400
Pro	Asp	Ala	Ser	Val	Gly	Ala	Pro	Pro	Asp	Gly	Tyr	Asn	Gln	Gln	Gly
				405					410					415	
Gln	Asp	Trp	Ser	Gln	Pro	Pro	Trp	His	Pro	Val	Arg	Leu	Ala	Glu	Glu
			420					425					430		

002290"0420960



```
<220>
<221> CDS
<222> (101)..(1264)
```



<400> 413

gtcctatgct tgctggaagg aagcaaataa cctcagaaag atg gca gaa gtg gtg 115  
Met Ala Glu Val Val  
1 5

cat tat caa gaa aat gca ggt caa gca gtt aaa aaa att gaa gga aga 163  
His Tyr Gln Glu Asn Ala Gly Gln Ala Val Lys Lys Ile Glu Gly Arg  
10 15 20

att gtt acc ccc cac ggg gtg att gat ggc ttt ctc caa ctc gaa aac 211  
Ile Val Thr Pro His Gly Val Ile Asp Gly Phe Leu Gln Leu Glu Asn  
25 30 35

ggc atc atc acg gaa ctc tct gga gaa cca gca cct aaa aac gca gga 259  
Gly Ile Ile Thr Glu Leu Ser Gly Glu Pro Ala Pro Lys Asn Ala Gly  
40 45 50

ttc cac ccc gaa ctc ccc acg att gtt ccc agt ttt att gat ctt cat 307  
Phe His Pro Glu Leu Pro Thr Ile Val Pro Ser Phe Ile Asp Leu His  
55 60 65

aat cac ggt gga aac ggt ggc gcg ttt cct acg gga acg cag gac cag 355  
Asn His Gly Gly Asn Gly Gly Ala Phe Pro Thr Gly Thr Gln Asp Gln  
70 75 80 85

gcg agg aat gcc gcg cag tat cac cgc gaa cat ggc acg acc gtg atg 403  
Ala Arg Asn Ala Ala Gln Tyr His Arg Glu His Gly Thr Thr Val Met  
90 95 100

```

ttg gca agc atg gtt tcg gcg ccg gct gac gca ctg gca gcg cag gtg    451
Leu Ala Ser Met Val Ser Ala Pro Ala Asp Ala Leu Ala Ala Gln Val
      105                      110                      115

```

gaa aac ctt att ccc ttg tgt gaa gag ggc ctg ctg tgc ggc att cac 499  
Glu Asn Leu Ile Pro Leu Cys Glu Glu Gly Leu Leu Cys Gly Ile His  
120 125 130

ctc gag ggt cct ttc atc aac gca tgc cgt tgt ggt gct caa aac ccg 547  
Leu Glu Gly Pro Phe Ile Asn Ala Cys Arg Cys Gly Ala Gln Asn Pro  
135 140 145

gat ttt att ttt ccc ggc aac cca aca gat ctt gcc cag gtg atc cat 595  
Asp Phe Ile Phe Pro Gly Asn Pro Thr Asp Leu Ala Gln Val Ile His  
150 155 160 165

gcg gga aaa ggt tgg atc aaa tcg atc aca gta gcg ccg gaa act gac 643  
Ala Gly Lys Gly Trp Ile Lys Ser Ile Thr Val Ala Pro Glu Thr Asp  
170 175 180

aat ctt act gag ctt ctc gat ctc tgc gca gcg cac cac atc att gct 691  
Asn Leu Thr Glu Leu Leu Asp Leu Cys Ala Ala His His Ile Ile Ala  
185 190 195

tcc ttc ggg cac act gat gca gat ttt gat acc act acc agc gca att 739  
Ser Phe Gly His Thr Asp Ala Asp Phe Asp Thr Thr Thr Ser Ala Ile  
200 205 210

SECRET



gcc	ttg	gct	aaa	gag	aaa	aat	gtg	acg	gtc	acg	gct	acg	cat	ttg	ttc	787																																															
Ala	Leu	Ala	Lys	Glu	Lys	Asn	Val	Thr	Val	Thr	Ala	Thr	His	Leu	Phe																																																
215																220																225																															
aat	gcg	atg	cct	ccg	ctg	cat	cat	agg	gat	ccc	ggc	agc	gtg	ggc	gct	835																																															
Asn	Ala	Met	Pro	Pro	Leu	His	His	Arg	Asp	Pro	Gly	Ser	Val	Gly	Ala																																																
230																235																240																245															
ttg	ctt	gct	gcg	gca	cgt	gcc	ggg	gac	gca	tat	gtt	gag	ttg	atc	gcc	883																																															
Leu	Leu	Ala	Ala	Ala	Arg	Ala	Gly	Asp	Ala	Tyr	Val	Glu	Leu	Ile	Ala																																																
250																255																260																															
gac	ggc	gtg	cat	ttg	gcc	gat	gga	acg	gtc	gat	cta	gct	cgt	tcc	aac	931																																															
Asp	Gly	Val	His	Leu	Ala	Asp	Gly	Thr	Val	Asp	Leu	Ala	Arg	Ser	Asn																																																
265																270																275																															
aac	gcc	ttt	ttc	atc	acg	gac	gcc	atg	gaa	gcc	gcc	gga	atg	cca	gac	979																																															
Asn	Ala	Phe	Phe	Ile	Thr	Asp	Ala	Met	Glu	Ala	Ala	Gly	Met	Pro	Asp																																																
280																285																290																															
ggt	gag	tac	att	ttg	ggc	gtt	ttg	aac	gtc	acc	gtc	acc	gat	ggc	gtc	1027																																															
Gly	Glu	Tyr	Ile	Leu	Gly	Val	Leu	Asn	Val	Thr	Val	Thr	Asp	Gly	Val																																																
295																300																305																															
gcc	cgt	ctg	cgc	gat	ggc	ggc	gcc	atc	gcc	ggg	ggt	acc	agc	aca	cta	1075																																															
Ala	Arg	Leu	Arg	Asp	Gly	Gly	Ala	Ile	Ala	Gly	Gly	Thr	Ser	Thr	Leu																																																
310																315																320																325															
gcg	agt	cag	ttc	gtg	cac	cac	gtg	cgc	agg	ggt	atg	acg	ctt	atc	gac	1123																																															
Ala	Ser	Gln	Phe	Val	His	His	Val	Arg	Arg	Gly	Met	Thr	Leu	Ile	Asp																																																
330																335																340																															
gcg	acc	ctc	cac	acc	tca	acc	gtc	gcc	gcc	aaa	att	ctc	gga	ctt	agc	1171																																															
Ala	Thr	Leu	His	Thr	Ser	Thr	Val	Ala	Ala	Lys	Ile	Leu	Gly	Leu	Ser																																																
345																350																355																															
gat	cac	gaa	atc	gtt	aaa	tcc	aac	cct	gta	aat	ttt	gtg	gtc	ttt	gac	1219																																															
Asp	His	Glu	Ile	Val	Lys	Ser	Asn	Pro	Val	Asn	Phe	Val	Val	Phe	Asp																																																
360																365																370																															
tca	aac	ggc	cag	tta	caa	cag	gtc	cat	tta	gac	cat	caa	gta	att		1264																																															
Ser	Asn	Gly	Gln	Leu	Gln	Gln	Val	His	Leu	Asp	His	Gln	Val	Ile																																																	
375																380																385																															
taaatac																gag caaaaacttttc																ctg																1287															

```
<210> 414
<211> 388
<212> PRT
<213> Corynebacterium glutamicum
```

```

<400> 414
Met  Ala  Glu  Val  Val  His  Tyr  Gln  Glu  Asn  Ala  Gly  Gln  Ala  Val  Lys
   1              5              10              15

Lys  Ile  Glu  Gly  Arg  Ile  Val  Thr  Pro  His  Gly  Val  Ile  Asp  Gly  Phe
              20              25              30

Leu  Gln  Leu  Glu  Asn  Gly  Ile  Ile  Thr  Glu  Leu  Ser  Gly  Glu  Pro  Ala
          35              40              45

```



Pro	Lys	Asn	Ala	Gly	Phe	His	Pro	Glu	Leu	Pro	Thr	Ile	Val	Pro	Ser
50						55					60				
Phe	Ile	Asp	Leu	His	Asn	His	Gly	Gly	Asn	Gly	Gly	Ala	Phe	Pro	Thr
65					70					75					80
Gly	Thr	Gln	Asp	Gln	Ala	Arg	Asn	Ala	Ala	Gln	Tyr	His	Arg	Glu	His
				85					90					95	
Gly	Thr	Thr	Val	Met	Leu	Ala	Ser	Met	Val	Ser	Ala	Pro	Ala	Asp	Ala
			100					105					110		
Leu	Ala	Ala	Gln	Val	Glu	Asn	Leu	Ile	Pro	Leu	Cys	Glu	Glu	Gly	Leu
		115					120					125			
Leu	Cys	Gly	Ile	His	Leu	Glu	Gly	Pro	Phe	Ile	Asn	Ala	Cys	Arg	Cys
	130					135					140				
Gly	Ala	Gln	Asn	Pro	Asp	Phe	Ile	Phe	Pro	Gly	Asn	Pro	Thr	Asp	Leu
145					150					155					160
Ala	Gln	Val	Ile	His	Ala	Gly	Lys	Gly	Trp	Ile	Lys	Ser	Ile	Thr	Val
				165					170					175	
Ala	Pro	Glu	Thr	Asp	Asn	Leu	Thr	Glu	Leu	Leu	Asp	Leu	Cys	Ala	Ala
			180					185					190		
His	His	Ile	Ile	Ala	Ser	Phe	Gly	His	Thr	Asp	Ala	Asp	Phe	Asp	Thr
		195					200					205			
Thr	Thr	Ser	Ala	Ile	Ala	Leu	Ala	Lys	Glu	Lys	Asn	Val	Thr	Val	Thr
						215					220				
Ala	Thr	His	Leu	Phe	Asn	Ala	Met	Pro	Pro	Leu	His	His	Arg	Asp	Pro
225					230					235					240
Gly	Ser	Val	Gly	Ala	Leu	Leu	Ala	Ala	Ala	Arg	Ala	Gly	Asp	Ala	Tyr
				245					250					255	
Val	Glu	Leu	Ile	Ala	Asp	Gly	Val	His	Leu	Ala	Asp	Gly	Thr	Val	Asp
			260					265					270		
Leu	Ala	Arg	Ser	Asn	Asn	Ala	Phe	Phe	Ile	Thr	Asp	Ala	Met	Glu	Ala
		275					280					285			
Ala	Gly	Met	Pro	Asp	Gly	Glu	Tyr	Ile	Leu	Gly	Val	Leu	Asn	Val	Thr
		290				295					300				
Val	Thr	Asp	Gly	Val	Ala	Arg	Leu	Arg	Asp	Gly	Gly	Ala	Ile	Ala	Gly
305					310					315					320
Gly	Thr	Ser	Thr	Leu	Ala	Ser	Gln	Phe	Val	His	His	Val	Arg	Arg	Gly
				325					330					335	
Met	Thr	Leu	Ile	Asp	Ala	Thr	Leu	His	Thr	Ser	Thr	Val	Ala	Ala	Lys
			340					345					350		
Ile	Leu	Gly	Leu	Ser	Asp	His	Glu	Ile	Val	Lys	Ser	Asn	Pro	Val	Asn
		355					360					365			



Phe Val Val Phe Asp Ser Asn Gly Gln Leu Gln Gln Val His Leu Asp  
 370 375 380

His Gln Val Ile  
 385

<210> 415

<211> 1287

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1264)

<223> FRXA00043

<400> 415

aacagcaggc ctcaagtccg aagataatta acctaaatcc gtagacataa gacatcatac 60

gtcctatgct tgctggaagg aagcaaataa cctcagaaag atg gca gaa gtg gtg 115  
 Met Ala Glu Val Val  
 1 5

cat tat caa gaa aat gca ggt caa gca gtt aaa aaa att gaa gga aga 163  
 His Tyr Gln Glu Asn Ala Gly Gln Ala Val Lys Lys Ile Glu Gly Arg  
 10 15 20

att gtt acc ccc cac ggg gtg att gat ggc ttt ctc caa ctc gaa aac 211  
 Ile Val Thr Pro His Gly Val Ile Asp Gly Phe Leu Gln Leu Glu Asn  
 25 30 35

ggc atc atc acg gaa ctc tct gga gaa cca gca cct aaa aac gca gga 259  
 Gly Ile Ile Thr Glu Leu Ser Gly Glu Pro Ala Pro Lys Asn Ala Gly  
 40 45 50

ttc cac ccc gaa ctc ccc acg att gtt ccc agt ttt att gat ctt cat 307  
 Phe His Pro Glu Leu Pro Thr Ile Val Pro Ser Phe Ile Asp Leu His  
 55 60 65

aat cac ggt gga aac ggt ggc gcg ttt cct acg gga acg cag gac cag 355  
 Asn His Gly Gly Asn Gly Gly Ala Phe Pro Thr Gly Thr Gln Asp Gln  
 70 75 80 85

gcg agg aat gcc gcg cag tat cac cgc gaa cat ggc acg acc gtg atg 403  
 Ala Arg Asn Ala Ala Gln Tyr His Arg Glu His Gly Thr Thr Val Met  
 90 95 100

ttg gca agc atg gtt tcg gcg ccg gct gac gca ctg gca gcg cag gtg 451  
 Leu Ala Ser Met Val Ser Ala Pro Ala Asp Ala Leu Ala Ala Gln Val  
 105 110 115

gaa aac ctt att ccc ttg tgt gaa gag ggc ctg ctg tgc ggc att cac 499  
 Glu Asn Leu Ile Pro Leu Cys Glu Glu Gly Leu Leu Cys Gly Ile His  
 120 125 130

ctc gag ggt cct ttc atc aac gca tgc cgt tgt ggt gct caa aac ccg 547  
 Leu Glu Gly Pro Phe Ile Asn Ala Cys Arg Cys Gly Ala Gln Asn Pro  
 135 140 145

gat ttt att ttt ccc ggc aac cca aca gat ctt gcc cag gtg atc cat 595

00E290"0420960



**00000000000000000000**



<400>	416														
Met 1	Ala	Glu	Val	Val 5	His	Tyr	Gln	Glu	Asn 10	Ala	Gly	Gln	Ala	Val 15	Lys
Lys	Ile	Glu	Gly 20	Arg	Ile	Val	Thr	Pro 25	His	Gly	Val	Ile	Asp 30	Gly	Phe
Leu	Gln	Leu 35	Glu	Asn	Gly	Ile	Ile 40	Thr	Glu	Leu	Ser	Gly 45	Glu	Pro	Ala
Pro	Lys 50	Asn	Ala	Gly	Phe	His 55	Pro	Glu	Leu	Pro	Thr 60	Ile	Val	Pro	Ser
Phe 65	Ile	Asp	Leu	His	Asn 70	His	Gly	Gly	Asn	Gly 75	Gly	Ala	Phe	Pro	Thr 80
Gly	Thr	Gln	Asp	Gln 85	Ala	Arg	Asn	Ala	Ala 90	Gln	Tyr	His	Arg	Glu 95	His
Gly	Thr	Thr	Val 100	Met	Leu	Ala	Ser	Met 105	Val	Ser	Ala	Pro	Ala 110	Asp	Ala
Leu	Ala	Ala 115	Gln	Val	Glu	Asn	Leu 120	Ile	Pro	Leu	Cys	Glu 125	Glu	Gly	Leu
Leu 130	Cys	Gly	Ile	His	Leu	Glu 135	Gly	Pro	Phe	Ile	Asn 140	Ala	Cys	Arg	Cys
Gly 145	Ala	Gln	Asn	Pro	Asp 150	Phe	Ile	Phe	Pro	Gly 155	Asn	Pro	Thr	Asp	Leu 160
Ala	Gln	Val	Ile	His 165	Ala	Gly	Lys	Gly	Trp 170	Ile	Lys	Ser	Ile	Thr 175	Val
Ala	Pro	Glu	Thr 180	Asp	Asn	Leu	Thr	Glu 185	Leu	Leu	Asp	Leu	Cys 190	Ala	Ala
His	His	Ile 195	Ile	Ala	Ser	Phe	Gly 200	His	Thr	Asp	Ala	Asp 205	Phe	Asp	Thr
Thr	Thr 210	Ser	Ala	Ile	Ala	Leu 215	Ala	Lys	Glu	Lys	Asn 220	Val	Thr	Val	Thr
Ala 225	Thr	His	Leu	Phe	Asn 230	Ala	Met	Pro	Pro	Leu 235	His	His	Arg	Asp	Pro 240
Gly	Ser	Val	Gly	Ala 245	Leu	Leu	Ala	Ala	Ala 250	Arg	Ala	Gly	Asp	Ala 255	Tyr
Val	Glu	Leu	Ile 260	Ala	Asp	Gly	Val	His 265	Leu	Ala	Asp	Gly	Thr 270	Val	Asp
Leu	Ala	Arg 275	Ser	Asn	Asn	Ala	Phe 280	Phe	Ile	Thr	Asp	Ala 285	Met	Glu	Ala



aca ttg ttg gac aga ttt atc atg ttt tcc aga ggt atc cgc gcg gaa 403  
Thr Leu Leu Asp Arg Phe Ile Met Phe Ser Arg Gly Ile Arg Ala Glu

**THE UNIVERSITY OF CHICAGO**



**00000000000000000000000000000000**



[illegible]

```
<210> 418
<211> 487
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 418  
Met Met Glu Gln Asp Leu Ser Tyr Arg Glu Ile Leu Pro Leu Asn Ala  
1 5 10 15  
Ser Glu Glu Lys Lys Lys Ala Ala Leu Ile Asp Ala Ile Glu Gly Leu  
20 25 30  
Arg Val Arg Asp Pro Leu Leu Ser Ala Ser Ile Ala Phe Thr Arg Gly  
35 40 45  
Gln Lys Val Ala Phe Ile Ala Val Val Val Gly Phe Ile Leu Met Leu  
50 55 60  
Ile Phe Ala Arg Gln Ala Ala Leu Ile Gly Leu Ser Ala Thr Cys Thr



65					70					75					80
Phe	Met	Tyr	Leu	Ile	Thr	Leu	Leu	Asp	Arg	Phe	Ile	Met	Phe	Ser	Arg
				85					90					95	
Gly	Ile	Arg	Ala	Glu	Ser	Ile	Ile	Gln	Val	Ser	Asp	Glu	Asp	Ala	Leu
			100					105					110		
Ala	Phe	Pro	Glu	Asp	Lys	Leu	Lys	Thr	Tyr	Thr	Val	Leu	Val	Pro	Ala
		115					120					125			
Tyr	Gly	Glu	Pro	Glu	Val	Ile	Ala	Gln	Leu	Leu	Ala	Ser	Met	His	Ala
	130					135					140				
Phe	Asp	Tyr	Pro	Lys	His	Leu	Leu	Gln	Val	Leu	Leu	Met	Leu	Glu	Glu
145					150					155					160
Asp	Asp	Leu	Pro	Thr	Ile	Ala	Ala	Ala	Glu	Ala	Ala	Gly	Val	Asp	Gln
				165					170					175	
Val	Ala	Thr	Ile	Ile	Lys	Val	Pro	Pro	Ala	Gln	Pro	Arg	Thr	Lys	Pro
			180					185					190		
Lys	Ala	Cys	Asn	Tyr	Gly	Leu	His	Phe	Ala	Thr	Gly	Glu	Ile	Val	Thr
		195					200					205			
Ile	Phe	Asp	Ala	Glu	Asp	Met	Pro	Asp	Pro	Leu	Gln	Leu	Arg	Arg	Val
	210					215					220				
Val	Val	Ala	Phe	Glu	Arg	Ser	Ala	Ser	Asn	Thr	Val	Cys	Val	Gln	Ser
225					230					235					240
Arg	Leu	Ser	Tyr	Arg	Asn	Ala	Arg	Gln	Asn	Leu	Leu	Thr	Ala	Trp	Phe
				245					250					255	
Thr	Ile	Glu	Tyr	Asp	Val	Trp	Phe	Asn	Phe	Leu	Leu	Pro	Gly	Val	Met
			260					265					270		
Arg	Met	Asn	Ala	Pro	Val	Pro	Leu	Gly	Gly	Thr	Ser	Asn	His	Leu	Leu
		275					280					285			
Thr	Gly	Val	Leu	Lys	Asp	Leu	Gly	Ala	Trp	Asp	Pro	Phe	Asn	Val	Thr
	290					295					300				
Glu	Asn	Ala	Asp	Leu	Gly	Val	Pro	Ile	Ala	Ala	Lys	Gly	Tyr	Ser	Thr
305					310					315					320
Ala	Val	Leu	Asp	Ser	Val	Thr	Trp	Glu	Glu	Ala	Asn	Ser	Asp	Thr	Ile
				325					330					335	
Asn	Trp	Leu	Arg	Gln	Arg	Ser	Arg	Trp	Tyr	Lys	Gly	Tyr	Leu	Gln	Thr
			340					345					350		
Trp	Leu	Val	Tyr	Met	Arg	Arg	Pro	Lys	Trp	Leu	Val	Gln	Glu	Leu	Gly
		355					360					365			
Ile	Ile	Pro	Ala	Val	Arg	Phe	Thr	Phe	Leu	Met	Ala	Gly	Thr	Pro	Ile
	370					375					380				
Ile	Ala	Val	Leu	Asn	Leu	Leu	Phe	Trp	Tyr	Leu	Ser	Leu	Thr	Trp	Ile
385					390					395					400

00602740-062300



Leu Gly Gln Pro Gly Thr Ile Glu Gln Met Phe Pro Pro Ala Val Tyr  
 405 410 415

Tyr Pro Ala Leu Val Cys Leu Val Val Ala Asn Ala Ala Thr Ile Phe  
 420 425 430

Met Asn Leu Ile Gly Cys Arg Glu Gly Arg Asp Pro Leu Leu Leu Ile  
 435 440 445

Ala Val Leu Thr Phe Pro Leu Tyr Trp Leu Leu Met Ser Ile Ala Ala  
 450 455 460

Leu Lys Gly Thr Trp Gln Leu Ile Thr Arg Pro Ser Tyr Trp Glu Lys  
 465 470 475 480

Thr Ala His Gly Leu Glu Ala  
 485

<210> 419  
 <211> 689  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (19)..(666)  
 <223> FRXA01839

<400> 419  
 ttccctgctgc caggtgtcatg cgc atg aac gca cct gtc cca ttg ggc ggt 51  
 Met Arg Met Asn Ala Pro Val Pro Leu Gly Gly  
 1 5 10

acc tcc aac cat ctg ctc acg ggt gtc ctg aaa gat ctc ggc gcg tgg 99  
 Thr Ser Asn His Leu Leu Thr Gly Val Leu Lys Asp Leu Gly Ala Trp  
 15 20 25

gat cct ttc aat gtc aca gaa gat gcg gac ctc ggc gta cgc atc gcg 147  
 Asp Pro Phe Asn Val Thr Glu Asp Ala Asp Leu Gly Val Arg Ile Ala  
 30 35 40

gca aag gga tat tcc acc gcg gtg ttg gat tcg gtg acg tgg gag gaa 195  
 Ala Lys Gly Tyr Ser Thr Ala Val Leu Asp Ser Val Thr Trp Glu Glu  
 45 50 55

gca aac tcc gac acc atc aac tgg ttg cgc cag cgt tct cgc tgg tac 243  
 Ala Asn Ser Asp Thr Ile Asn Trp Leu Arg Gln Arg Ser Arg Trp Tyr  
 60 65 70 75

aag ggc tat ctg caa aca tgg ctt gtg tat atg cgc agg cca aag tgg 291  
 Lys Gly Tyr Leu Gln Thr Trp Leu Val Tyr Met Arg Arg Pro Lys Trp  
 80 85 90

tta gtc caa gag ctt ggc atc att cct gct gtg cgt ttt acc ttc ctc 339  
 Leu Val Gln Glu Leu Gly Ile Ile Pro Ala Val Arg Phe Thr Phe Leu  
 95 100 105

atg gca ggc acc ccg atc att gcg gtg ctc aat ctg ctc ttt tgg tac 387  
 Met Ala Gly Thr Pro Ile Ile Ala Val Leu Asn Leu Leu Phe Trp Tyr

00602740.062300



110	115	120	
ttg tcg ctc acg tgg att ctg ggc cag ccc ggc acc att gag cag atg			435
Leu Ser Leu Thr Trp Ile Leu Gly Gln Pro Gly Thr Ile Glu Gln Met			
125	130	135	
ttc cca cct gcg gtg tac tac cca gcg ttg gtg tgt ttg gtg gtg gcc			483
Phe Pro Pro Ala Val Tyr Tyr Pro Ala Leu Val Cys Leu Val Val Ala			
140	145	150	155
aat gct gcg acc atc ttt atg aat ctc att ggc tgc cgg gaa ggc cgc			531
Asn Ala Ala Thr Ile Phe Met Asn Leu Ile Gly Cys Arg Glu Gly Arg			
	160	165	170
gac ccc ttg ctg ctc atc gcg gtt ctc acg ttc ccg ctg tat tgg ctg			579
Asp Pro Leu Leu Leu Ile Ala Val Leu Thr Phe Pro Leu Tyr Trp Leu			
	175	180	185
ctc atg agc att gca gcg ttg aaa ggc acg tgg caa ttg atc acg cga			627
Leu Met Ser Ile Ala Ala Leu Lys Gly Thr Trp Gln Leu Ile Thr Arg			
	190	195	200
cca tcc tat tgg gag aaa act gcc cac gga ttg gag gcg taagcgggtgc			676
Pro Ser Tyr Trp Glu Lys Thr Ala His Gly Leu Glu Ala			
205	210	215	
ccatcgtcaa acc			689
<210> 420			
<211> 216			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 420			
Met Arg Met Asn Ala Pro Val Pro Leu Gly Gly Thr Ser Asn His Leu			
1	5	10	15
Leu Thr Gly Val Leu Lys Asp Leu Gly Ala Trp Asp Pro Phe Asn Val			
	20	25	30
Thr Glu Asp Ala Asp Leu Gly Val Arg Ile Ala Ala Lys Gly Tyr Ser			
	35	40	45
Thr Ala Val Leu Asp Ser Val Thr Trp Glu Glu Ala Asn Ser Asp Thr			
	50	55	60
Ile Asn Trp Leu Arg Gln Arg Ser Arg Trp Tyr Lys Gly Tyr Leu Gln			
	65	70	75
Thr Trp Leu Val Tyr Met Arg Arg Pro Lys Trp Leu Val Gln Glu Leu			
	85	90	95
Gly Ile Ile Pro Ala Val Arg Phe Thr Phe Leu Met Ala Gly Thr Pro			
	100	105	110
Ile Ile Ala Val Leu Asn Leu Leu Phe Trp Tyr Leu Ser Leu Thr Trp			
	115	120	125
Ile Leu Gly Gln Pro Gly Thr Ile Glu Gln Met Phe Pro Pro Ala Val			
	130	135	140

09602740.062300



Tyr Tyr Pro Ala Leu Val Cys Leu Val Val Ala Asn Ala Ala Thr Ile  
 145 150 155 160  
 Phe Met Asn Leu Ile Gly Cys Arg Glu Gly Arg Asp Pro Leu Leu Leu  
 165 170 175  
 Ile Ala Val Leu Thr Phe Pro Leu Tyr Trp Leu Leu Met Ser Ile Ala  
 180 185 190  
 Ala Leu Lys Gly Thr Trp Gln Leu Ile Thr Arg Pro Ser Tyr Trp Glu  
 195 200 205  
 Lys Thr Ala His Gly Leu Glu Ala  
 210 215

<210> 421  
 <211> 1050  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1027)  
 <223> RXA01859

<400> 421  
 tacgccccagg gtttccatat tggtaaatct aagccgattg atgaatttat agctacttat 60  
 ctcgagacga accaaaccgc tacctggggg taggaagaat atg aaa aag aag agc 115  
 Met Lys Lys Lys Ser  
 1 5  
 ttt cca atc gca aga gtc atc ggt atc ggc gtc ctt ggc atc gcc ggg 163  
 Phe Pro Ile Ala Arg Val Ile Gly Ile Gly Val Leu Gly Ile Ala Gly  
 10 15 20  
 atg gga ata ttg ttg cta tgg ctt gca gtt acc ctg tct gat cca gca 211  
 Met Gly Ile Leu Leu Leu Trp Leu Ala Val Thr Leu Ser Asp Pro Ala  
 25 30 35  
 tca ccg ggt gcc aaa gaa acc gaa gtc ttt gat agg tgg aaa gtg ctc 259  
 Ser Pro Gly Ala Lys Glu Thr Glu Val Phe Asp Arg Trp Lys Val Leu  
 40 45 50  
 ttt gat gac tat att cca cca gtc agg gta ttg gtt gct gcg att atc 307  
 Phe Asp Asp Tyr Ile Pro Pro Val Arg Val Leu Val Ala Ala Ile Ile  
 55 60 65  
 gtt gca tta att ttc gtc ttt atc gct gcc aca gtg gaa cga acc gta 355  
 Val Ala Leu Ile Phe Val Phe Ile Ala Ala Thr Val Glu Arg Thr Val  
 70 75 80 85  
 acc aac cgc tac cga agc tcc gta gac ggc gaa aga gtg cca tta gcg 403  
 Thr Asn Arg Tyr Arg Ser Ser Val Asp Gly Glu Arg Val Pro Leu Ala  
 90 95 100  
 ccg aag att gtg atg gca gaa acc cga ggg gta ttt cat gga ccg att 451  
 Pro Lys Ile Val Met Ala Glu Thr Arg Gly Val Phe His Gly Pro Ile  
 105 110 115

003290" 04/20/96 09502740.062300



<400> 422  
Met Lys Lys Lys Ser Phe Pro Ile Ala Arg Val Ile Gly Ile Gly Val  
1 5 10 15



[illegible]

<210>	423
<211>	882
<212>	DNA



$\langle 220 \rangle$ 

&lt;221&gt; CDS

<222> (101) .. (859)

<223> RXA00042

<400> 423

[illegible]



gga aaa gcc gac gcc atc cgc gga act gtg gaa ggc cca ctg acc gcc 739  
 Gly Lys Ala Asp Ala Ile Arg Gly Thr Val Glu Gly Pro Leu Thr Ala  
           200                          205                          210

atg tgc cca ggt tcc atc ctg cag atg cac aac aat gcc acc atc atc 787  
 Met Cys Pro Gly Ser Ile Leu Gln Met His Asn Asn Ala Thr Ile Ile  
           215                          220                          225

gtt gat gaa gca gca gca tcc aag ctg gaa aac gct gat cac tac cgt 835  
 Val Asp Glu Ala Ala Ala Ser Lys Leu Glu Asn Ala Asp His Tyr Arg  
           230                          235                          240                          245

ctc atg gag caa tta aag ctg cgc tagaaacaaa aaggaaagta gtg 882  
 Leu Met Glu Gln Leu Lys Leu Arg  
                                   250

<210> 424

<211> 253

<212> PRT

<213> Corynebacterium glutamicum

<400> 424

Met Asp Ile Ile Ile Cys Lys Asp Glu Gln Glu Val Gly Lys Ala Ala  
   1                          5                          10                          15

Ala Ala Leu Ile Ala Pro Phe Ala Thr Lys Gly Gly Thr Leu Gly Leu  
                           20                          25                          30

Ala Thr Gly Ser Ser Pro Leu Ser Thr Tyr Gln Glu Leu Ile Arg Met  
           35                          40                          45

Tyr Glu Ala Gly Glu Val Ser Phe Lys Asn Cys Lys Ala Phe Leu Leu  
           50                          55                          60

Asp Glu Tyr Val Gly Leu Thr Arg Asp Asp Glu Asn Ser Tyr Phe Lys  
           65                          70                          75                          80

Thr Ile Arg Lys Glu Phe Thr Asp His Ile Asp Ile Val Asp Glu Glu  
                           85                          90                          95

Val Tyr Ser Pro Asp Gly Ala Asn Pro Asp Pro Tyr Glu Ala Ala Ala  
           100                          105                          110

Glu Tyr Glu Ala Lys Ile Ala Ala Glu Ser Val Asp Val Gln Ile Leu  
           115                          120                          125

Gly Ile Gly Gly Asn Gly His Ile Ala Phe Asn Glu Pro Ser Ser Ser  
           130                          135                          140

Leu Ser Gly Leu Thr Lys Val Gln Ala Leu His Pro Lys Thr Val Glu  
           145                          150                          155                          160

Asp Asn Ala Arg Phe Phe Asn Thr Ile Glu Glu Val Pro Thr His Ala  
                           165                          170                          175

Leu Thr Gln Gly Leu Gly Thr Leu Ser Arg Ala Gln Asn Ile Val Leu  
           180                          185                          190

Val Ala Thr Gly Glu Gly Lys Ala Asp Ala Ile Arg Gly Thr Val Glu

09602740 062300



<400> 425																
ttgcgtgctg caacttaatt atggtcctcc cagctcagtg tgctgtgtgg attgtttatt																60
ctcgtccatt aagtgatcga gaaaaagttg ttgtaaagtc																115
Met Arg Met Cys Gly 1 5																
att gtt gga tat att ggc caa gcg ggc gac tcc cgt gat tac ttt gct																163
Ile Val Gly Tyr Ile Gly Gln Ala Gly Asp Ser Arg Asp Tyr Phe Ala 10 15 20																
cta gat gta gtt gtt gaa gga cta cgt cgc ctg gaa tac cgc gga tat																211
Leu Asp Val Val Val Glu Gly Leu Arg Arg Leu Glu Tyr Arg Gly Tyr 25 30 35																
gac tcc gca ggt att gct att cac gcc aat ggt gag att agc tac cga																259
Asp Ser Ala Gly Ile Ala Ile His Ala Asn Gly Glu Ile Ser Tyr Arg 40 45 50																
aag aag gcc gga aag gtt gct gca cta gat gca gaa atc gct aaa gca																307
Lys Lys Ala Gly Lys Val Ala Ala Leu Asp Ala Glu Ile Ala Lys Ala 55 60 65																
cct ctt cca gat tct att ttg gga att gga cac acc cgt tgg gca act																355
Pro Leu Pro Asp Ser Ile Leu Gly Ile Gly His Thr Arg Trp Ala Thr 70 75 80 85																
cat ggt ggc cca acc gat gtc aac gct cac ccc cac gtt gtt tcc aat																403
His Gly Gly Pro Thr Asp Val Asn Ala His Pro His Val Val Ser Asn 90 95 100																
ggc aag ctt gcc gta gta cac aac ggc atc atc gaa aac ttt gcg gaa																451
Gly Lys Leu Ala Val Val His Asn Gly Ile Ile Glu Asn Phe Ala Glu 105 110 115																
ctg cgc tct gag ctt tcc gct aag ggc tac aac ttt gta tcc gat acc																499
Leu Arg Ser Glu Leu Ser Ala Lys Gly Tyr Asn Phe Val Ser Asp Thr 120 125 130																

[illegible]



**096074-240-069**



[illegible]



<210> 426  
<211> 625  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 426

Met	Arg	Met	Cys	Gly	Ile	Val	Gly	Tyr	Ile	Gly	Gln	Ala	Gly	Asp	Ser
1				5					10					15	
Arg	Asp	Tyr	Phe	Ala	Leu	Asp	Val	Val	Val	Glu	Gly	Leu	Arg	Arg	Leu
			20					25					30		
Glu	Tyr	Arg	Gly	Tyr	Asp	Ser	Ala	Gly	Ile	Ala	Ile	His	Ala	Asn	Gly
		35					40					45			
Glu	Ile	Ser	Tyr	Arg	Lys	Lys	Ala	Gly	Lys	Val	Ala	Ala	Leu	Asp	Ala
	50					55					60				
Glu	Ile	Ala	Lys	Ala	Pro	Leu	Pro	Asp	Ser	Ile	Leu	Gly	Ile	Gly	His
65					70					75					80
Thr	Arg	Trp	Ala	Thr	His	Gly	Gly	Pro	Thr	Asp	Val	Asn	Ala	His	Pro
				85					90					95	
His	Val	Val	Ser	Asn	Gly	Lys	Leu	Ala	Val	Val	His	Asn	Gly	Ile	Ile
			100					105					110		
Glu	Asn	Phe	Ala	Glu	Leu	Arg	Ser	Glu	Leu	Ser	Ala	Lys	Gly	Tyr	Asn
		115					120					125			
Phe	Val	Ser	Asp	Thr	Asp	Thr	Glu	Val	Ala	Ala	Ser	Leu	Leu	Ala	Glu
	130					135					140				
Ile	Tyr	Asn	Thr	Gln	Ala	Asn	Gly	Asp	Leu	Thr	Leu	Ala	Met	Gln	Leu
145				150						155					160
Thr	Gly	Gln	Arg	Leu	Glu	Gly	Ala	Phe	Thr	Leu	Leu	Ala	Ile	His	Ala
				165					170					175	
Asp	His	Asp	Asp	Arg	Ile	Val	Ala	Ala	Arg	Arg	Asn	Ser	Pro	Leu	Val
			180					185					190		
Ile	Gly	Val	Gly	Glu	Gly	Glu	Asn	Phe	Leu	Gly	Ser	Asp	Val	Ser	Gly
		195					200					205			
Phe	Ile	Asp	Tyr	Thr	Arg	Lys	Ala	Val	Glu	Leu	Ala	Asn	Asp	Gln	Val
	210					215					220				
Val	Thr	Ile	Thr	Ala	Asp	Asp	Tyr	Ala	Ile	Thr	Asn	Phe	Asp	Gly	Ser
225				230						235					240
Glu	Ala	Val	Gly	Lys	Pro	Phe	Asp	Val	Glu	Trp	Asp	Ala	Ala	Ala	Ala
				245					250				255		
Glu	Lys	Gly	Gly	Phe	Gly	Ser	Phe	Met	Glu	Lys	Glu	Ile	His	Asp	Gln
			260					265					270		

**THE UNIVERSITY OF CHICAGO**



Pro Ala Ala Val Arg Asp Thr Leu Met Gly Arg Leu Asp Glu Asp Gly  
 275 280 285  
 Lys Leu Val Leu Asp Glu Leu Arg Ile Asp Glu Ala Ile Leu Arg Ser  
 290 295 300  
 Val Asp Lys Ile Val Ile Val Ala Cys Gly Thr Ala Ala Tyr Ala Gly  
 305 310 315 320  
 Gln Val Ala Arg Tyr Ala Ile Glu His Trp Cys Arg Ile Pro Thr Glu  
 325 330 335  
 Val Glu Leu Ala His Glu Phe Arg Tyr Arg Asp Pro Ile Leu Asn Glu  
 340 345 350  
 Lys Thr Leu Val Val Ala Leu Ser Gln Ser Gly Glu Thr Met Asp Thr  
 355 360 365  
 Leu Met Ala Val Arg His Ala Arg Glu Gln Gly Ala Lys Val Val Ala  
 370 375 380  
 Ile Cys Asn Thr Val Gly Ser Thr Leu Pro Arg Glu Ala Asp Ala Ser  
 385 390 395 400  
 Leu Tyr Thr Tyr Ala Gly Pro Glu Ile Ala Val Ala Ser Thr Lys Ala  
 405 410 415  
 Phe Leu Ala Gln Ile Thr Ala Ser Tyr Leu Leu Gly Leu Tyr Leu Ala  
 420 425 430  
 Gln Leu Arg Gly Asn Lys Phe Ala Asp Glu Val Ser Ser Ile Leu Asp  
 435 440 445  
 Ser Leu Arg Glu Met Pro Glu Lys Ile Gln Gln Val Ile Asp Ala Glu  
 450 455 460  
 Glu Gln Ile Lys Lys Leu Gly Gln Asp Met Ala Asp Ala Lys Ser Val  
 465 470 475 480  
 Leu Phe Leu Gly Arg His Val Gly Phe Pro Val Ala Leu Glu Gly Ala  
 485 490 495  
 Leu Lys Leu Lys Glu Ile Ala Tyr Leu His Ala Glu Gly Phe Ala Ala  
 500 505 510  
 Gly Glu Leu Lys His Gly Pro Ile Ala Leu Val Glu Glu Gly Gln Pro  
 515 520 525  
 Ile Phe Val Ile Val Pro Ser Pro Arg Gly Arg Asp Ser Leu His Ser  
 530 535 540  
 Lys Val Val Ser Asn Ile Gln Glu Ile Arg Ala Arg Gly Ala Val Thr  
 545 550 555 560  
 Ile Val Ile Ala Glu Glu Gly Asp Glu Ala Val Asn Asp Tyr Ala Asn  
 565 570 575  
 Phe Ile Ile Arg Ile Pro Gln Ala Pro Thr Leu Met Gln Pro Leu Leu  
 580 585 590

002290" 04220960



Glu  
625

```
<220>  
<221> CDS  
<222> (1) .. (666)  
<223> RXN03179
```

<400> 427																
gct	cgt	gag	gca	tgg	cgc	att	ttc	atg	tcc	cac	tgg	gat	ctc	tac	gca	48
Ala	Arg	Glu	Ala	Trp	Arg	Ile	Phe	Met	Ser	His	Trp	Asp	Leu	Tyr	Ala	
1				5					10					15		
gga	acc	gca	act	ggc	tac	tgg	gtg	gag	cag	gaa	ttt	gag	cac	gtt	ttc	96
Gly	Thr	Ala	Thr	Gly	Tyr	Trp	Val	Glu	Gln	Glu	Phe	Glu	His	Val	Phe	
			20					25					30			
ggc	atc	aac	gcg	gag	cgc	ctg	aat	gtt	ggc	acc	cca	gaa	cat	gct	gac	144
Gly	Ile	Asn	Ala	Glu	Arg	Leu	Asn	Val	Gly	Thr	Pro	Glu	His	Ala	Asp	
		35					40					45				
gcc	atc	ttt	gat	gag	ctg	acc	gat	att	ctt	gcc	aag	cca	gat	ttc	cga	192
Ala	Ile	Phe	Asp	Glu	Leu	Thr	Asp	Ile	Leu	Ala	Lys	Pro	Asp	Phe	Arg	
	50					55					60					
cca	cgc	gca	ctg	gct	gag	cag	ttc	aac	ttg	gaa	gtt	cta	gcc	acc	acc	240
Pro	Arg	Ala	Leu	Ala	Glu	Gln	Phe	Asn	Leu	Glu	Val	Leu	Ala	Thr	Thr	
65					70					75					80	
gac	gat	ccg	ctc	gat	gac	ctg	gca	gat	cac	aag	gca	ctg	gca	gat	gat	288
Asp	Asp	Pro	Leu	Asp	Asp	Leu	Ala	Asp	His	Lys	Ala	Leu	Ala	Asp	Asp	
				85					90					95		
cca	acc	ttc	tcc	cct	cgt	gtg	ctc	cct	acc	ttc	cgc	cca	gac	gca	tac	336
Pro	Thr	Phe	Ser	Pro	Arg	Val	Leu	Pro	Thr	Phe	Arg	Pro	Asp	Ala	Tyr	
			100					105					110			
acc	aag	atg	tac	aac	gct	ggt	tgg	gca	gaa	aaa	acc	acc	aag	ctt	atc	384
Thr	Lys	Met	Tyr	Asn	Ala	Gly	Trp	Ala	Glu	Lys	Thr	Thr	Lys	Leu	Ile	
		115					120					125				
gat	acc	gca	ggt	gac	ggc	aag	gca	ggc	tgg	gag	ggt	tac	ctt	cag	gca	432
Asp	Thr	Ala	Gly	Asp	Gly	Lys	Ala	Gly	Trp	Glu	Gly	Tyr	Leu	Gln	Ala	
	130					135					140					
atg	cgc	aac	cgc	cgc	cag	tac	ttc	atc	aat	cac	ggt	gca	acc	tcc	gcg	480
Met	Arg	Asn	Arg	Arg	Gln	Tyr	Phe	Ile	Asn	His	Gly	Ala	Thr	Ser	Ala	
145					150					155					160	

**THE UNIVERSITY OF CHICAGO**



cca aga aga cgg ctg gtc atg acc atc cac cag gtg tgt acc 666  
Pro Arg Arg Arg Leu Val Met Thr Ile His Gln Val Cys Thr  
210 215 220

<213> Corynebacterium glutamicum

Glu Met His Ala Phe Glu Ala Asn Thr Thr Tyr Arg Ser Arg Lys Cys  
195 200 205

[illegible]



<400> 429																
gct	cgt	gag	gca	tgg	cgc	att	ttc	atg	tcc	cac	tgg	gat	ctc	tac	gca	48
Ala	Arg	Glu	Ala	Trp	Arg	Ile	Phe	Met	Ser	His	Trp	Asp	Leu	Tyr	Ala	
1				5					10					15		
gga	acc	gca	act	ggc	tac	tgg	gtg	gag	cag	gaa	ttt	gag	cac	gtt	ttc	96
Gly	Thr	Ala	Thr	Gly	Tyr	Trp	Val	Glu	Gln	Glu	Phe	Glu	His	Val	Phe	
			20					25					30			
ggc	atc	aac	gcg	gag	cgc	ctg	aat	gtt	ggc	acc	cca	gaa	cat	gct	gac	144
Gly	Ile	Asn	Ala	Glu	Arg	Leu	Asn	Val	Gly	Thr	Pro	Glu	His	Ala	Asp	
		35					40					45				
gcc	atc	ttt	gat	gag	ctg	acc	gat	att	ctt	gcc	aag	cca	gat	ttc	cga	192
Ala	Ile	Phe	Asp	Glu	Leu	Thr	Asp	Ile	Leu	Ala	Lys	Pro	Asp	Phe	Arg	
	50					55					60					
cca	cgc	gca	ctg	gct	gag	cag	ttc	aac	ttg	gaa	gtt	cta	gcc	acc	acc	240
Pro	Arg	Ala	Leu	Ala	Glu	Gln	Phe	Asn	Leu	Glu	Val	Leu	Ala	Thr	Thr	
65					70					75					80	
gac	gat	ccg	ctc	gat	gac	ctg	gca	gat	cac	aag	gca	ctg	gca	gat	gat	288
Asp	Asp	Pro	Leu	Asp	Asp	Leu	Ala	Asp	His	Lys	Ala	Leu	Ala	Asp	Asp	
				85					90					95		
cca	acc	ttc	tcc	cct	cgt	gtg	ctc	cct	acc	ttc	cgc	cca	gac	gca	tac	336
Pro	Thr	Phe	Ser	Pro	Arg	Val	Leu	Pro	Thr	Phe	Arg	Pro	Asp	Ala	Tyr	
			100					105					110			
acc	aag	atg	tac	aac	gct	ggc	tgg	gca	gaa	aaa	acc	acc	aag	ctt	atc	384
Thr	Lys	Met	Tyr	Asn	Ala	Gly	Trp	Ala	Glu	Lys	Thr	Thr	Lys	Leu	Ile	
		115					120				125					
gat	acc	gca	ggc	gac	ggc	aag	gca	ggc	tgg	gag	ggc	tac	ctt	cag	gca	432
Asp	Thr	Ala	Gly	Asp	Gly	Lys	Ala	Gly	Trp	Glu	Gly	Tyr	Leu	Gln	Ala	
	130					135					140					
atg	cgc	aac	cgc	cgc	cag	tac	ttc	atc	aat	cac	ggc	gca	acc	tcc	gcg	480
Met	Arg	Asn	Arg	Arg	Gln	Tyr	Phe	Ile	Asn	His	Gly	Ala	Thr	Ser	Ala	
145					150					155					160	
gac	cac	ggc	ctc	cac	gac	acc	gac	acc	acc	cca	ctg	agc	cac	aaa	gat	528
Asp	His	Gly	Leu	His	Asp	Thr	Asp	Thr	Thr	Pro	Leu	Ser	His	Lys	Asp	
				165					170					175		
gcc	caq	aaq	atc	ttq	qac	aaq	ggt	ctc	gct	qqc	aca	qca	acc	ttq	gct	576



Ala Gln Lys Ile Leu Asp Lys Gly Leu Ala Gly Thr Ala Thr Leu Ala  
180 185 190

gaa atg cat gcc ttc gaa gcc aac acc acc tac cgt ttc gcg gaa atg 624  
Glu Met His Ala Phe Glu Ala Asn Thr Thr Tyr Arg Phe Ala Glu Met  
195 200 205

tcc caa gaa gac ggc ctg gtc atg acc atc cac cca ggt gtg tac cgc 672  
Ser Gln Glu Asp Gly Leu Val Met Thr Ile His Pro Gly Val Tyr Arg  
210 215 220

<210> 430

<211> 224

<212> PRT

<213> Corynebacterium glutamicum

<400> 430

Ala Arg Glu Ala Trp Arg Ile Phe Met Ser His Trp Asp Leu Tyr Ala  
1 5 10 15

Gly Thr Ala Thr Gly Tyr Trp Val Glu Gln Glu Phe Glu His Val Phe  
20 25 30

Gly Ile Asn Ala Glu Arg Leu Asn Val Gly Thr Pro Glu His Ala Asp  
35 40 45

Ala Ile Phe Asp Glu Leu Thr Asp Ile Leu Ala Lys Pro Asp Phe Arg  
50 55 60

Pro Arg Ala Leu Ala Glu Gln Phe Asn Leu Glu Val Leu Ala Thr Thr  
65 70 75 80

Asp Asp Pro Leu Asp Asp Leu Ala Asp His Lys Ala Leu Ala Asp Asp  
85 90 95

Pro Thr Phe Ser Pro Arg Val Leu Pro Thr Phe Arg Pro Asp Ala Tyr  
100 105 110

Thr Lys Met Tyr Asn Ala Gly Trp Ala Glu Lys Thr Thr Lys Leu Ile  
115 120 125

Asp Thr Ala Gly Asp Gly Lys Ala Gly Trp Glu Gly Tyr Leu Gln Ala  
130 135 140

Met Arg Asn Arg Arg Gln Tyr Phe Ile Asn His Gly Ala Thr Ser Ala  
145 150 155 160

Asp His Gly Leu His Asp Thr Asp Thr Thr Pro Leu Ser His Lys Asp  
165 170 175

Ala Gln Lys Ile Leu Asp Lys Gly Leu Ala Gly Thr Ala Thr Leu Ala  
180 185 190

Glu Met His Ala Phe Glu Ala Asn Thr Thr Tyr Arg Phe Ala Glu Met  
195 200 205

Ser Gln Glu Asp Gly Leu Val Met Thr Ile His Pro Gly Val Tyr Arg  
210 215 220

00602740"062300



```
<220>  
<221> CDS  
<222> (1) .. (510)  
<223> RXN03180
```

tqt 533



```
<210> 432
<211> 170
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 432															
Phe	Gly	Glu	Asn	Lys	Asp	Leu	Ile	Ser	Asp	Ser	Ser	Phe	Asn	Arg	Trp
1				5					10					15	
Leu	Arg	Thr	Val	Ser	Leu	Gly	Ser	Thr	Gln	Asp	Ala	Asp	Met	Ala	Ala
			20					25					30		
Ala	Ser	Asn	Leu	Ala	Ala	Asn	Ser	Lys	Met	Ala	Arg	Gln	Asn	Thr	Arg
		35					40					45			
Asp	Ile	Leu	Asp	Ala	Val	Ser	Asp	Gly	Gly	Val	Met	Leu	Gly	Arg	Asn
	50					55					60				
Gly	Ala	Leu	Val	Leu	Gly	Pro	Val	Val	Gly	Thr	Leu	His	Ile	Lys	Phe
65					70					75					80
Ile	Ala	Pro	Leu	Asn	Lys	Arg	Val	Glu	Arg	Val	Met	Tyr	Lys	Thr	Gly
				85					90					95	
Leu	Ser	Glu	Ala	Ala	Ala	Ala	Glu	Gln	Cys	Ala	Leu	Glu	Asp	Arg	Leu
			100					105					110		
Arg	Glu	Glu	Met	Ala	His	Ala	Leu	Tyr	Gln	Trp	Asn	Pro	Gly	Arg	Asp
		115					120					125			
Glu	Asn	Tyr	Asp	Leu	Val	Ile	Asn	Thr	Gly	Ser	Met	Thr	Tyr	Glu	Gln
	130					135					140				
Ile	Val	Asp	Leu	Val	Val	Glu	Thr	Tyr	Ala	Arg	Lys	Tyr	Pro	Leu	His
145					150					155					160
Val	Arg	Ile	Ile	Pro	Asn	Gly	Lys	Asp	Gln						
				165					170						

```
<210> 433
<211> 533
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (1)..(510)  
<223> FRXA02873
```

<400> 433																
ttc	ggt	gag	aac	aaa	gat	ctc	atc	tct	gac	agc	agt	ttc	aac	cgc	tgg	48
Phe	Gly	Glu	Asn	Lys	Asp	Leu	Ile	Ser	Asp	Ser	Ser	Phe	Asn	Arg	Trp	
1				5					10					15		
ctg	cgt	acg	gtt	tcc	ctc	gga	tcg	acc	cag	gat	gcc	gat	atg	gct	gca	96
Leu	Arg	Thr	Val	Ser	Leu	Gly	Ser	Thr	Gln	Asp	Ala	Asp	Met	Ala	Ala	
			20					25					30			
gct	tcc	aac	ttg	gca	gcc	aat	tct	aaa	atg	gcc	cgc	cag	aac	acc	cgc	144
Ala	Ser	Asn	Leu	Ala	Ala	Asn	Ser	Lys	Met	Ala	Arg	Gln	Asn	Thr	Arg	



<400> 434																
Phe	Gly	Glu	Asn	Lys	Asp	Leu	Ile	Ser	Asp	Ser	Ser	Phe	Asn	Arg	Trp	
1				5					10					15		
Leu	Arg	Thr	Val	Ser	Leu	Gly	Ser	Thr	Gln	Asp	Ala	Asp	Met	Ala	Ala	
			20					25					30			
Ala	Ser	Asn	Leu	Ala	Ala	Asn	Ser	Lys	Met	Ala	Arg	Gln	Asn	Thr	Arg	
		35					40					45				
Asp	Ile	Leu	Asp	Ala	Val	Ser	Asp	Gly	Gly	Val	Met	Leu	Gly	Arg	Asn	
	50					55					60					
Gly	Ala	Leu	Val	Leu	Gly	Pro	Val	Val	Gly	Thr	Leu	His	Ile	Lys	Phe	
65					70					75					80	
Ile	Ala	Pro	Leu	Asn	Lys	Arg	Val	Glu	Arg	Val	Met	Tyr	Lys	Thr	Gly	
				85					90					95		

[illegible]



```
<210> 435
<211> 798
<212> DNA
<213> Corynebacterium glutamicum
```

<400> 435																
tgcaccacgc cagctgcaac cctgcgcggt ggtctctgggaa gttgggtggag gggatcgtcg																60
aaaagcgtag gcactaaagt tctcctgcac aatggaggat atg gac aat gac ttt																115
Met Asp Asn Asp Phe																5
gaa tct atc gag aaa atg agc agc ggc gat tgg tac gtg gct acc ggc																163
Glu Ser Ile Glu Lys Met Ser Ser Gly Asp Trp Tyr Val Ala Thr Gly																10 15 20
gcg gaa cgt gaa gaa gtg gca caa aaa aca gcg tta ctt ttc cac gaa																211
Ala Glu Arg Glu Glu Val Ala Gln Lys Thr Ala Leu Leu Phe His Glu																25 30 35
tac aac caa att gga cct aca gac ccc gca cga act gcc gaa ata cta																259
Tyr Asn Gln Ile Gly Pro Thr Asp Pro Ala Arg Thr Ala Glu Ile Leu																40 45 50
aga act gta cta aat cct gcc agc gga acc tgc acg atc aaa gcg cca																307
Arg Thr Val Leu Asn Pro Ala Ser Gly Thr Cys Thr Ile Lys Ala Pro																55 60 65
gcc atc att gaa tac ggc ttc aac acc acg atc ggc gag cat gtg ttc																355
Ala Ile Ile Glu Tyr Gly Phe Asn Thr Thr Ile Gly Glu His Val Phe																70 75 80 85
atc aac ttt ggc ctc acc att tta gat atc gca ccg gtt cgc atc ggg																403
Ile Asn Phe Gly Leu Thr Ile Leu Asp Ile Ala Pro Val Arg Ile Gly																90 95 100
gca cgc agc atg ctc ggg cca aac tgt cag ctc ttc acc gca ggt cac																451
Ala Arg Ser Met Leu Gly Pro Asn Cys Gln Leu Phe Thr Ala Gly His																105 110 115

[illegible]



ccg gtc gat gac tgg gaa atg cgc tcc ggt ggg tgg gaa aat ggc gca 499  
 Pro Val Asp Asp Trp Glu Met Arg Ser Gly Gly Trp Glu Asn Gly Ala  
 120 125 130

ccc att tcc att ggc gag gat acg tgg ctg ggt gga aat gtc acc gtc 547  
 Pro Ile Ser Ile Gly Glu Asp Thr Trp Leu Gly Gly Asn Val Thr Val  
 135 140 145

gtt ggt ggc gtg agc att ggc gat agg tgt gtg att ggc gcg ggg ccc 595  
 Val Gly Gly Val Ser Ile Gly Asp Arg Cys Val Ile Gly Ala Gly Pro  
 150 155 160 165

gtg gtg acc aag gat att ccg gat gat tct att gct gtg ggc aac cct 643  
 Val Val Thr Lys Asp Ile Pro Asp Asp Ser Ile Ala Val Gly Asn Pro  
 170 175 180

gcg cga gta gtg cgg aaa cgt gat gat agc cgg ctc gaa cgt tcg cag 691  
 Ala Arg Val Val Arg Lys Arg Asp Asp Ser Arg Leu Glu Arg Ser Gln  
 185 190 195

ctg cca gaa ggt gct tcc gtg gat gcg ttg ggg att ctt cct aca aaa 739  
 Leu Pro Glu Gly Ala Ser Val Asp Ala Leu Gly Ile Leu Pro Thr Lys  
 200 205 210

tca cct agg ctg tca gaa aat att gcc gaa aaa tat taaatacgca 785  
 Ser Pro Arg Leu Ser Glu Asn Ile Ala Glu Lys Tyr  
 215 220 225

ggcactaaga aga 798

<210> 436  
 <211> 225  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 436  
 Met Asp Asn Asp Phe Glu Ser Ile Glu Lys Met Ser Ser Gly Asp Trp  
 1 5 10 15

Tyr Val Ala Thr Gly Ala Glu Arg Glu Glu Val Ala Gln Lys Thr Ala  
 20 25 30

Leu Leu Phe His Glu Tyr Asn Gln Ile Gly Pro Thr Asp Pro Ala Arg  
 35 40 45

Thr Ala Glu Ile Leu Arg Thr Val Leu Asn Pro Ala Ser Gly Thr Cys  
 50 55 60

Thr Ile Lys Ala Pro Ala Ile Ile Glu Tyr Gly Phe Asn Thr Thr Ile  
 65 70 75 80

Gly Glu His Val Phe Ile Asn Phe Gly Leu Thr Ile Leu Asp Ile Ala  
 85 90 95

Pro Val Arg Ile Gly Ala Arg Ser Met Leu Gly Pro Asn Cys Gln Leu  
 100 105 110

Phe Thr Ala Gly His Pro Val Asp Asp Trp Glu Met Arg Ser Gly Gly  
 115 120 125

09602740.062300



Trp Glu Asn Gly Ala Pro Ile Ser Ile Gly Glu Asp Thr Trp Leu Gly  
 130 135 140

Gly Asn Val Thr Val Val Gly Gly Val Ser Ile Gly Asp Arg Cys Val  
 145 150 155 160

Ile Gly Ala Gly Pro Val Val Thr Lys Asp Ile Pro Asp Asp Ser Ile  
 165 170 175

Ala Val Gly Asn Pro Ala Arg Val Val Arg Lys Arg Asp Asp Ser Arg  
 180 185 190

Leu Glu Arg Ser Gln Leu Pro Glu Gly Ala Ser Val Asp Ala Leu Gly  
 195 200 205

Ile Leu Pro Thr Lys Ser Pro Arg Leu Ser Glu Asn Ile Ala Glu Lys  
 210 215 220

Tyr  
 225

<210> 437  
 <211> 891  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(868)  
 <223> RXA02666

<400> 437  
 gctcggcgac gaggaagaga agaaggacgc attcgacgac ttcgacgatt ccgacgtgga 60

tcttgacgat ctgagcttcg acgacgaaga ttagacgccc atg tcg tct aca cga 115  
 Met Ser Ser Thr Arg  
 1 5

atc ccc gtc atc gca ctc ctc gcg gcg gcg ggg cgc gga acc cgc ctc 163  
 Ile Pro Val Ile Ala Leu Leu Ala Ala Gly Arg Gly Thr Arg Leu  
 10 15 20

ggc gga ccc atc ccc aaa gca ttc gtc acg ttg cgt gaa cgc aca ctt 211  
 Gly Gly Pro Ile Pro Lys Ala Phe Val Thr Leu Arg Glu Arg Thr Leu  
 25 30 35

tta gag cgc tcg ctc caa gcc atg ctc acc tcc gaa agc gtc gac gaa 259  
 Leu Glu Arg Ser Leu Gln Ala Met Leu Thr Ser Glu Ser Val Asp Glu  
 40 45 50

atc atc atc ctc gtc agc ccc gac atg gaa acc tac gcc cgc gat ttg 307  
 Ile Ile Ile Leu Val Ser Pro Asp Met Glu Thr Tyr Ala Arg Asp Leu  
 55 60 65

ctg cgc aaa cgc ggt ctt ttg aac gac ccc gaa ggg gta cgc gta cgg 355  
 Leu Arg Lys Arg Gly Leu Leu Asn Asp Pro Glu Gly Val Arg Val Arg  
 70 75 80 85

ctc gtg cac ggc ggc ggg gag cgc gcg gac tcg gtc tgg gca ggc ctt 403  
 Leu Val His Gly Gly Gly Glu Arg Ala Asp Ser Val Trp Ala Gly Leu

009602740.062300



	90	95	100	
cag gca att tcg ctt gac gac gcc acc ccc gat gca att gtc tta atc				451
Gln Ala Ile Ser Leu Asp Asp Ala Thr Pro Asp Ala Ile Val Leu Ile				
	105	110	115	
cac gac agc gcc cga gcg ctc aca cca ccc ggc atg att gcg cgc gtg				499
His Asp Ser Ala Arg Ala Leu Thr Pro Pro Gly Met Ile Ala Arg Val				
	120	125	130	
gtg cgc aaa gtc cac gaa ggc gcc acc gca gtc atc cca gta ctg cca				547
Val Arg Lys Val His Glu Gly Ala Thr Ala Val Ile Pro Val Leu Pro				
	135	140	145	
gta tcg gac acc atc aaa cga gtg tcc cct gat ggc gga gta gtt gtc				595
Val Ser Asp Thr Ile Lys Arg Val Ser Pro Asp Gly Gly Val Val Val				
	150	155	160	165
gac aca ccc aac cgt gca gaa ctt cgc gcc gtc caa acc cca caa ggc				643
Asp Thr Pro Asn Arg Ala Glu Leu Arg Ala Val Gln Thr Pro Gln Gly				
	170	175	180	
ttc ctg ctg tcc gaa ctt gtt gca gcg aat gag aaa ttc ttc gcc gac				691
Phe Leu Leu Ser Glu Leu Val Ala Ala Asn Glu Lys Phe Phe Ala Asp				
	185	190	195	
ccc aac cca ggc ttc atc cca acc gat gac gcc agc ttg atg gaa tgg				739
Pro Asn Pro Gly Phe Ile Pro Thr Asp Asp Ala Ser Leu Met Glu Trp				
	200	205	210	
tac ggc gca gat gta gtc tgc gta caa ggc gac cca atg gcg ttt aaa				787
Tyr Gly Ala Asp Val Val Cys Val Gln Gly Asp Pro Met Ala Phe Lys				
	215	220	225	
gta aca acc ccc att gat atg atg ctg gca caa cgc atc acc gac gaa				835
Val Thr Thr Pro Ile Asp Met Met Leu Ala Gln Arg Ile Thr Asp Glu				
	230	235	240	245
gcc gaa ccc aca ata ttt gag gta cca ggt gac taacccaatc atccccgcg				888
Ala Glu Pro Thr Ile Phe Glu Val Pro Gly Asp				
	250	255		
tag				891

&lt;210&gt; 438

&lt;211&gt; 256

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 438

Met	Ser	Ser	Thr	Arg	Ile	Pro	Val	Ile	Ala	Leu	Leu	Ala	Ala	Ala	Gly
1				5					10						15

Arg	Gly	Thr	Arg	Leu	Gly	Gly	Pro	Ile	Pro	Lys	Ala	Phe	Val	Thr	Leu
			20					25					30		

Arg	Glu	Arg	Thr	Leu	Leu	Glu	Arg	Ser	Leu	Gln	Ala	Met	Leu	Thr	Ser
		35					40					45			

Glu	Ser	Val	Asp	Glu	Ile	Ile	Ile	Leu	Val	Ser	Pro	Asp	Met	Glu	Thr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

09602740.062300



```
<210> 439
<211> 1065
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(1042)
<223> RXA00202
```

```

<400> 439
ctggcagcag attgtcatcg gttgtgtcat cgcgcttgcg gtgggcttcg atgtcatccg 60
aaacaaaacc tctaagtaat tcttgaaagg aaattttcac atg tac gct cgt aaa 115
                                         Met Tyr Ala Arg Lys
                                         1                               5
ctt att gct ctg tcc gct tct gtc gtt ttg gct ttc agc ttg tct gct 163
Leu Ile Ala Leu Ser Ala Ser Val Val Leu Ala Phe Ser Leu Ser Ala

```



	10	15	20	
tgc aac cgt gaa tct tct ggc acc agc gca gac ggc ggt tct gcg gat	25	30	35	211
Cys Asn Arg Glu Ser Ser Gly Thr Ser Ala Asp Gly Gly Ser Ala Asp				
ggg tcg atc acc ttg gct ctg tct acc cag acc aac ccg ttc ttt gtg	40	45	50	259
Gly Ser Ile Thr Leu Ala Leu Ser Thr Gln Thr Asn Pro Phe Phe Val				
cag ctt cgt gat ggt gcc cag gaa aag gct gat gaa ttg ggc gtg acc	55	60	65	307
Gln Leu Arg Asp Gly Ala Gln Glu Lys Ala Asp Glu Leu Gly Val Thr				
ctc aat gtt cag gat gct tcc gat gac gct gca acg cag gcc aac cag	70	75	80	355
Leu Asn Val Gln Asp Ala Ser Asp Asp Ala Ala Thr Gln Ala Asn Gln				
ctc aac aac gct gtc acc acc ggt gct ggc gtg gtg att gtc aac cca	90	95	100	403
Leu Asn Asn Ala Val Thr Thr Gly Ala Gly Val Val Ile Val Asn Pro				
act gat tct gat gct gtg gtg ccg tcg gtg gaa gct ctc aac cag gct	105	110	115	451
Thr Asp Ser Asp Ala Val Val Pro Ser Val Glu Ala Leu Asn Gln Ala				
gac att cct gtt gtg gct gtc gac cgt tcc tcc aat ggt ggc gag gtg	120	125	130	499
Asp Ile Pro Val Val Ala Val Asp Arg Ser Ser Asn Gly Gly Glu Val				
gcg tcc ttc gtg gca tct gac aac gtt gct ggc ggc gcg cag gct gct	135	140	145	547
Ala Ser Phe Val Ala Ser Asp Asn Val Ala Gly Gly Ala Gln Ala Ala				
gca gcc ctg gca gag gcg atc ggt ggc gaa ggt gaa atc ctc atg ctg	150	155	160	595
Ala Ala Leu Ala Glu Ala Ile Gly Gly Glu Glu Ile Leu Met Leu				
caa ggc att gcg gga tcc tct gca tca cgt gat cgt gga cag gga ttt	170	175	180	643
Gln Gly Ile Ala Gly Ser Ser Ala Ser Arg Asp Arg Gly Gln Gly Phe				
gaa gag gag atc gct aag cat gag ggc att tcc att gtg gct aag cag	185	190	195	691
Glu Glu Glu Ile Ala Lys His Glu Gly Ile Ser Ile Val Ala Lys Gln				
acc gcc aac ttt gac cgc ggt gag ggc ctg gac gtg gca act aac ctg	200	205	210	739
Thr Ala Asn Phe Asp Arg Gly Glu Gly Leu Asp Val Ala Thr Asn Leu				
ctg cag gca cac ccc aat gtg aag gcg atc ttc gcg gaa aac gat gag	215	220	225	787
Leu Gln Ala His Pro Asn Val Lys Ala Ile Phe Ala Glu Asn Asp Glu				
atg gcg ttg ggc gca atc gaa gcc ctg ggt gct cgt gct ggt gaa gat	230	235	240	835
Met Ala Leu Gly Ala Ile Glu Ala Leu Gly Ala Arg Ala Gly Glu Asp				
gtc atc gtt gtc ggt ttc gat ggc acc aat gat ggt ctg gca gcg gtt	250	255	260	883
Val Ile Val Val Gly Phe Asp Gly Thr Asn Asp Gly Leu Ala Ala Val				

0052290" 04220960



```
<210> 440
<211> 314
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 440															
Met 1	Tyr	Ala	Arg	Lys 5	Leu	Ile	Ala	Leu	Ser 10	Ala	Ser	Val	Val	Leu 15	Ala
Phe	Ser	Leu	Ser 20	Ala	Cys	Asn	Arg	Glu 25	Ser	Ser	Gly	Thr	Ser 30	Ala	Asp
Gly	Gly	Ser 35	Ala	Asp	Gly	Ser	Ile 40	Thr	Leu	Ala	Leu	Ser 45	Thr	Gln	Thr
Asn	Pro 50	Phe	Phe	Val	Gln	Leu 55	Arg	Asp	Gly	Ala	Gln 60	Glu	Lys	Ala	Asp
Glu 65	Leu	Gly	Val	Thr	Leu 70	Asn	Val	Gln	Asp	Ala 75	Ser	Asp	Asp	Ala	Ala 80
Thr	Gln	Ala	Asn	Gln 85	Leu	Asn	Asn	Ala	Val 90	Thr	Thr	Gly	Ala	Gly 95	Val
Val	Ile	Val	Asn 100	Pro	Thr	Asp	Ser	Asp 105	Ala	Val	Val	Pro	Ser 110	Val	Glu
Ala	Leu	Asn 115	Gln	Ala	Asp	Ile	Pro 120	Val	Val	Ala	Val	Asp 125	Arg	Ser	Ser
Asn	Gly 130	Gly	Glu	Val	Ala	Ser 135	Phe	Val	Ala	Ser	Asp 140	Asn	Val	Ala	Gly
Gly 145	Ala	Gln	Ala	Ala 150	Ala	Ala	Leu	Ala	Glu 155	Ala	Ile	Gly	Gly	Glu	Gly 160
Glu	Ile	Leu	Met	Leu 165	Gln	Gly	Ile	Ala	Gly 170	Ser	Ser	Ala	Ser	Arg 175	Asp
Arg	Gly	Gln	Gly 180	Phe	Glu	Glu	Glu	Ile 185	Ala	Lys	His	Glu	Gly 190	Ile	Ser
Ile	Val	Ala	Lys	Gln	Thr	Ala	Asn	Phe	Asp	Arg	Gly	Glu	Gly	Leu	Asp



```
<210> 441
<211> 963
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(940)
<223> RXA02440
```

<400> 441																
gctgttaatc acgggttggt cagctaccgg gggagcacca cgggcaacag atgggggcac																60
aggcggagga accgtcgata cgcctcgggt ggttgtcgcg																115
Met Val Ser His Gly																5
1																
gcg ccg ggc gat act ttt tgg gat ttg gtc cga aaa ggt gct gaa gac																163
Ala Pro Gly Asp Thr Phe Trp Asp Leu Val Arg Lys Gly Ala Glu Asp																
10 15 20																
gcc gcc caa aaa gac aac gtt gaa ctc cgc tat tcc tct aat ccg gaa																211
Ala Ala Gln Lys Asp Asn Val Glu Leu Arg Tyr Ser Ser Asn Pro Glu																
25 30 35																
atc cct gaa caa tcc aac ctc gtg caa aat gcc atc gat tca cgc gtc																259
Ile Pro Glu Gln Ser Asn Leu Val Gln Asn Ala Ile Asp Ser Arg Val																
40 45 50																
gac ggc atc gcc atg acc atg cct aat gct caa tca cta gga ccg gtc																307
Asp Gly Ile Ala Met Thr Met Pro Asn Ala Gln Ser Leu Gly Pro Val																
55 60 65																
gct caa aag gcc gtg gat gcg ggc att cct gtg gtt ggt ctc aac gct																355
Ala Gln Lys Ala Val Asp Ala Gly Ile Pro Val Val Gly Leu Asn Ala																
70 75 80 85																



```
<210> 442
<211> 280
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 442  
Met Val Ser His Gly Ala Pro Gly Asp Thr Phe Trp Asp Leu Val Arg  
1 5 10 15



```
<220>  
<221> CDS  
<222> (101)..(1459)
```



&lt;223&gt; RXN01569

&lt;400&gt; 443

```

aaggcctaga gcagaccatc gattggtacc gcgaaaacga ggcctggtgg cgccctgccca 60
agaacaacgt cgaagctacc tacgctaagc agggacaata atg gaa tac ggt aaa 115
                                         Met Glu Tyr Gly Lys
                                         1                               5
caa ctc acc tcc cac acc acc gac atc gaa ggc cta ctg gtt ttc gat 163
Gln Leu Thr Ser His Thr Thr Asp Ile Glu Gly Leu Leu Val Phe Asp
                        10                        15                        20
ttc ccc gtc cac ggc gac aac cgc ggc tgg ttc aag gaa aat tgg cag 211
Phe Pro Val His Gly Asp Asn Arg Gly Trp Phe Lys Glu Asn Trp Gln
                        25                        30                        35
cgc acc aag atg acc aac ctg ggg ctg ccc gat ttt ggc ccc gtc caa 259
Arg Thr Lys Met Thr Asn Leu Gly Leu Pro Asp Phe Gly Pro Val Gln
                        40                        45                        50
aac aac atg agt ttc aac gcc acc gcc ggc acg act cgc ggc atg cac 307
Asn Asn Met Ser Phe Asn Ala Thr Ala Gly Thr Thr Arg Gly Met His
                        55                        60                        65
gct gag ccg tgg gat aaa ttt gtg tcc gtc gcg gtg ggt tcc gtt ttc 355
Ala Glu Pro Trp Asp Lys Phe Val Ser Val Ala Val Gly Ser Val Phe
      70                        75                        80                        85
gga gct tgg gtg gat ctg cgc gcg ggc tcg agc acg tac ggt aac gtc 403
Gly Ala Trp Val Asp Leu Arg Ala Gly Ser Ser Thr Tyr Gly Asn Val
                        90                        95                        100
gta acg caa aaa att acc cct gac gtg gga gtt tac gtc ccg cgt ggt 451
Val Thr Gln Lys Ile Thr Pro Asp Val Gly Val Tyr Val Pro Arg Gly
                        105                        110                        115
gtg gca aac ggc ttc cag gcg ctc gag gac ggc acg ctg tac acc tac 499
Val Ala Asn Gly Phe Gln Ala Leu Glu Asp Gly Thr Leu Tyr Thr Tyr
                        120                        125                        130
ctc gtc aac gat cat tgg tcc ccc gac gcg cat tac gcc aac gtc aac 547
Leu Val Asn Asp His Trp Ser Pro Asp Ala His Tyr Ala Asn Val Asn
      135                        140                        145
ctc aac atg atc gac tgg ccg ctg ccc atc acc gag atc tcc gaa aaa 595
Leu Asn Met Ile Asp Trp Pro Leu Pro Ile Thr Glu Ile Ser Glu Lys
      150                        155                        160                        165
gat aaa aaa cat cca gcg ctt atc gac gcc acc ccc ctg ccc gcc cgc 643
Asp Lys Lys His Pro Ala Leu Ile Asp Ala Thr Pro Leu Pro Ala Arg
                        170                        175                        180
aag gtt ctc gtg gtc ggc gcc ggc gga caa ctg gga acc gcg cta cgc 691
Lys Val Leu Val Val Gly Ala Gly Gly Gln Leu Gly Thr Ala Leu Arg
                        185                        190                        195
gcg cag ttc cca gac gcg gaa ttt gtc acg cgc caa gaa ctc gat atc 739
Ala Gln Phe Pro Asp Ala Glu Phe Val Thr Arg Gln Glu Leu Asp Ile
                        200                        205                        210

```

09602740-062300



acc tca gat ctc acc gag gct cgc gcg tgg aaa caa tac tcc acc atc 787  
 Thr Ser Asp Leu Thr Glu Ala Arg Ala Trp Lys Gln Tyr Ser Thr Ile  
 215 220 225

ata aac gcc gcc gcc tac act gcc gtt gac cag gca gaa cac gac cgc 835  
 Ile Asn Ala Ala Ala Tyr Thr Ala Val Asp Gln Ala Glu His Asp Arg  
 230 235 240 245

gca gca gcg tgg gac atc aac gca gcg gca gtg gct aac ctc gcg acc 883  
 Ala Ala Ala Trp Asp Ile Asn Ala Ala Val Ala Asn Leu Ala Thr  
 250 255 260

atc gcg cgc gac aac aac ctc acc ctc gtg cac gtg tcc tca gat tat 931  
 Ile Ala Arg Asp Asn Asn Leu Thr Leu Val His Val Ser Ser Asp Tyr  
 265 270 275

gtc ttc gac ggt gcg gcc gaa tcc tac gat gaa aac gca ccg ttt tcc 979  
 Val Phe Asp Gly Ala Ala Glu Ser Tyr Asp Glu Asn Ala Pro Phe Ser  
 280 285 290

cca ctc ggc gtg tac ggc caa tcc aaa gca gcc ggc gac atc gga gac 1027  
 Pro Leu Gly Val Tyr Gly Gln Ser Lys Ala Ala Gly Asp Ile Gly Asp  
 295 300 305

acc acc gca ccg cgc cac tac att gtg cgc acc agc tgg gtg att ggc 1075  
 Thr Thr Ala Pro Arg His Tyr Ile Val Arg Thr Ser Trp Val Ile Gly  
 310 315 320 325

gat ggc aat aat ttt gtc cgc acc atg aaa tcc ctc gac gaa cgc ggc 1123  
 Asp Gly Asn Asn Phe Val Arg Thr Met Lys Ser Leu Asp Glu Arg Gly  
 330 335 340

atc gca cca tca gta gtt gat gat caa atc ggc cgc cta tcc ttc acc 1171  
 Ile Ala Pro Ser Val Val Asp Asp Gln Ile Gly Arg Leu Ser Phe Thr  
 345 350 355

gaa gac atc gca gcc ggc atc gcg cac ctt ttg gaa gtg ggt gca gca 1219  
 Glu Asp Ile Ala Ala Gly Ile Ala His Leu Leu Glu Val Gly Ala Ala  
 360 365 370

tat ggc acc tac aac ctc acc aac acc ggc gaa ccc gca agc tgg gcc 1267  
 Tyr Gly Thr Tyr Asn Leu Thr Asn Thr Gly Glu Pro Ala Ser Trp Ala  
 375 380 385

gat gtt gcc cgc gca gta ttt tcc gac ccc acc aaa gtt acc ggc gtg 1315  
 Asp Val Ala Arg Ala Val Phe Ser Asp Pro Thr Lys Val Thr Gly Val  
 390 395 400 405

agc acc gcc gag tac ttc gcc aac aaa gac gca gcg ccc cgc cca ctg 1363  
 Ser Thr Ala Glu Tyr Phe Ala Asn Lys Asp Ala Ala Pro Arg Pro Leu  
 410 415 420

aac tcc gtt ttg gat ctc ggc aaa atc gaa gcc acc gga ttt agc gca 1411  
 Asn Ser Val Leu Asp Leu Gly Lys Ile Glu Ala Thr Gly Phe Ser Ala  
 425 430 435

ccg acc tgg cag acc cgc ctc aac gac tac ctc aag gaa ctc tca aag 1459  
 Pro Thr Trp Gln Thr Arg Leu Asn Asp Tyr Leu Lys Glu Leu Ser Lys  
 440 445 450

tgaaaggcat catcctcgca ggt 1482

09602740 062300



&lt;210&gt; 444

&lt;211&gt; 453

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 444

Met Glu Tyr Gly Lys Gln Leu Thr Ser His Thr Thr Asp Ile Glu Gly  
 1 5 10 15

Leu Leu Val Phe Asp Phe Pro Val His Gly Asp Asn Arg Gly Trp Phe  
 20 25 30

Lys Glu Asn Trp Gln Arg Thr Lys Met Thr Asn Leu Gly Leu Pro Asp  
 35 40 45

Phe Gly Pro Val Gln Asn Asn Met Ser Phe Asn Ala Thr Ala Gly Thr  
 50 55 60

Thr Arg Gly Met His Ala Glu Pro Trp Asp Lys Phe Val Ser Val Ala  
 65 70 75 80

Val Gly Ser Val Phe Gly Ala Trp Val Asp Leu Arg Ala Gly Ser Ser  
 85 90 95

Thr Tyr Gly Asn Val Val Thr Gln Lys Ile Thr Pro Asp Val Gly Val  
 100 105 110

Tyr Val Pro Arg Gly Val Ala Asn Gly Phe Gln Ala Leu Glu Asp Gly  
 115 120 125

Thr Leu Tyr Thr Tyr Leu Val Asn Asp His Trp Ser Pro Asp Ala His  
 130 135 140

Tyr Ala Asn Val Asn Leu Asn Met Ile Asp Trp Pro Leu Pro Ile Thr  
 145 150 155 160

Glu Ile Ser Glu Lys Asp Lys Lys His Pro Ala Leu Ile Asp Ala Thr  
 165 170 175

Pro Leu Pro Ala Arg Lys Val Leu Val Val Gly Ala Gly Gly Gln Leu  
 180 185 190

Gly Thr Ala Leu Arg Ala Gln Phe Pro Asp Ala Glu Phe Val Thr Arg  
 195 200 205

Gln Glu Leu Asp Ile Thr Ser Asp Leu Thr Glu Ala Arg Ala Trp Lys  
 210 215 220

Gln Tyr Ser Thr Ile Ile Asn Ala Ala Ala Tyr Thr Ala Val Asp Gln  
 225 230 235 240

Ala Glu His Asp Arg Ala Ala Ala Trp Asp Ile Asn Ala Ala Ala Val  
 245 250 255

Ala Asn Leu Ala Thr Ile Ala Arg Asp Asn Asn Leu Thr Leu Val His  
 260 265 270

Val Ser Ser Asp Tyr Val Phe Asp Gly Ala Ala Glu Ser Tyr Asp Glu  
 275 280 285

002290.0720960











&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1021)

&lt;223&gt; FRXA02055

&lt;400&gt; 447

```

aaggcctaga gcagaccatc gattggtacc gcgaaaacga ggccctggtgg cgccctgccca 60
agaacaacgt cgaagctacc tacgctaagc agggacaata atg gaa tac ggt aaa 115
                                         Met Glu Tyr Gly Lys
                                         1                               5

caa ctc acc tcc cac acc acc gac atc gaa ggc cta ctg gtt ttc gat 163
Gln Leu Thr Ser His Thr Thr Asp Ile Glu Gly Leu Leu Val Phe Asp
                               10                               15                               20

ttc ccc gtc cac ggc gac aac cgc ggc tgg ttc aag gaa aat tgg cag 211
Phe Pro Val His Gly Asp Asn Arg Gly Trp Phe Lys Glu Asn Trp Gln
                               25                               30                               35

cgc acc aag atg acc aac ctg ggg ctg ccc gat ttt ggc ccc gtc caa 259
Arg Thr Lys Met Thr Asn Leu Gly Leu Pro Asp Phe Gly Pro Val Gln
                               40                               45                               50

aac aac atg agt ttc aac gcc acc gcc ggc acg act cgc ggc atg cac 307
Asn Asn Met Ser Phe Asn Ala Thr Ala Gly Thr Thr Arg Gly Met His
                               55                               60                               65

gct gag ccg tgg gat aaa ttt gtg tcc gtc gcg gtg ggt tcc gtt ttc 355
Ala Glu Pro Trp Asp Lys Phe Val Ser Val Ala Val Gly Ser Val Phe
                               70                               75                               80                               85

gga gct tgg gtg gat ctg cgc gcg ggc tgc agc acg tac ggt aac gtc 403
Gly Ala Trp Val Asp Leu Arg Ala Gly Ser Ser Thr Tyr Gly Asn Val
                               90                               95                               100

gta acg caa aaa att acc cct gac gtg gga gtt tac gtc ccg cgt ggt 451
Val Thr Gln Lys Ile Thr Pro Asp Val Gly Val Tyr Val Pro Arg Gly
                               105                               110                               115

gtg gca aac ggc ttc cag gcg ctc gag gac ggc acg ctg tac acc tac 499
Val Ala Asn Gly Phe Gln Ala Leu Glu Asp Gly Thr Leu Tyr Thr Tyr
                               120                               125                               130

ctc gtc aac gat cat tgg tcc ccc gac gcg cat tac gcc aac gtc aac 547
Leu Val Asn Asp His Trp Ser Pro Asp Ala His Tyr Ala Asn Val Asn
                               135                               140                               145

ctc aac atg atc gac tgg ccg ctg ccc atc acc gag atc tcc gaa aaa 595
Leu Asn Met Ile Asp Trp Pro Leu Pro Ile Thr Glu Ile Ser Glu Lys
                               150                               155                               160                               165

gat aaa aaa cat cca gcg ctt atc gac gcc acc ccc ctg ccc gcc cgc 643
Asp Lys Lys His Pro Ala Leu Ile Asp Ala Thr Pro Leu Pro Ala Arg
                               170                               175                               180

aag gtt ctc gtg gtc ggc gcc ggc gga caa ctg gga acc gcg cta cgc 691
Lys Val Leu Val Val Gly Ala Gly Gly Gln Leu Gly Thr Ala Leu Arg
                               185                               190                               195

```

09602740-062300



gcg cag ttc cca gac gcg gaa ttt gtc acg cgc caa gaa ctc gat atc 739  
 Ala Gln Phe Pro Asp Ala Glu Phe Val Thr Arg Gln Glu Leu Asp Ile  
 200 205 210

acc tca gat ctc acc gag gct cgc gcg tgg aaa caa tac tcc acc atc 787  
 Thr Ser Asp Leu Thr Glu Ala Arg Ala Trp Lys Gln Tyr Ser Thr Ile  
 215 220 225

ata aac gcc gcc gcc tac act gcc gtt gac cag gca gaa cac gac cgc 835  
 Ile Asn Ala Ala Ala Tyr Thr Ala Val Asp Gln Ala Glu His Asp Arg  
 230 235 240 245

gca gca gcg tgg gac att aac gca gcg gca gtg gct acc tcg cga cca 883  
 Ala Ala Ala Trp Asp Ile Asn Ala Ala Val Ala Thr Ser Arg Pro  
 250 255 260

tcg cgc gcg aca aca acc tca ccc tcg tgc acg tgt cct cag att atg 931  
 Ser Arg Ala Thr Thr Thr Ser Pro Ser Cys Thr Cys Pro Gln Ile Met  
 265 270 275

tct tcg acg gtg cgg gcg aat cct acg atg aaa acg cac cgt ttt ccc 979  
 Ser Ser Thr Val Arg Ala Asn Pro Thr Met Lys Thr His Arg Phe Pro  
 280 285 290

cac tcg gcg tgt acg gcc aat cca aag cag ccg gcg aca tcg 1021  
 His Ser Ala Cys Thr Ala Asn Pro Lys Gln Pro Ala Thr Ser  
 295 300 305

taagcac 1028

<210> 448  
 <211> 307  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 448  
 Met Glu Tyr Gly Lys Gln Leu Thr Ser His Thr Thr Asp Ile Glu Gly  
 1 5 10 15  
 Leu Leu Val Phe Asp Phe Pro Val His Gly Asp Asn Arg Gly Trp Phe  
 20 25 30  
 Lys Glu Asn Trp Gln Arg Thr Lys Met Thr Asn Leu Gly Leu Pro Asp  
 35 40 45  
 Phe Gly Pro Val Gln Asn Asn Met Ser Phe Asn Ala Thr Ala Gly Thr  
 50 55 60  
 Thr Arg Gly Met His Ala Glu Pro Trp Asp Lys Phe Val Ser Val Ala  
 65 70 75 80  
 Val Gly Ser Val Phe Gly Ala Trp Val Asp Leu Arg Ala Gly Ser Ser  
 85 90 95  
 Thr Tyr Gly Asn Val Val Thr Gln Lys Ile Thr Pro Asp Val Gly Val  
 100 105 110  
 Tyr Val Pro Arg Gly Val Ala Asn Gly Phe Gln Ala Leu Glu Asp Gly  
 115 120 125

002290"0420960



```
<210> 449
<211> 1056
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101) .. (1033)
<223> RXA00825
```

```
<400> 449
cccgttcattg ctgggctttg gtgcggtgat ggcaactatt tgtctgatca ttgtgagttt 60
```

```
tagtgacgcg  cgattctgag  aaacaactaa  agtgagccac  atg  cgc  aca  gta  gtt      115
                Met  Arg  Thr  Val  Val
                1              5
```

acc ggc ggt gcc ggc ttc atc gga tcc cat ctc gtt gac ctt ttg atc 163  
Thr Gly Gly Ala Gly Phe Ile Gly Ser His Leu Val Asp Leu Leu Ile  
10 15 20

aag gaa ggc cac gag gtc gtt gtg atc gat aac ctc tcc cgc gga cgc 211  
Lys Glu Gly His Glu Val Val Val Ile Asp Asn Leu Ser Arg Gly Arg



**THE**  
**WORLD**  
**OF**  
**THE**  
**FUTURE**



```
<210> 450
<211> 311
<212> PRT
<213> Corynebacterium glutamicum
```

[illegible]







atc ggc acc ttt gtc ctg cta gaa gca gtc cgc aag cac aac aaa cgc 451  
 Ile Gly Thr Phe Val Leu Leu Glu Ala Val Arg Lys His Asn Lys Arg  
 105 110 115

ttc cac cac atc tcc acc gat gaa gtc ttc ggc gat cta gag ctg gat 499  
 Phe His His Ile Ser Thr Asp Glu Val Phe Gly Asp Leu Glu Leu Asp  
 120 125 130

gat cca aac cgc ttc act gaa acc acc gcc tac aag cca tcg tct cca 547  
 Asp Pro Asn Arg Phe Thr Glu Thr Thr Ala Tyr Lys Pro Ser Ser Pro  
 135 140 145

tat tct gca acc aag gca ggg tct gat cac ttg gta cac gca tgg atc 595  
 Tyr Ser Ala Thr Lys Ala Gly Ser Asp His Leu Val His Ala Trp Ile  
 150 155 160 165

cgc tcc ttc gga atc cag gca acc atg tct aac tgc tcc aac aat tac 643  
 Arg Ser Phe Gly Ile Gln Ala Thr Met Ser Asn Cys Ser Asn Asn Tyr  
 170 175 180

ggt ccc tac cag cac att gaa aag ttc atc ccc cgc cag atc acc aat 691  
 Gly Pro Tyr Gln His Ile Glu Lys Phe Ile Pro Arg Gln Ile Thr Asn  
 185 190 195

att ctg gcc ggc ctg aca cca aaa ctt tat gga acc ggc gag cag gtc 739  
 Ile Leu Ala Gly Leu Thr Pro Lys Leu Tyr Gly Thr Gly Glu Gln Val  
 200 205 210

cgc gac tgg atc cac gtc gat gat cac aat gac gcc gtc cac ctg atc 787  
 Arg Asp Trp Ile His Val Asp Asp His Asn Asp Ala Val His Leu Ile  
 215 220 225

ctg agt aag ggc aag atc ggc gaa acc tac atc atc ggc gcc gac aac 835  
 Leu Ser Lys Gly Lys Ile Gly Glu Thr Tyr Ile Ile Gly Ala Asp Asn  
 230 235 240 245

gat cat gtg aat aac aag cag gtc atc gag ctt att tgt gaa ctc atg 883  
 Asp His Val Asn Asn Lys Gln Val Ile Glu Leu Ile Cys Glu Leu Met  
 250 255 260

ggc ctc gac aaa aac gca tac gag cac gtc gca gac cgc ccc ggc cac 931  
 Gly Leu Asp Lys Asn Ala Tyr Glu His Val Ala Asp Arg Pro Gly His  
 265 270 275

gat atg cgt tac gcc atg gat tcc acc aag ctg cgc acc gag ctc ggc 979  
 Asp Met Arg Tyr Ala Met Asp Ser Thr Lys Leu Arg Thr Glu Leu Gly  
 280 285 290

tgg gca cct aaa tac acc gac gtt gat tcc ggc atg cgc aaa ggc cta 1027  
 Trp Ala Pro Lys Tyr Thr Asp Val Asp Ser Gly Met Arg Lys Gly Leu  
 295 300 305

gag cag acc atc gat tgg tac cgc gaa aac gag gcc tgg tgg cgc cct 1075  
 Glu Gln Thr Ile Asp Trp Tyr Arg Glu Asn Glu Ala Trp Trp Arg Pro  
 310 315 320 325

gcc aag aac aac gtc gaa gct acc tac gct aag cag gga caa 1117  
 Ala Lys Asn Asn Val Glu Ala Thr Tyr Ala Lys Gln Gly Gln  
 330 335

taatggaata cggtaaacaa ctc 1140

002290" 04220960



&lt;210&gt; 452

&lt;211&gt; 339

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 452

Met Thr Ser Leu Leu Val Thr Gly Gly Ala Gly Phe Ile Gly Ala Asn  
 1 5 10 15

Phe Val Arg Gln Thr Val Glu Gln His Pro Glu Tyr Thr His Ile Thr  
 20 25 30

Val Leu Asp Lys Leu Thr Tyr Ala Gly Asn Ala Asp Asn Leu Lys Gly  
 35 40 45

Leu Pro Asp Ser Lys Val Thr Leu Ile Glu Gly Asp Ile Cys Asp Ala  
 50 55 60

Glu Leu Val Asp Ser Leu Val Lys Asp His Asp Ile Thr Val His Phe  
 65 70 75 80

Ala Ala Glu Ser His Asn Asp Asn Ser Leu Asn Asp Pro Ser Pro Phe  
 85 90 95

Val His Thr Asn Leu Ile Gly Thr Phe Val Leu Leu Glu Ala Val Arg  
 100 105 110

Lys His Asn Lys Arg Phe His His Ile Ser Thr Asp Glu Val Phe Gly  
 115 120 125

Asp Leu Glu Leu Asp Asp Pro Asn Arg Phe Thr Glu Thr Thr Ala Tyr  
 130 135 140

Lys Pro Ser Ser Pro Tyr Ser Ala Thr Lys Ala Gly Ser Asp His Leu  
 145 150 155 160

Val His Ala Trp Ile Arg Ser Phe Gly Ile Gln Ala Thr Met Ser Asn  
 165 170 175

Cys Ser Asn Asn Tyr Gly Pro Tyr Gln His Ile Glu Lys Phe Ile Pro  
 180 185 190

Arg Gln Ile Thr Asn Ile Leu Ala Gly Leu Thr Pro Lys Leu Tyr Gly  
 195 200 205

Thr Gly Glu Gln Val Arg Asp Trp Ile His Val Asp Asp His Asn Asp  
 210 215 220

Ala Val His Leu Ile Leu Ser Lys Gly Lys Ile Gly Glu Thr Tyr Ile  
 225 230 235 240

Ile Gly Ala Asp Asn Asp His Val Asn Asn Lys Gln Val Ile Glu Leu  
 245 250 255

Ile Cys Glu Leu Met Gly Leu Asp Lys Asn Ala Tyr Glu His Val Ala  
 260 265 270

Asp Arg Pro Gly His Asp Met Arg Tyr Ala Met Asp Ser Thr Lys Leu  
 275 280 285

00602740-062200



<400> 453																
gcggtcattg	tgaccacaaa	tcgtgtggaa	ttgctgcggc	attccctcga	ggttgttgcc	60										
aatcaaacct atccggtgaa acacattgtg gtggtggata atg ggg cgg atc cta 115																
Met Gly Arg Ile Leu 5																
1																
gta	ttc	tat	agt	gtc	act	tta	gag	gtg	gcg	gga	gac	cgt	ccc	gtt	tac	163
Val	Phe	Tyr	Ser	Val	Thr	Leu	Glu	Val	Ala	Gly	Asp	Arg	Pro	Val	Tyr	
10 15 20																
acg	cct	tcg	cgc	acc	aat	ttg	ggc	gac	ggt	ggc	ggt	ttt	gct	ttt	ggt	211
Thr	Pro	Ser	Arg	Thr	Asn	Leu	Gly	Asp	Gly	Gly	Gly	Phe	Ala	Phe	Gly	
25 30 35																
ttt	ttg	acg	gcg	ttg	gcg	ctg	ggg	gcg	aac	gcg	gtg	tgg	tgc	aca	gac	259
Phe	Leu	Thr	Ala	Leu	Ala	Leu	Gly	Ala	Asn	Ala	Val	Trp	Cys	Thr	Asp	
40 45 50																
gat	gac	ggc	cgg	ccg	gag	ggg	cca	ggg	gtg	ttg	aag	acg	ctt	atc	gac	307
Asp	Asp	Gly	Arg	Pro	Glu	Gly	Pro	Gly	Val	Leu	Lys	Thr	Leu	Ile	Asp	
55 60 65																
gcc	gct	tct	cgg	cat	aat	ctg	gag	gag	gtt	tct	ccg	gtg	gta	tgc	aat	355
Ala	Ala	Ser	Arg	His	Asn	Leu	Glu	Glu	Val	Ser	Pro	Val	Val	Cys	Asn	
70 75 80 85																
gct	gat	gat	ccg	gag	cgg	ttg	gca	ttt	ccg	ctg	cgt	cgg	ggc	ttg	gag	403
Ala	Asp	Asp	Pro	Glu	Arg	Leu	Ala	Phe	Pro	Leu	Arg	Arg	Gly	Leu	Glu	
90 95 100																
tgg	cgt	cgg	atg	cgc	agt	gag	ttg	att	gat	cca	gcc	aac	ccg	gag	gat	451
Trp	Arg	Arg	Met	Arg	Ser	Glu	Leu	Ile	Asp	Pro	Ala	Asn	Pro	Glu	Asp	
105 110 115																
gat	ttg	ctg	ccg	ggc	atc	gcc	tcc	ttg	ttc	aat	ggt	gcc	ctg	atc	agc	499
Asp	Leu	Leu	Pro	Gly	Ile	Ala	Ser	Leu	Phe	Asn	Gly	Ala	Leu	Ile	Ser	



```
<210> 454
<211> 262
<212> PRT
<213> Corynebacterium glutamicum
```

```

<400> 454
Met Gly Arg Ile Leu Val Phe Tyr Ser Val Thr Leu Glu Val Ala Gly
  1          5          10          15
Asp Arg Pro Val Tyr Thr Pro Ser Arg Thr Asn Leu Gly Asp Gly Gly
          20          25          30
Gly Phe Ala Phe Gly Phe Leu Thr Ala Leu Ala Leu Gly Ala Asn Ala
          35          40          45
Val Trp Cys Thr Asp Asp Asp Gly Arg Pro Glu Gly Pro Gly Val Leu
          50          55          60
Lys Thr Leu Ile Asp Ala Ala Ser Arg His Asn Leu Glu Glu Val Ser
  65          70          75          80
Pro Val Val Cys Asn Ala Asp Asp Pro Glu Arg Leu Ala Phe Pro Leu

```



85 90 95

Arg Arg Gly Leu Glu Trp Arg Arg Met Arg Ser Glu Leu Ile Asp Pro  
100 105 110

Ala Asn Pro Glu Asp Asp Leu Leu Pro Gly Ile Ala Ser Leu Phe Asn  
115 120 125

Gly Ala Leu Ile Ser Ala Tyr Ala Met Glu Arg Ile Gly Val Pro Asp  
130 135 140

Tyr Arg Leu Phe Ile Arg Gly Asp Glu Val Glu Tyr His Arg Arg Leu  
145 150 155 160

Val Arg Ser Gly Leu Pro Phe Gly Thr Cys Leu Thr Thr Ala Tyr Leu  
165 170 175

His Pro Asp Gly Ser Asp Glu Phe Lys Pro Ile Leu Gly Gly Arg Met  
180 185 190

His Thr Gln Tyr Pro Asp Asn Asp Phe Lys Arg Phe Phe Thr Tyr Arg  
195 200 205

Asn Arg Gly Tyr Leu Met Ser Gln Pro Gly Met Arg Lys Leu Leu Pro  
210 215 220

Gln Glu Tyr Ala Arg Phe Ala Trp Phe Phe Leu Val Gln Lys Arg Asp  
225 230 235 240

Val Lys Gly Phe Arg Glu Trp Leu Arg Leu His Lys Leu Gly Arg Asp  
245 250 255

Glu Lys Phe Asn Arg Pro  
260

<210> 455  
<211> 555  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(532)  
<223> FRXA00427

<400> 455  
tgctgatgat ccggagcggg ttgcatttcc gctgcgctcgg ggcttggagt ggcgtcggat 60

gcgcagtgag ttgattgatc cagccaaccc ggaggatgat ttg ctg ccg ggc atc 115  
Leu Leu Pro Gly Ile  
1 5

gcc tcc ttg ttc aat ggt gcc ctg atc agc gct tat gca atg gag cgc 163  
Ala Ser Leu Phe Asn Gly Ala Leu Ile Ser Ala Tyr Ala Met Glu Arg  
10 15 20

att ggc gtg ccg gac tat cga ctg ttt att cgc ggc gat gag gtg gag 211  
Ile Gly Val Pro Asp Tyr Arg Leu Phe Ile Arg Gly Asp Glu Val Glu  
25 30 35

09602740-062300



tat	cac	cgc	cgt	ttg	gtg	cgt	tcc	ggg	ttg	ccg	ttt	ggg	acg	tgt	ttg	259
Tyr	His	Arg	Arg	Leu	Val	Arg	Ser	Gly	Leu	Pro	Phe	Gly	Thr	Cys	Leu	
		40					45					50				
acc	acg	gcg	tat	ttg	cac	ccg	gat	ggg	tct	gat	gag	ttc	aag	ccg	att	307
Thr	Thr	Ala	Tyr	Leu	His	Pro	Asp	Gly	Ser	Asp	Glu	Phe	Lys	Pro	Ile	
		55				60					65					
ctg	ggg	ggg	cgg	atg	cat	acg	cag	tat	ccg	gat	aat	gat	ttc	aag	agg	355
Leu	Gly	Gly	Arg	Met	His	Thr	Gln	Tyr	Pro	Asp	Asn	Asp	Phe	Lys	Arg	
					75					80					85	
ttt	ttc	acc	tac	cgc	aac	cgt	ggc	tac	ctg	atg	agc	cag	ccg	gga	atg	403
Phe	Phe	Thr	Tyr	Arg	Asn	Arg	Gly	Tyr	Leu	Met	Ser	Gln	Pro	Gly	Met	
				90					95					100		
cgc	aag	ctt	ctc	cct	cag	gaa	tat	gcg	cgc	ttt	gcg	tgg	ttc	ttc	ctg	451
Arg	Lys	Leu	Leu	Pro	Gln	Glu	Tyr	Ala	Arg	Phe	Ala	Trp	Phe	Phe	Leu	
			105					110					115			
gtt	cag	aaa	cgg	gat	gtg	aag	gga	ttc	cgg	gag	tgg	ctg	cgc	ctg	cac	499
Val	Gln	Lys	Arg	Asp	Val	Lys	Gly	Phe	Arg	Glu	Trp	Leu	Arg	Leu	His	
		120					125					130				
aaa	ctg	ggc	cgc	gac	gag	aaa	ttc	aat	agg	ccc	tagatcagtt	ttagtagttc				552
Lys	Leu	Gly	Arg	Asp	Glu	Lys	Phe	Asn	Arg	Pro						
		135				140										
ctc																555
<210>	456															
<211>	144															
<212>	PRT															
<213>	Corynebacterium glutamicum															
<400>	456															
Leu	Leu	Pro	Gly	Ile	Ala	Ser	Leu	Phe	Asn	Gly	Ala	Leu	Ile	Ser	Ala	
1				5					10					15		
Tyr	Ala	Met	Glu	Arg	Ile	Gly	Val	Pro	Asp	Tyr	Arg	Leu	Phe	Ile	Arg	
			20					25					30			
Gly	Asp	Glu	Val	Glu	Tyr	His	Arg	Arg	Leu	Val	Arg	Ser	Gly	Leu	Pro	
		35					40					45				
Phe	Gly	Thr	Cys	Leu	Thr	Thr	Ala	Tyr	Leu	His	Pro	Asp	Gly	Ser	Asp	
	50					55					60					
Glu	Phe	Lys	Pro	Ile	Leu	Gly	Gly	Arg	Met	His	Thr	Gln	Tyr	Pro	Asp	
	65				70					75					80	
Asn	Asp	Phe	Lys	Arg	Phe	Phe	Thr	Tyr	Arg	Asn	Arg	Gly	Tyr	Leu	Met	
				85					90					95		
Ser	Gln	Pro	Gly	Met	Arg	Lys	Leu	Leu	Pro	Gln	Glu	Tyr	Ala	Arg	Phe	
			100					105					110			
Ala	Trp	Phe	Phe	Leu	Val	Gln	Lys	Arg	Asp	Val	Lys	Gly	Phe	Arg	Glu	
		115				</										

```
<210> 456
<211> 144
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 456															
Leu	Leu	Pro	Gly	Ile	Ala	Ser	Leu	Phe	Asn	Gly	Ala	Leu	Ile	Ser	Ala
1				5					10					15	
Tyr	Ala	Met	Glu	Arg	Ile	Gly	Val	Pro	Asp	Tyr	Arg	Leu	Phe	Ile	Arg
			20					25					30		
Gly	Asp	Glu	Val	Glu	Tyr	His	Arg	Arg	Leu	Val	Arg	Ser	Gly	Leu	Pro
		35					40					45			
Phe	Gly	Thr	Cys	Leu	Thr	Thr	Ala	Tyr	Leu	His	Pro	Asp	Gly	Ser	Asp
	50					55					60				
Glu	Phe	Lys	Pro	Ile	Leu	Gly	Gly	Arg	Met	His	Thr	Gln	Tyr	Pro	Asp
65					70					75					80
Asn	Asp	Phe	Lys	Arg	Phe	Phe	Thr	Tyr	Arg	Asn	Arg	Gly	Tyr	Leu	Met
				85					90					95	
Ser	Gln	Pro	Gly	Met	Arg	Lys	Leu	Leu	Pro	Gln	Glu	Tyr	Ala	Arg	Phe
			100					105					110		
Ala	Trp	Phe	Phe	Leu	Val	Gln	Lys	Arg	Asp	Val	Lys	Gly	Phe	Arg	Glu
		115					120					125			



$\langle 210 \rangle$	458
$\langle 211 \rangle$	128

**SECRET**



<212> PRT

<213> Corynebacterium glutamicum

<400> 458

Met Ile Gln Ala Ala Leu Trp Ile Val Leu Phe Leu Phe Ala Asp Arg  
1 5 10 15

Leu Ser Asn Pro Leu Val Phe Val Ser Ala Ile Met Phe Ala Ile Ser  
20 25 30

Phe Ser Ser Pro Val Ala Asn Phe Gly Phe Asp Thr Ile Cys Glu Lys  
35 40 45

Leu Asp Arg Arg Val Met Val Ala Gly Thr Gly Met Ala Asn Met Ser  
50 55 60

Ala Tyr Ile Cys Ala Met Leu Ala Thr Gln Ile Ile Gly Phe Leu Leu  
65 70 75 80

Asp Trp Asn Ala Asp Gly His Ala Tyr Thr Trp Ser Asn Phe Gln Val  
85 90 95

Ala Trp Leu Gly Leu Gly Ala Val Trp Leu Ala Gly Met Ile Gly Leu  
100 105 110

Ala Val Cys Leu Leu Leu Gln Arg Arg Lys Asn Ile Ala Phe Arg Arg  
115 120 125

<210> 459

<211> 615

<212> DNA

<213> Corynebacterium glutamicum

 $\langle 220 \rangle$ 

<221> CDS

<222> (101) . . (592)

<223> RXA00328

<400> 459

gtcacgggat ttgttgtagc ccgactcaag ggtggaccgg gccgcagatt actcgcccaq 60

attaggtcta ccaaggactt ttaaagatcg ggtaaacct gtg ggc gtt gaa agg 115  
Val Gly Val Glu Arg  
1 5

ggc aag gtc tct gcc aag gca cta gtt gtc tgg ttg acg gca atg tgc 163  
Gly Lys Val Ser Ala Lys Ala Leu Val Val Trp Leu Thr Ala Met Cys  
10 15 20

gtg	tac	atc	gtg	gcc	att	gct	ggt	cga	aca	tca	ttt	ggt	gtc	gcc	gga	211
Val	Tyr	Ile	Val	Ala	Ile	Ala	Gly	Arg	Thr	Ser	Phe	Gly	Val	Ala	Gly	
			25				30						35			

gtg	cat	gcg	atc	gat	cgc	ttt	gat	atc	gac	gcc	tcc	cgg	ttg	gcc	gtg	259
Val	His	Ala	Ile	Asp	Arg	Phe	Asp	Ile	Asp	Ala	Ser	Arg	Leu	Ala	Val	
		40					45					50				

0960240 092300



```
<210> 460
<211> 164
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 460															
Val	Gly	Val	Glu	Arg	Gly	Lys	Val	Ser	Ala	Lys	Ala	Leu	Val	Val	Trp
1				5					10					15	
Leu	Thr	Ala	Met	Cys	Val	Tyr	Ile	Val	Ala	Ile	Ala	Gly	Arg	Thr	Ser
			20					25					30		
Phe	Gly	Val	Ala	Gly	Val	His	Ala	Ile	Asp	Arg	Phe	Asp	Ile	Asp	Ala
		35					40					45			
Ser	Arg	Leu	Ala	Val	Phe	Thr	Ser	Val	Gln	Val	Gly	Val	Tyr	Val	Leu
	50					55					60				
Ala	Gln	Ile	Pro	Met	Gly	Met	Leu	Val	Asp	Arg	Phe	Asp	Ala	Arg	Lys
65					70					75					80
Leu	Leu	Leu	Ala	Gly	Ala	Leu	Ile	Leu	Ala	Ala	Gly	Gln	Leu	Ile	Leu
				85					90					95	
Gly	Phe	Thr	Asp	Ser	Tyr	Met	Ile	Ala	Ile	Phe	Ala	Arg	Val	Leu	Ile
			100					105					110		
Ser	Val	Gly	Asp	Ser	Ser	Ala	Phe	Leu	Ser	Val	Met	Arg	Leu	Leu	Pro
		115					120					125			



Tyr Ser Thr Pro

```
<220>
<221> CDS
<222> (101)..(1324)
<223> RXA00329
```

cct ttc atg gcg ttg ttg ggt gcg cag ggt tgg cct gtg gcg ttt gtc 547  
Pro Phe Met Ala Leu Leu Gly Ala Gln Gly Trp Pro Val Ala Phe Val

[illegible]



135	140	145	
agc ctt ggt tcc gtg gtg gca ctc att gcg atc gca gcg ctg gtg gcc Ser Leu Gly Ser Val Val Ala Leu Ile Ala Ile Ala Ala Leu Val Ala 150 155 160 165			595
ggt cgg gat act cca gat cct cag cca aaa cct gtc gaa tca gct cag Val Arg Asp Thr Pro Asp Pro Gln Pro Lys Pro Val Glu Ser Ala Gln 170 175 180			643
gaa gca gat aaa cca agc ctg cgc gcg agt ttg aag ttg att gtc cgc Glu Ala Asp Lys Pro Ser Leu Arg Ala Ser Leu Lys Leu Ile Val Arg 185 190 195			691
aat ccg att acg tgg cag ggt ttc ttc att cac tac gta ttg atg gtg Asn Pro Ile Thr Trp Gln Gly Phe Phe Ile His Tyr Val Leu Met Val 200 205 210			739
tgg cag acc gtg ttc tcc atg atg tgg ggc gtc ccg ctg atg act ttg Trp Gln Thr Val Phe Ser Met Met Trp Gly Val Pro Leu Met Thr Leu 215 220 225			787
ggc atg gga ctg tct gca acg acg gct ggt ttg gtg ttg agc atc aac Gly Met Gly Leu Ser Ala Thr Thr Ala Gly Leu Val Leu Ser Ile Asn 230 235 240 245			835
acg ctg tgc atg gtg gta tgc gcg cca atc atc gga ata att tcc gca Thr Leu Cys Met Val Val Ser Ala Pro Ile Ile Gly Ile Ile Ser Ala 250 255 260			883
cgc ctt ggg tat cgc cgt gac gtg gtc gcc att gcg ctg tgc ttt gtt Arg Leu Gly Tyr Arg Arg Asp Val Val Ala Ile Ala Leu Ser Phe Val 265 270 275			931
caa tcc gca gta tgg ctg gtg ttc ttg gcc tcc gat gca cct cgt ggt Gln Ser Ala Val Trp Leu Val Phe Leu Ala Ser Asp Ala Pro Arg Gly 280 285 290			979
ttg atg gct atc atc ttg gtc aac atc gtc atg ggt ctg act act gcg Leu Met Ala Ile Ile Leu Val Asn Ile Val Met Gly Leu Thr Thr Ala 295 300 305			1027
gct tct ggt tat ggc ttt gac acc att cgt gag cgc cta gat cgc aag Ala Ser Gly Tyr Gly Phe Asp Thr Ile Arg Glu Arg Leu Asp Arg Lys 310 315 320 325			1075
att ttg gct gcg ggc acg gga ctg gca aac atg ggt gga ttc ttg tca Ile Leu Ala Ala Gly Thr Gly Leu Ala Asn Met Gly Gly Phe Leu Ser 330 335 340			1123
tgc atg gtt gca gcg cag gtt atg ggg ttc ctt ctt gat cac agc gcg Ser Met Val Ala Ala Gln Val Met Gly Phe Leu Leu Asp His Ser Ala 345 350 355			1171
cat ggt agc acc tat act tgg gtg gac ttc cgt ttt ggt ttc ctt gcg His Gly Ser Thr Tyr Thr Trp Val Asp Phe Arg Phe Gly Phe Leu Ala 360 365 370			1219
att ctt gtc aca tgg gcc gtc gga gtc acg gga ttt gtt gta gcc cga Ile Leu Val Thr Trp Ala Val Gly Val Thr Gly Phe Val Val Ala Arg 375 380 385			1267

09602740-062300



ctc aag ggt gga ccg ggc cgc aga tta ctc gcc cag att agg tct acc 1315  
 Leu Lys Gly Gly Pro Gly Arg Arg Leu Leu Ala Gln Ile Arg Ser Thr  
 390 395 400 405

aag gac ttt taaagatcgg gtaaaacctg tgg 1347  
 Lys Asp Phe

<210> 462

<211> 408

<212> PRT

<213> Corynebacterium glutamicum

<400> 462

Met Ala Ala Ile Thr Ser Arg Thr Ser Phe Gly Val Ala Gly Val Glu  
 1 5 10 15

Ala Ile Asp Arg Phe Gln Val Asp Ala Thr Arg Ile Ala Val Phe Thr  
 20 25 30

Ser Val Gln Val Gly Val Tyr Ala Phe Ala Gln Ile Pro Met Gly Ile  
 35 40 45

Leu Ile Asp Lys Phe Gly Pro Arg Lys Leu Leu Ala Ile Gly Ala Leu  
 50 55 60

Val Met Gly Ile Gly Gln Leu Ile Leu Gly Phe Thr Asp Ser Tyr Ser  
 65 70 75 80

Ile Ala Ile Ile Ala Arg Val Phe Ile Gly Ala Gly Asp Ala Ser Ile  
 85 90 95

Phe Leu Ser Val Met Arg Ile Leu Pro Phe Trp Phe Pro Leu Lys His  
 100 105 110

Thr Pro Ile Phe Thr Gln Leu Thr Thr Cys Leu Gly Gln Leu Gly Gln  
 115 120 125

Phe Phe Ser Ala Val Pro Phe Met Ala Leu Leu Gly Ala Gln Gly Trp  
 130 135 140

Pro Val Ala Phe Val Ser Leu Gly Ser Val Val Ala Leu Ile Ala Ile  
 145 150 155 160

Ala Ala Leu Val Ala Val Arg Asp Thr Pro Asp Pro Gln Pro Lys Pro  
 165 170 175

Val Glu Ser Ala Gln Glu Ala Asp Lys Pro Ser Leu Arg Ala Ser Leu  
 180 185 190

Lys Leu Ile Val Arg Asn Pro Ile Thr Trp Gln Gly Phe Phe Ile His  
 195 200 205

Tyr Val Leu Met Val Trp Gln Thr Val Phe Ser Met Met Trp Gly Val  
 210 215 220

Pro Leu Met Thr Leu Gly Met Gly Leu Ser Ala Thr Thr Ala Gly Leu  
 225 230 235 240

09602740-062300







060740-0230



Table 1. Demographic characteristics of the study population	
Age (years)	65.0 ± 1.5
Gender	
Male	50 (50.0%)
Female	50 (50.0%)
Education (years)	12.0 ± 1.0
Marital status	
Married	40 (80.0%)
Single	10 (20.0%)
Occupation	
Retired	40 (80.0%)
Unemployed	10 (20.0%)
Income (USD/month)	1,200 ± 200
Health status	
Good	40 (80.0%)
Poor	10 (20.0%)
Comorbidities	
Hypertension	30 (60.0%)
Diabetes	20 (40.0%)
Cholesterol	15 (30.0%)
Smoking status	
Smoker	10 (20.0%)
Non-smoker	40 (80.0%)
Alcohol consumption	
Regular	5 (10.0%)
Occasional	15 (30.0%)
Never	30 (60.0%)



[illegible]

<210> 464

<211> 714

&lt;212&gt; PRT

<213> Corynebacterium glutamicum

<400> 464

Leu Lys Lys His Val Thr Ser Ala Val Thr Ala Val Val Thr Ala Phe  
1 5 10 15

Ser Thr Ala Ala Leu Gly Leu Ser Ile Ala Val Ser Pro Ala Val Ala  
20 25 30

[illegible]



Gln Val Ala Asn Pro Ala Pro Asp Leu Ser Ala Pro Tyr Thr Trp Val  
 35 40 45  
 Glu Glu Phe Asp Ser Glu Asp Ala Leu Lys Gly Trp Asn Ile Phe Arg  
 50 55 60  
 Gln Pro Asp Tyr Gly Ser Asp Lys Val Leu Tyr Thr Glu Asp Ala Leu  
 65 70 75 80  
 Ser Ile Glu Asp Gly Lys Leu Thr Ile Thr Thr Gln Arg His Cys Val  
 85 90 95  
 Asp Glu Asp Phe Ala Ile Ser Asp Pro Val Asn Arg Gly Lys Leu Asn  
 100 105 110  
 Asp Ser Thr Ala Gln Val Glu Pro Cys Ala Pro Gly Gln Phe Glu Lys  
 115 120 125  
 Phe Thr Ser Ala Arg Ile Val Thr Pro Lys Ile Ala Arg Gly Glu Phe  
 130 135 140  
 Asp Leu Ser Val Thr Ala Thr Leu Asn Thr Gly Gly Val Glu Gly Val  
 145 150 155 160  
 Arg Ser Ala Ile Trp Met Gln Asn Gly Glu Gln Ala Cys Ser Ser Ala  
 165 170 175  
 Thr Asn Asn Gly Leu Tyr Gly Glu Leu Asp Leu Val Glu His Phe Ser  
 180 185 190  
 Tyr Asp Leu Arg Ser Pro Trp Ser Pro Ser Asn Thr His Leu Gly Cys  
 195 200 205  
 Asp Pro Glu Ser Val Asn Gly Thr Asn Arg Ala Pro Arg Glu Leu Lys  
 210 215 220  
 Leu Asp Glu Ser Leu Asp Gly Val Glu His Thr Trp Thr Val Ser Thr  
 225 230 235 240  
 Thr Arg Asp Gly Val Glu Tyr Phe Ile Asp Asp Glu Ala Ile Asn Arg  
 245 250 255  
 Gln Ser Trp Arg Asn Asp Val Thr Leu Gly His Ala Glu Ile Asp Asp  
 260 265 270  
 Phe Gly Ile Ser Ala Gln Thr Phe Asp Glu Ile Val Asp Arg Glu Trp  
 275 280 285  
 Thr Leu Thr Leu Asn Gln Lys Val Glu Ser Ala Asp Trp Ala Lys Pro  
 290 295 300  
 Arg Ser Ser Glu Glu Asp Phe Pro Val Arg Ser Met Val Ile Asp Arg  
 305 310 315 320  
 Ile Glu Val Thr Gly Ser Pro Ala Val Ser Glu Asp Thr Pro Met Pro  
 325 330 335  
 Asp Thr Thr Gln Leu Leu Thr Gln Asp Thr Leu Glu Tyr Leu Gly Arg  
 340 345 350  
 Met Pro Val Leu Glu Arg Tyr Glu Pro Ala Ser Ala Asp Phe Ala Asp

006290" 0420960







```

<400> 466
Leu Gly Val Gly Thr Pro Gln Gln Lys Gly Thr Tyr Ala Ala Asp Leu
  1          5          10          15
Thr Tyr Val Arg Gln Val Val Glu Asp Leu Val Pro Leu Leu Glu Gly
          20          25          30

```



Glu	His	Ile	Ile	Phe	Gly	Lys	Ser	Thr	Val	Pro	Val	Gly	Thr	Ala	Glu
		35					40					45			
Gln	Leu	Gln	Glu	Leu	Ala	Asp	Ser	Leu	Val	Lys	Pro	Gly	Ser	His	Val
	50					55					60				
Glu	Ile	Ala	Trp	Asn	Pro	Glu	Phe	Leu	Arg	Glu	Gly	Tyr	Ala	Val	Lys
65					70					75					80
Asp	Thr	Ile	Thr	Pro	Asp	Arg	Ile	Val	Val	Gly	Val	Arg	Glu		
				85					90						

```
<210> 467
<211> 801
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(778)  
<223> RXN03056
```

<400> 467																
ttactatcac tggtttttgca gatgagatcg cacatgatct cgacgaacag atttccttac 60																
ttaaataaact gaagaacagc tcgcggaagc taaagccaaa ttg gat gcc gca gga 115 Leu Asp Ala Ala Gly 1 5																
att tca ctt tca gcc gtt gga tcc gac ttc ggc aag atc aac atc acc 163 Ile Ser Leu Ser Ala Val Gly Ser Asp Phe Gly Lys Ile Asn Ile Thr 10 15 20																
gat cct ttt gaa gat cac ttg gag cgc gca cgc cac ggt gtt gag gtc 211 Asp Pro Phe Glu Asp His Leu Glu Arg Ala Arg His Gly Val Glu Val 25 30 35																
gct aag ctc ttc ggc gcg aaa tac atc cgc atg ttc tcc ttc ttt att 259 Ala Lys Leu Phe Gly Ala Lys Tyr Ile Arg Met Phe Ser Phe Phe Ile 40 45 50																
gca gaa ggc gac aac cct gaa agc ttc cgc aaa gaa gta ctc tcc cgc 307 Ala Glu Gly Asp Asn Pro Glu Ser Phe Arg Lys Glu Val Leu Ser Arg 55 60 65																
acc cac gca atg gtc gaa ctc gca gaa gcc ggc ggc atc acc ctc ctc 355 Thr His Ala Met Val Glu Leu Ala Glu Ala Gly Gly Ile Thr Leu Leu 70 75 80 85																
cac gaa aat gaa aag gga atc tat ggc gac tcc ccg cag cgc gtg aag 403 His Glu Asn Glu Lys Gly Ile Tyr Gly Asp Ser Pro Gln Arg Val Lys 90 95 100																
gat tta atc acc agc atc gac tcc cct aac tac cgc gca atc tac gac 451 Asp Leu Ile Thr Ser Ile Asp Ser Pro Asn Tyr Arg Ala Ile Tyr Asp 105 110 115																
gca gct aac tac gtg caa acc gga ttc aag cct ttt gat gag gca tgg 499 Ala Ala Asn Tyr Val Gln Thr Gly Phe Lys Pro Phe Asp Glu Ala Trp																



069078-2



Ile Lys Asp Ala Thr Ile Pro Asp Ala Glu His Pro Ile Gly Ile Ile  
 145 150 155 160

Lys Pro Ala Gly Gln Gly Asp Gly Gln Tyr Pro Glu Leu Leu Ala Ala  
 165 170 175

Leu Asn Ala Asp Gly Tyr Asn Gly Phe Val Ser Ile Glu Pro His Leu  
 180 185 190

Gly Asp Phe Asp Glu Phe Gly Gly Leu Cys Gly Pro Asp Leu Trp Thr  
 195 200 205

Ser Ala Cys Asp Ala Leu Ala Gly Ile Leu Asn Asn Ile Asn Ala Glu  
 210 215 220

Tyr Asn  
 225

<210> 469  
 <211> 687  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(664)  
 <223> RXN03030

<400> 469  
 gaagatgaag cagaaaagat cattggtgcg ccagaggttt ctgcattggg caacaaagca 60

cagcttgatt ccgtcacctt gctgcgtaac aaccccatcc gtg ctg cca ctg gat 115  
 Val Leu Pro Leu Asp  
 1 5

cct gca gca agc ctg aag atc tac cca ttg gtt act ggc cgt acc aag 163  
 Pro Ala Ala Ser Leu Lys Ile Tyr Pro Leu Val Thr Gly Arg Thr Lys  
 10 15 20

atc gac gag gtt caa cta cag ctg gaa gca gcc att cgc gca gaa ctc 211  
 Ile Asp Glu Val Gln Leu Gln Leu Glu Ala Ala Ile Arg Ala Glu Leu  
 25 30 35

cca ggg gta acc ttg gtg tct tcc gag tca gaa gca gat ctt gca atc 259  
 Pro Gly Val Thr Leu Val Ser Ser Glu Ser Glu Ala Asp Leu Ala Ile  
 40 45 50

gtg tgg gct cgc cct gaa att gca ctg ttt gaa gat gac ctc gaa ggt 307  
 Val Trp Ala Arg Pro Glu Ile Ala Leu Phe Glu Asp Asp Leu Glu Gly  
 55 60 65

gtt tcc ctc tct gtt gac cct cgt gcc aat ggt gtc gat gtg gaa cgc 355  
 Val Ser Leu Ser Val Asp Pro Arg Ala Asn Gly Val Asp Val Glu Arg  
 70 75 80 85

gtt cag gct gtg gaa gct gca gtc cca acc atc ttg gct gtg aac ttc 403  
 Val Gln Ala Val Glu Ala Ala Val Pro Thr Ile Leu Ala Val Asn Phe  
 90 95 100

09602740-062200



[illegible]

<210> 470  
<211> 188  
<212> PRT  
<213> *Corynebacterium glutamicum*

<400> 470															
Val 1	Leu	Pro	Leu	Asp 5	Pro	Ala	Ala	Ser	Leu 10	Lys	Ile	Tyr	Pro	Leu 15	Val
Thr	Gly	Arg	Thr 20	Lys	Ile	Asp	Glu	Val 25	Gln	Leu	Gln	Leu	Glu 30	Ala	Ala
Ile	Arg	Ala 35	Glu	Leu	Pro	Gly	Val 40	Thr	Leu	Val	Ser	Ser 45	Glu	Ser	Glu
Ala	Asp 50	Leu	Ala	Ile	Val	Trp 55	Ala	Arg	Pro	Glu	Ile 60	Ala	Leu	Phe	Glu
Asp 65	Asp	Leu	Glu	Gly	Val 70	Ser	Leu	Ser	Val	Asp 75	Pro	Arg	Ala	Asn	Gly 80
Val	Asp	Val	Glu	Arg 85	Val	Gln	Ala	Val	Glu 90	Ala	Ala	Val	Pro	Thr 95	Ile
Leu	Ala	Val	Asn 100	Phe	Thr	Asn	Pro	Trp 105	Val	Leu	Ser	Glu 110	Ile	Glu	Pro
Gly	Ala 115	Ala	Ala	Val	Val	Gly	Thr 120	Phe	Glu	Ile	Lys	Pro 125	Glu	Phe	Leu
Leu	Lys 130	Ala	Leu	Thr	Gly	Gln 135	Glu	Gly	Gly	Pro	Lys 140	Gly	Lys	Leu	Pro
Leu 145	Thr	Val	Pro	Ala	Ser 150	Met	Gln	Ala	Ile	Ala 155	Asp	Ser	Pro	Arg	Asp 160

	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2423	2424	2425	2426	2427	2428	2429	2430	2431	2432	2433	2434	2435	2436	2437	2438	2439	2440	2441	2442	2
--	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	---



Gly Met Ala Tyr Lys Tyr Gly His Gly Leu Asn Phe  
180 185

```
<220>
<221> CDS
<222> (101)..(1039)
<223> RXN00401
```

<400> 471															
cttttaagca tttcaacatg ccaaactaat -cttggacagg tatcactggc tcctcttaga 60															
ctccaaagtg tcttagaaaa cactcaccca aggagccctc atg gca cgc ttt tca 115															
Met Ala Arg Phe Ser 5															
cca caa gat ctc gca gac cac ctc aag gat gga ctg ctc tct ttc ccg 163															
Pro Gln Asp Leu Ala Asp His Leu Lys Asp Gly Leu Leu Ser Phe Pro 20															
gcc acc gct ttc caa gat gac ctc gaa gta gat gaa gct gct tat gtc 211															
Ala Thr Ala Phe Gln Asp Asp Leu Glu Val Asp Glu Ala Ala Tyr Val 35															
gag cac att gaa tgg cag tcc agc tac cca gtc gcc ggc ctc ttc gca 259															
Glu His Ile Glu Trp Gln Ser Ser Tyr Pro Val Ala Gly Leu Phe Ala 50															
gct ggc ggt act ggc gaa gga ttc agc ctt acc gtt gag gaa aac cac 307															
Ala Gly Gly Thr Gly Glu Gly Phe Ser Leu Thr Val Glu Glu Asn His 65															
cgt gtc act caa ctt gca gtt cag gcg tcc agc ccg gaa gtt ccc gtg 355															
Arg Val Thr Gln Leu Ala Val Gln Ala Ser Ser Pro Glu Val Pro Val 85															
ttg ggg tct gct act ggc tca act aag tct gcc atc gca aac gca cag 403															
Leu Gly Ser Ala Thr Gly Ser Thr Lys Ser Ala Ile Ala Asn Ala Gln 100															
ggc gca gag gca gca ggc gct gaa ggt gtc ctc ctg ctt cct ccc tac 451															
Gly Ala Glu Ala Ala Gly Ala Glu Gly Val Leu Leu Leu Pro Pro Tyr 115															
ctc acc gaa tgc gac gca gaa ggc ctg tac aac cat gca gcc gca gtc 499															
Leu Thr Glu Cys Asp Ala Glu Gly Leu Tyr Asn His Ala Ala Ala Val 130															
tgt gaa tcc act tct ctt ggt gtc atc gtg tac aac cgt gcc aat gcc 547															
Cys Glu Ser Thr Ser Leu Gly Val Ile Val Tyr Asn Arg Ala Asn Ala 145															
atc tac tcc cca qaq qtt atc gct cqa ctc tct qaq cgc tac ccc aac 595															

[illegible]



<400> 472

Met	Ala	Arg	Phe	Ser	Pro	Gln	Asp	Leu	Ala	Asp	His	Leu	Lys	Asp	Gly
1				5					10					15	
Leu	Leu	Ser	Phe	Pro	Ala	Thr	Ala	Phe	Gln	Asp	Asp	Leu	Glu	Val	Asp
			20					25					30		
Glu	Ala	Ala	Tyr	Val	Glu	His	Ile	Glu	Trp	Gln	Ser	Ser	Tyr	Pro	Val
		35					40					45			
Ala	Gly	Leu	Phe	Ala	Ala	Gly	Gly	Thr	Gly	Glu	Gly	Phe	Ser	Leu	Thr
	50					55					60				



```
<210> 473
<211> 924
<212> DNA
<213> Corynebacterium glutamicum
<220>
<221> CDS
<222> (101)..(901)
<223> RXN02125
<400> 473
```



[illegible]



cct gtg tat tcc ggc aag tagaaagatt tttatcatgg gac 924  
Pro Val Tyr Ser Gly Lys  
265

<210> 474

<211> 267

&lt;212&gt; PRT

<213> Corynebacterium glutamicum

<400> 474

Met Val Ala Thr Ser Gln Phe Ile Asp Asp Ser Glu Ala Ala Gln Ala  
1 5 10 15

Val Arg Ala Ala Ile Val Ala Gly Tyr Arg Asn Ile Asp Thr Ala Leu  
20 25 30

Ala Tyr Gly Asn Glu Arg Gly Val Gly Glu Gly Ile Arg Thr Ala Gly  
35 40 45

Val Pro Arg Glu Glu Leu Phe Ile Ser Thr Lys Leu Ala Ala Glu Ile  
50 55 60

Lys Asp Tyr Asp Gly Ala Val Ala Ala Ile Asp Glu Ser Leu Ala Lys  
65 70 75 80

Ile Gly Leu Asp Tyr Val Asp Leu Met Leu Ile His Ser Pro Gln Pro  
85 90 95

Trp Ser Asp Phe Arg Gly Gly Asp Tyr Ser Glu Gly Asn Arg Glu Ala  
100 105 110

Trp Arg Ala Leu Glu Asp Ala Tyr Lys Ala Gly Lys Ile Arg Ser Ile  
115 120 125

Gly Val Ser Asn Phe Leu Glu Ala Asp Leu Glu Asn Ile Leu Asp Ser  
130 135 140

Ala Thr Val Ala Pro His Val Asn Gln Leu Leu Val His Val Gly Asn  
145 150 155 160

Thr Pro Ser Glu Leu Ile Ser Phe Cys Asp Ser Lys Gly Ile Leu Val  
165 170 175

Glu Ala Tyr Ser Pro Ile Ala His Gly Glu Met Leu Lys Asn Gln Gln  
180 185 190

Val Lys Ala Ile Ala Asp Lys Tyr Asn Val Ser Ile Pro Gln Leu Cys  
195 200 205

Ile Arg Tyr Thr Ile Gln Leu Gly Thr Val Ser Leu Pro Lys Thr Ala  
210 215 220



Glu His Ser Gly Phe Pro Val Tyr Ser Gly Lys  
260 265

```
<220>
<221> CDS
<222> (101) .. (3538)
<223> RXN00200
```

<400> 475																
aacccggagt	catttgatca	gatgtggcag	accaagcaag	tgggaccttt	cgtaggtggta	60										
acgcacaatg agtaattcct caccaaacga cccaagccct						atg	cgc	caa	gtc	ggc	115					
						Met	Arg	Gln	Val	Gly						
						1				5						
ggc	aat	ggg	ggc	cat	caa	cta	gac	tcg	atc	aac	gtg	tca	gat	gta	ggt	163
Gly	Asn	Gly	Gly	His	Gln	Leu	Asp	Ser	Ile	Asn	Val	Ser	Asp	Val	Val	
						10			15					20		
gag tcg aag aaa cta aag ggt tct gcg caa gaa ccc ccg cag gtt gcc 211																
Glu Ser Lys Lys Leu Lys Gly Ser Ala Gln Glu Pro Pro Gln Val Ala																
						25			30				35			
ccg ggc tgg ctg aag aaa ctg gct atc tca tca ggt ctg ctt ggc ctg 259																
Pro Gly Trp Leu Lys Lys Leu Ala Ile Ser Ser Gly Leu Leu Gly Leu																
						40			45				50			
ttg atg ttt gtg ctg ttg cct ttc ctg cca gtg aac cag gtg cag tct 307																
Leu Met Phe Val Leu Leu Pro Phe Leu Pro Val Asn Gln Val Gln Ser																
						55			60			65				
tcg ctg tca tgg cca caa aat ggt gag ctt tcc agc gtt aac gcc ccg 355																
Ser Leu Ser Trp Pro Gln Asn Gly Glu Leu Ser Ser Val Asn Ala Pro																
						70			75			80			85	
ctg att tcc tac gca ccg cag tcg atg gat gcg tcc atc cct gtg tcc 403																
Leu Ile Ser Tyr Ala Pro Gln Ser Met Asp Ala Ser Ile Pro Val Ser																
						90			95					100		
gcg ctg gac agt ctc aat gac aat cag tcg ttg gtg atg ggc acg ttg 451																
Ala Leu Asp Ser Leu Asn Asp Asn Gln Ser Leu Val Met Gly Thr Leu																
						105			110				115			
cct ctg gac agt acg gac gcc acc aac cgt ggt ctg ttt gtg cgc acc 499																
Pro Leu Asp Ser Thr Asp Ala Thr Asn Arg Gly Leu Phe Val Arg Thr																
						120			125				130			
atc gac ggt aac ctt gac gtg att gtt cgc ggt gag gtg ctg ttg gat 547																

[illegible]



0630 0640 0650 0700 0710 0720 0730 0740 0750



**D E F I N I T I O N**



0360240-0600



[illegible]



<400> 476															
Met	Arg	Gln	Val	Gly	Gly	Asn	Gly	Gly	His	Gln	Leu	Asp	Ser	Ile	Asn
1				5					10					15	
Val	Ser	Asp	Val	Val	Glu	Ser	Lys	Lys	Leu	Lys	Gly	Ser	Ala	Gln	Glu
			20					25					30		
Pro	Pro	Gln	Val	Ala	Pro	Gly	Trp	Leu	Lys	Lys	Leu	Ala	Ile	Ser	Ser
		35					40					45			
Gly	Leu	Leu	Gly	Leu	Leu	Met	Phe	Val	Leu	Leu	Pro	Phe	Leu	Pro	Val
	50					55					60				
Asn	Gln	Val	Gln	Ser	Ser	Leu	Ser	Trp	Pro	Gln	Asn	Gly	Glu	Leu	Ser
65					70					75					80
Ser	Val	Asn	Ala	Pro	Leu	Ile	Ser	Tyr	Ala	Pro	Gln	Ser	Met	Asp	Ala
				85					90					95	
Ser	Ile	Pro	Val	Ser	Ala	Leu	Asp	Ser	Leu	Asn	Asp	Asn	Gln	Ser	Leu
			100					105					110		
Val	Met	Gly	Thr	Leu	Pro	Leu	Asp	Ser	Thr	Asp	Ala	Thr	Asn	Arg	Gly
		115					120					125			
Leu	Phe	Val	Arg	Thr	Ile	Asp	Gly	Asn	Leu	Asp	Val	Ile	Val	Arg	Gly
	130					135					140				
Glu	Val	Leu	Leu	Asp	Leu	Ser	Pro	Thr	Glu	Val	Asn	Arg	Leu	Pro	Asp
145					150					155					160
Asp	Ala	Ile	Leu	Glu	Ile	Ser	Ser	Thr	Glu	Glu	Thr	Thr	Ser	Ala	Glu
				165					170					175	
Ile	Thr	Gly	Thr	Ala	Phe	Ser	Gly	Glu	Thr	Glu	Gly	Asp	Glu	Arg	Pro
			180					185					190		
Gln	Val	Thr	Gly	Val	Tyr	Thr	Glu	Leu	Val	Asp	Asp	Pro	Ser	Thr	Ala
		195					200					205			
Ser	Ala	Leu	Ala	Ser	Ala	Gly	Leu	Asn	Val	Asp	Ile	Glu	Ile	Asn	Ser
	210					215					220				
Arg	Phe	Thr	Ser	Ser	Pro	Ser	Leu	Leu	Lys	Tyr	Ala	Ala	Ile	Phe	Ile

**090706Z**



225					230						235				240
Gly	Leu	Ala	Ser	Val	Leu	Val	Ser	Leu	Trp	Thr	Leu	His	Arg	Met	Asp
				245					250					255	
Ile	Leu	Asp	Gly	Arg	Lys	Ala	His	Arg	Phe	Leu	Pro	Ala	Asn	Trp	Tyr
			260					265					270		
Lys	Leu	Lys	Pro	Leu	Asp	Gly	Val	Val	Val	Ala	Ile	Leu	Val	Phe	Trp
		275					280					285			
His	Phe	Leu	Gly	Ala	Asn	Thr	Ser	Asp	Asp	Gly	Phe	Ile	Met	Thr	Met
	290					295					300				
Ala	Arg	Val	Ser	Gln	Asn	Ala	Asp	Tyr	Met	Ala	Asn	Tyr	Tyr	Arg	Trp
305					310					315					320
Phe	Gly	Val	Pro	Glu	Ser	Pro	Phe	Gly	Ala	Pro	Tyr	Tyr	Asp	Leu	Leu
				325					330					335	
Ala	Leu	Met	Ala	Tyr	Ile	Ser	Thr	Ser	Ser	Ile	Trp	Leu	Arg	Leu	Pro
			340					345					350		
Ala	Leu	Leu	Ala	Gly	Leu	Ile	Met	Trp	Phe	Val	Ile	Thr	Arg	Glu	Val
		355					360					365			
Met	Pro	Arg	Phe	Gly	Ser	Leu	Val	Asn	Gly	Arg	Arg	Val	Ala	His	Trp
	370					375					380				
Ser	Ala	Ala	Met	Val	Phe	Leu	Ala	Phe	Trp	Leu	Pro	Tyr	Asn	Asn	Gly
385					390					395					400
Thr	Arg	Pro	Glu	Pro	Ile	Ile	Ala	Met	Gly	Ala	Leu	Leu	Ala	Trp	Val
				405					410					415	
Ser	Phe	Glu	Arg	Ala	Ile	Ala	Thr	Ser	Arg	Leu	Leu	Pro	Ala	Ala	Ile
			420					425					430		
Gly	Val	Ile	Ile	Ala	Thr	Ile	Ser	Leu	Ala	Ser	Gly	Pro	Thr	Gly	Leu
		435					440					445			
Met	Ala	Val	Ala	Ala	Leu	Leu	Val	Ser	Leu	Ser	Ala	Leu	Ile	Arg	Ile
	450					455					460				
Leu	Tyr	Arg	Arg	Leu	Pro	Leu	Ile	Gly	Ala	Ser	Arg	Gly	Ala	Ser	Lys
465					470					475					480
Ser	Lys	Val	Phe	Gly	Ala	Ser	Met	Ala	Met	Leu	Ala	Pro	Phe	Leu	Ala
				485					490					495	
Ser	Gly	Thr	Ala	Ile	Leu	Ile	Ala	Val	Phe	Gly	Asp	Gln	Thr	Leu	Ser
			500					505					510		
Thr	Val	Met	Glu	Ser	Ile	Ser	Val	Arg	Ser	Ala	Lys	Gly	Pro	Ala	Leu
		515					520					525			
Thr	Trp	Tyr	His	Glu	Tyr	Val	Arg	Tyr	Gln	Thr	Val	Met	Glu	Gln	Thr
	530					535					540				
Val	Asp	Gly	Ser	Phe	Thr	Arg	Arg	Phe	Ala	Val	Leu	Met	Leu	Met	Ala
545					550					555					560

002290"0420950







```
<210> 477
<211> 1509
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1486)
<223> RXN01175
```



&lt;400&gt; 477

tcgcgtctct tagtcgatct gctcccatc cataggttgg gagaaaactt aactgttatt 60

ccattcctta aaacaccgat atcgtgctat gaataggggt gtg agt tgg aca gtt 115  
Val Ser Trp Thr Val  
1 5

gat atc cct aaa gaa gtt ctc cct gat ttg cca cca ttg cca gaa ggc 163  
Asp Ile Pro Lys Glu Val Leu Pro Asp Leu Pro Pro Leu Pro Glu Gly  
10 15 20

atg cag cag cag ttc gag gac acc att tcc cgt gac gct aag cag caa 211  
Met Gln Gln Gln Phe Glu Asp Thr Ile Ser Arg Asp Ala Lys Gln Gln  
25 30 35

cct acg tgg gat cgt gca cag gca gaa aac gtg cgc aag atc ctt gag 259  
Pro Thr Trp Asp Arg Ala Gln Ala Glu Asn Val Arg Lys Ile Leu Glu  
40 45 50

tcg gtt cct cca atc gtt gtt gcc cct gag gta ctt gag ctg aag cag 307  
Ser Val Pro Pro Ile Val Val Ala Pro Glu Val Leu Glu Leu Lys Gln  
55 60 65

aag ctt gct gat gtt gcc aac ggt aag gcc ttc ctc ttg cag ggt ggt 355  
Lys Leu Ala Asp Val Ala Asn Gly Lys Ala Phe Leu Leu Gln Gly Gly  
70 75 80 85

gac tgt gcg gaa act ttc gag tca aac act gag ccg cac att cgc gcc 403  
Asp Cys Ala Glu Thr Phe Glu Ser Asn Thr Glu Pro His Ile Arg Ala  
90 95 100

aac gta aag act ctg ctg cag atg gca gtt gtt ttg acc tac ggt gca 451  
Asn Val Lys Thr Leu Leu Gln Met Ala Val Val Leu Thr Tyr Gly Ala  
105 110 115

tcc act cct gtg atc aag atg gct cgt att gct ggt cag tac gca aag 499  
Ser Thr Pro Val Ile Lys Met Ala Arg Ile Ala Gly Gln Tyr Ala Lys  
120 125 130

cct cgc tct tct gat ctg gat gga aat ggt ctg cca aac tac cgt ggc 547  
Pro Arg Ser Ser Asp Leu Asp Gly Asn Gly Leu Pro Asn Tyr Arg Gly  
135 140 145

gat atc gtc aac ggt gtg gag gca acc cca gag gct cgt cgc cac gat 595  
Asp Ile Val Asn Gly Val Glu Ala Thr Pro Glu Ala Arg Arg His Asp  
150 155 160 165

cct gcc cgc atg atc cgt gct tac gct aac gct tct gct gcg atg aac 643  
Pro Ala Arg Met Ile Arg Ala Tyr Ala Asn Ala Ser Ala Ala Met Asn  
170 175 180

ttg gtg cgc gcg ctc acc agc tct ggc acc gct gat ctt tac cgt ctc 691  
Leu Val Arg Ala Leu Thr Ser Ser Gly Thr Ala Asp Leu Tyr Arg Leu  
185 190 195

agc gag tgg aac cgc gag ttc gtt gcg aac tcc cca gct ggt gca cgc 739  
Ser Glu Trp Asn Arg Glu Phe Val Ala Asn Ser Pro Ala Gly Ala Arg  
200 205 210

tac gag gct ctt gct cgt gag atc gac tcc ggt ctg cgc ttc atg gaa 787

09602740-062300



**THE UNIVERSITY OF CHICAGO**



460

1509

<400> 478															
Val 1	Ser	Trp	Thr	Val 5	Asp	Ile	Pro	Lys	Glu 10	Val	Leu	Pro	Asp	Leu 15	Pro
Pro	Leu	Pro	Glu 20	Gly	Met	Gln	Gln	Gln 25	Phe	Glu	Asp	Thr	Ile 30	Ser	Arg
Asp	Ala	Lys 35	Gln	Gln	Pro	Thr	Trp 40	Asp	Arg	Ala	Gln	Ala 45	Glu	Asn	Val
Arg	Lys 50	Ile	Leu	Glu	Ser	Val 55	Pro	Pro	Ile	Val	Val 60	Ala	Pro	Glu	Val
Leu 65	Glu	Leu	Lys	Gln	Lys 70	Leu	Ala	Asp	Val	Ala 75	Asn	Gly	Lys	Ala	Phe 80
Leu	Leu	Gln	Gly	Gly 85	Asp	Cys	Ala	Glu	Thr 90	Phe	Glu	Ser	Asn	Thr 95	Glu
Pro	His	Ile 100	Arg	Ala	Asn	Val	Lys	Thr 105	Leu	Leu	Gln	Met	Ala 110	Val	Val
Leu	Thr	Tyr 115	Gly	Ala	Ser	Thr	Pro 120	Val	Ile	Lys	Met	Ala 125	Arg	Ile	Ala
Gly 130	Gln	Tyr	Ala	Lys	Pro	Arg 135	Ser	Ser	Asp	Leu	Asp 140	Gly	Asn	Gly	Leu
Pro 145	Asn	Tyr	Arg	Gly	Asp 150	Ile	Val	Asn	Gly	Val 155	Glu	Ala	Thr	Pro	Glu 160
Ala	Arg	Arg	His	Asp 165	Pro	Ala	Arg	Met	Ile 170	Arg	Ala	Tyr	Ala	Asn 175	Ala
Ser	Ala	Ala	Met 180	Asn	Leu	Val	Arg	Ala 185	Leu	Thr	Ser	Ser	Gly 190	Thr	Ala
Asp	Leu	Tyr 195	Arg	Leu	Ser	Glu	Trp 200	Asn	Arg	Glu	Phe	Val 205	Ala	Asn	Ser
Pro 210	Ala	Gly	Ala	Arg	Tyr	Glu 215	Ala	Leu	Ala	Arg	Glu 220	Ile	Asp	Ser	Gly
Leu 225	Arg	Phe	Met	Glu	Ala 230	Cys	Gly	Val	Ser	Asp 235	Glu	Ser	Leu	Arg	Ala 240
Ala	Asp	Ile	Tyr	Cys 245	Ser	His	Glu	Ala	Leu 250	Leu	Val	Asp	Tyr	Glu 255	Arg
Ser	Met	Leu	Arg 260	Leu	Ala	Thr	Asp	Glu 265	Glu	Gly	Asn	Glu	Glu 270	Leu	Tyr



cga gac acc cac gtt gtg atg gca gac aat ggt tct gtg gac ggt gtt 211  
Arg Asp Thr His Val Val Met Ala Asp Asn Gly Ser Val Asp Gly Val













[illegible]



qac 984

<400> 480															
Val 1	Thr	Tyr	Ser	Pro 5	Gly	Lys	Tyr	Leu	Ala 10	Ser	Phe	Leu	Asp	Ser 15	Leu
Pro	Gly	Ala	Thr 20	Ser	Arg	Asp	Thr	His 25	Val	Val	Met	Ala	Asp 30	Asn	Gly
Ser	Val	Asp 35	Gly	Val	Pro	Glu	Gln 40	Ala	Ala	Ala	Ser	Arg 45	Ser	Asn	Val
Glu	Phe 50	Leu	Ser	Thr	Gly	Gly 55	Asn	Leu	Gly	Tyr	Gly 60	Thr	Ala	Ile	Asn
Ile 65	Ala	Ala	Arg	Ser	Leu 70	Arg	Ala	Arg	Arg	Glu 75	Ala	Gly	Glu	Ile	Asp 80
Gly	Glu	Phe	Phe	Leu 85	Val	Ser	Asn	Pro	Asp 90	Val	Val	Phe	Asp	Glu 95	Asp
Ser	Ile	Asp	Gln 100	Leu	Leu	Glu	Cys	Ala 105	Lys	Arg	His	Pro	Glu 110	Ala	Gly
Ala	Val	Gly 115	Pro	Leu	Ile	Arg	Glu 120	Ala	Asp	Gly	Ser	Ala 125	Tyr	Pro	Ser
Ala	Arg 130	Ala	Val	Pro	Thr	Leu 135	Ala	Asn	Gly	Ile	Gly 140	His	Ala	Leu	Leu
Gly 145	Ala	Val	Trp	Lys 150	Ser	Asn	Pro	Trp	Ser	Ala 155	Ala	Tyr	Arg	Asp	Asp 160
Glu	Asp	Met	Asp	Thr 165	Glu	Arg	Thr	Ala	Gly 170	Trp	Leu	Ser	Gly	Ser 175	Cys
Leu	Leu	Leu	Arg 180	Trp	Asp	Ala	Phe	Asp 185	Arg	Val	Gly	Gly	Phe 190	Asp	Glu
Arg	Tyr 195	Phe	Met	Tyr	Met	Glu	Asp 200	Val	Asp	Leu	Gly	Asp 205	Arg	Leu	Val
Arg	Ala 210	Gly	Phe	Thr	Asn	Val 215	Phe	Cys	Pro	Ser	Ala 220	Gln	Ile	Ile	His
Ala 225	Lys	Gly	His	Val	Ala 230	Gly	Lys	Asn	Pro	Glu 235	Asn	Met	Leu	Pro	Ala 240
His	His	Glu	Ser	Ala 245	Tyr	Arg	Phe	Gln	Ala 250	Asp	Arg	Leu	Ala	Lys 255	Pro

[illegible]



Trp Gln Ala Pro Ile Arg Leu Ala Leu Arg Ile Gly Leu Lys Leu Arg  
260 265 270

Ala Gly Val Ala Val Gly Val Ser Lys Met Arg Thr Lys Ala Ser  
275 280 285

<210> 481

<211> 1002

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(979)

<223> RXN01631

<400> 481

gccagttgag gatgctctca cagtcgctcg cattgtcagt gcatgctacg aatccgacaa 60

caaccagggc atttccgtaa acatctaaga ggagcactcc atg aaa cca caa ctt 115  
Met Lys Pro Gln Leu  
1 5

att gca tct tgc tgg acc agc gcg gga gac gcc gca ccc gat cgt gac 163  
Ile Ala Ser Cys Trp Thr Ser Ala Gly Asp Ala Ala Pro Asp Arg Asp  
10 15 20

gat ctc agc agc cca gta gca atc gat gag cgc atc gct cta gtc gct 211  
Asp Leu Ser Ser Pro Val Ala Ile Asp Glu Arg Ile Ala Leu Val Ala  
25 30 35

gaa acc ggt tgg gca ggc att ggg ctt gtt cac gcc gat ctc atc aaa 259  
Glu Thr Gly Trp Ala Gly Ile Gly Leu Val His Ala Asp Leu Ile Lys  
40 45 50

gca cgc gac acc att ggc tac gag gaa ttg cgc cga cgc atc cac gct 307  
Ala Arg Asp Thr Ile Gly Tyr Glu Glu Leu Arg Arg Arg Ile His Ala  
55 60 65

gca gga att gaa atc att gag gtg gag ttc ctc aat ggt tgg tgg gcg 355  
Ala Gly Ile Glu Ile Ile Glu Val Glu Phe Leu Asn Gly Trp Trp Ala  
70 75 80 85

act ggt gcg gaa cgc caa gag tcc gat gcc gtt cgt gcg gat ctg ttt 403  
Thr Gly Ala Glu Arg Gln Glu Ser Asp Ala Val Arg Ala Asp Leu Phe  
90 95 100

gct gcg gcg caa gct ctt ggt tcc cca cac att aag gtc gga gca gga 451  
Ala Ala Ala Gln Ala Leu Gly Ser Pro His Ile Lys Val Gly Ala Gly  
105 110 115

gag ggc acc aat ggt gtg gtt ccc att gct cac atg gcc agt gcg ttt 499  
Glu Gly Thr Asn Gly Val Val Pro Ile Ala His Met Ala Ser Ala Phe  
120 125 130

act gat ctc gct gcg gaa gct gaa gct cat ggc gtc aag ctc gcg ttg 547  
Thr Asp Leu Ala Ala Glu Ala Glu Ala His Gly Val Lys Leu Ala Leu  
135 140 145

09602740-062300



gaa gca act ccg ttt tct cac ctg aag acc atc tac gac gcg ctg gaa 595  
 Glu Ala Thr Pro Phe Ser His Leu Lys Thr Ile Tyr Asp Ala Leu Glu  
 150 155 160 165  
  
 gtt gtc agc cat tcc gat agc cca tcg gct gga ctc atg gtt gat atc 643  
 Val Val Ser His Ser Asp Ser Pro Ser Ala Gly Leu Met Val Asp Ile  
 170 175 180  
  
 tgg cac acc gcg aaa atc gga atc ccc aac gat gaa ctg tgg cgc aac 691  
 Trp His Thr Ala Lys Ile Gly Ile Pro Asn Asp Glu Leu Trp Arg Asn  
 185 190 195  
  
 att cca ctg tcc aag gtc aac gca gtg gag gtt gat gat ggt ttc att 739  
 Ile Pro Leu Ser Lys Val Asn Ala Val Glu Val Asp Asp Gly Phe Ile  
 200 205 210  
  
 gac acc cca att gat ctt ttc gat gac tcc acc aac cgt cgc gcg tac 787  
 Asp Thr Pro Ile Asp Leu Phe Asp Asp Ser Thr Asn Arg Arg Ala Tyr  
 215 220 225  
  
 tgc ggt gaa ggc gaa ttt gat ccc gca agc ttc atc cgt ggc gcc atc 835  
 Cys Gly Glu Gly Glu Phe Asp Pro Ala Ser Phe Ile Arg Gly Ala Ile  
 230 235 240 245  
  
 gac gcc ggt tgg acg ggc gca tat ggt gtg gaa att att tcc gca gag 883  
 Asp Ala Gly Trp Thr Gly Ala Tyr Gly Val Glu Ile Ile Ser Ala Glu  
 250 255 260  
  
 cac cga agc ctc ccg gtg aaa gaa ggg ctg caa cgt gct ttc gac acc 931  
 His Arg Ser Leu Pro Val Lys Glu Gly Leu Gln Arg Ala Phe Asp Thr  
 265 270 275  
  
 acc atc gca gcg ttt gaa caa gct gct cgt ctc gcc ccc tcc act aac 979  
 Thr Ile Ala Ala Phe Glu Gln Ala Ala Arg Leu Ala Pro Ser Thr Asn  
 280 285 290  
  
 tgatctttga aaggctgaaa aaa 1002

&lt;210&gt; 482

&lt;211&gt; 293

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 482

Met Lys Pro Gln Leu Ile Ala Ser Cys Trp Thr Ser Ala Gly Asp Ala  
 1 5 10 15  
  
 Ala Pro Asp Arg Asp Asp Leu Ser Ser Pro Val Ala Ile Asp Glu Arg  
 20 25 30  
  
 Ile Ala Leu Val Ala Glu Thr Gly Trp Ala Gly Ile Gly Leu Val His  
 35 40 45  
  
 Ala Asp Leu Ile Lys Ala Arg Asp Thr Ile Gly Tyr Glu Glu Leu Arg  
 50 55 60  
  
 Arg Arg Ile His Ala Ala Gly Ile Glu Ile Ile Glu Val Glu Phe Leu  
 65 70 75 80  
  
 Asn Gly Trp Trp Ala Thr Gly Ala Glu Arg Gln Glu Ser Asp Ala Val

00E290"0420960



[illegible]

```
<210> 483
<211> 990
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(967)
<223> RXN01593
```

```

<400> 483
atatgacagc cttctttcttg atctagatgg aaccgtctac gagggcggcc gagccattga 60

gcacgtagtt tctgcgctct ctggcgccgg cctaccgcgc atg tat gtc acc aat 115
                               Met Tyr Val Thr Asn
                               1           5

aat gcc tcc cgt gct ccg gag gtg gtg gct gcg caa ctc cgt gag att 163
Asn Ala Ser Arg Ala Pro Glu Val Val Ala Ala Gln Leu Arg Glu Ile

```



	10	15	20	
ggc ctt gcc gac acc act gcg gac aat gtg atg aca tct gct caa gct	211			
Gly Leu Ala Asp Thr Thr Ala Asp Asn Val Met Thr Ser Ala Gln Ala				
	25	30	35	
gcc tgc aag atg gcg gcg gag aag att ccc gct gga tcc aag gtg tat	259			
Ala Cys Lys Met Ala Ala Glu Lys Ile Pro Ala Gly Ser Lys Val Tyr				
	40	45	50	
gtt ttg ggt tca gaa tcc ttc cgc gag cta gct act gaa gct ggt ttt	307			
Val Leu Gly Ser Glu Ser Phe Arg Glu Leu Ala Thr Glu Ala Gly Phe				
	55	60	65	
gtg gtg gtt gat tcg gct gat gat aaa cct gtg gct gtg ctt cac ggc	355			
Val Val Val Asp Ser Ala Asp Asp Lys Pro Val Ala Val Leu His Gly				
	70	75	80	85
cac aac cct gag acc ggt tgg gct cag ttg agc gag gct gcg ctg tca	403			
His Asn Pro Glu Thr Gly Trp Ala Gln Leu Ser Glu Ala Ala Leu Ser				
	90	95	100	
att aat gct ggc gcg cag tat ttt gca tca aat ttg gat tcc acc ctt	451			
Ile Asn Ala Gly Ala Gln Tyr Phe Ala Ser Asn Leu Asp Ser Thr Leu				
	105	110	115	
ccc atg gaa gcg ggt cgt cac att ggc aac ggt tcc atg gtg gct gcc	499			
Pro Met Glu Arg Gly Arg His Ile Gly Asn Gly Ser Met Val Ala Ala				
	120	125	130	
gtg gtc aac gcg act ggc gta aag cct ctt tcc gca ggt aag cca ggc	547			
Val Val Asn Ala Thr Gly Val Lys Pro Leu Ser Ala Gly Lys Pro Gly				
	135	140	145	
ccc gcg atg ttc tat gcg ggg gct gaa act ctt aat tct tca aag cct	595			
Pro Ala Met Phe Tyr Ala Gly Ala Glu Thr Leu Asn Ser Ser Lys Pro				
	150	155	160	165
ttg gct gtc ggc gat cgt ctc gat acc gat atc gcc ggc gga aac gct	643			
Leu Ala Val Gly Asp Arg Leu Asp Thr Asp Ile Ala Gly Gly Asn Ala				
	170	175	180	
gca ggc atg gac aca ttc cag gtc ctg acc ggc gtc agc ggc tac tac	691			
Ala Gly Met Asp Thr Phe Gln Val Leu Thr Gly Val Ser Gly Tyr Tyr				
	185	190	195	
gat ttg gtg gcg gcc att ccc aga gca gcg ccc cac cta tat cgc cac	739			
Asp Leu Val Arg Ala Ile Pro Arg Ala Ala Pro His Leu Tyr Arg His				
	200	205	210	
ctc gat gca gga tct cta cag cga tcc ggg cga gct caa gcc agg tgc	787			
Leu Asp Ala Gly Ser Leu Gln Arg Ser Gly Arg Ala Gln Ala Arg Cys				
	215	220	225	
cca ggg cgg ttt ttc agc gct tat cga cgg cga cac cct ggt cat ttc	835			
Pro Gly Arg Phe Phe Ser Ala Tyr Arg Arg Arg His Pro Gly His Phe				
	230	235	240	245
cgg cgg cga tgc cgg cgc aac tcc ggt tgc agc act ccg cac tgc gtt	883			
Arg Arg Arg Cys Arg Arg Asn Ser Gly Cys Ser Thr Pro His Cys Val				
	250	255	260	

000290" 0420960



tca gag gta gct gct act gca ttg cag agc tgg tgg taaacggtga 977  
Ser Glu Val Ala Ala Thr Ala Leu Gln Ser Trp Trp  
280 285

```
<210> 484
<211> 289
<212> PRT
<213> Corynebacterium glutamicum
```

[illegible]



<400> 485																	
ggacgcttat	tggtgagcat	tcggattacg	ccggtggtgt	ggtgctggcg	gctaatagcga	60											
attgccggac						tgcggctgcc	gtcaataaag	aaccgcgacg	atg	ttg	tta	acg	tat	115			
									Met	Leu	Leu	Thr	Tyr	5			
									1								
gcg	ttt	gtg	gat	gtg	gag	gga	ggc	gtc	gaa	aag	cat	tct	tta	agc	act	163	
Ala	Phe	Val	Asp	Val	Glu	Gly	Gly	Val	Glu	Lys	His	Ser	Leu	Ser	Thr		
				10					15					20			
gcg	gac	att	gca	gct	cgc	gca	cac	gcc	cat	atg	aaa	tcc	cat	gat	gtt	211	
Ala	Asp	Ile	Ala	Ala	Arg	Ala	His	Ala	His	Met	Lys	Ser	His	Asp	Val		
			25				30				35						
ttg	ggg	cgg	cag	act	acg	ccg	cct	cag	ccg	gag	ggc	ggc	gtt	gct	gcc	259	
Leu	Gly	Arg	Gln	Thr	Thr	Pro	Pro	Gln	Pro	Glu	Gly	Gly	Val	Ala	Ala		
		40					45					50					
cgg	ttg	ggc	ggg	att	gcg	tgg	aca	atg	atc	cat	aag	caa	atg	ctt	tcg	307	
Arg	Leu	Gly	Gly	Ile	Ala	Trp	Thr	Met	Ile	His	Lys	Gln	Met	Leu	Ser		
		55					60					65					
cgt	gac	aca	aaa	ggc	ctg	gat	atc	acc	gtg	ttg	agc	acc	att	cct	gag	355	
Arg	Asp	Thr	Lys	Gly	Leu	Asp	Ile	Thr	Val	Leu	Ser	Thr	Ile	Pro	Glu		
70					75					80					85		
ggg	gtg	ggg	ctg	ggt	gaa	aat	tcc	gcc	atg	gat	gtg	gcg	ctc	gca	ttg	403	
Gly	Val	Gly	Leu	Gly	Glu	Asn	Ser	Ala	Met	Asp	Val	Ala	Leu	Ala	Leu		
				90					95					100			
gcg	ctg	tat	cgg	gaa	aat	att	gag	gaa	gcc	ccc	acg	aag	gcg	cgc	att	451	
Ala	Leu	Tyr	Arg	Glu	Asn	Ile	Glu	Glu	Ala	Pro	Thr	Lys	Ala	Arg	Ile		
			105				110				115						
gcg	qag	att	tgt	tcg	caq	tcc	qca	ttc	atg	ttc	aqt	qag	act	tca	qtg	499	

[illegible]



Ala	Glu	Ile	Cys	Ser	Gln	Ser	Ala	Phe	Met	Phe	Ser	Glu	Thr	Ser	Val	
		120					125					130				
ttg	cgt	gcg	cgg	cac	acc	gtg	gcg	ttg	cgg	ggt	gaa	act	gga	cag	att	547
Leu	Arg	Ala	Arg	His	Thr	Val	Ala	Leu	Arg	Gly	Glu	Thr	Gly	Gln	Ile	
		135				140					145					
tcg	gtg	gtt	gat	tac	gcc	gat	ggg	tcg	gtc	act	cag	gcg	cca	cat	ccg	595
Ser	Val	Val	Asp	Tyr	Ala	Asp	Gly	Ser	Val	Thr	Gln	Ala	Pro	His	Pro	
		150			155					160					165	
gtg	agt	cgt	tcc	gct	ggg	ttg	tcg	gca	ttt	gtt	gtt	gct	gcg	caa	act	643
Val	Ser	Arg	Ser	Ala	Gly	Leu	Ser	Ala	Phe	Val	Val	Ala	Ala	Gln	Thr	
				170					175					180		
gaa	act	gat	ccg	agc	att	tac	cgc	gag	atc	tat	gct	cga	cat	gcg	ttt	691
Glu	Thr	Asp	Pro	Ser	Ile	Tyr	Arg	Glu	Ile	Tyr	Ala	Arg	His	Ala	Phe	
			185					190					195			
atc	gat	gaa	gct	gcg	cgc	gct	ttc	agt	gtg	gaa	tct	ttg	cgg	ttg	ctt	739
Ile	Asp	Glu	Ala	Ala	Arg	Ala	Phe	Ser	Val	Glu	Ser	Leu	Arg	Leu	Leu	
		200				205						210				
ccc	gac	gct	tcc	act	cgt	gtt	gtg	gat	tgg	ttg	cag	gcc	gtg	att	gag	787
Pro	Asp	Ala	Ser	Thr	Arg	Val	Val	Asp	Trp	Leu	Gln	Ala	Val	Ile	Glu	
		215				220					225					
gtg	act	ggg	cga	gag	gat	ctg	ccc	tcg	att	gaa	caa	gcc	cag	cgc	tgg	835
Val	Thr	Gly	Arg	Glu	Asp	Leu	Pro	Ser	Ile	Glu	Gln	Ala	Gln	Arg	Trp	
		230			235					240					245	
ttg	aat	ctg	tgg	gaa	aac	gaa	acc	cgg	cgc	gct	cag	agg	aca	gcc	aat	883
Leu	Asn	Leu	Trp	Glu	Asn	Glu	Thr	Arg	Arg	Ala	Gln	Arg	Thr	Ala	Asn	
				250					255					260		
gcc	ctg	cgt	tcg	aga	agg	ctg	agt	gag	ttt	tct	gag	ctg	ctg	atg	gaa	931
Ala	Leu	Arg	Ser	Arg	Arg	Leu	Ser	Glu	Phe	Ser	Glu	Leu	Leu	Met	Glu	
			265					270					275			
tcc	caa	gat	gat	ttg	agc	gac	acc	ttc	gat	ttc	ccc	cct	gct	gat	ttg	979
Ser	Gln	Asp	Asp	Leu	Ser	Asp	Thr	Phe	Asp	Phe	Pro	Pro	Ala	Asp	Leu	
		280				285					290					
gcg	ctt	gct	cgt	ttg	tgc	gtc	gag	cgg	ggt	gcc	aca	gct	gct	cgg	tcc	1027
Ala	Leu	Ala	Arg	Leu	Cys	Val	Glu	Arg	Gly	Ala	Thr	Ala	Ala	Arg	Ser	
		295			300						305					
acg	tca	gcg	cgc	ggg	gtg	att	gcg	ttg	gtt	gat	gcc	cat	cat	gcg	cac	1075
Thr	Ser	Ala	Arg	Gly	Val	Ile	Ala	Leu	Val	Asp	Ala	His	His	Ala	His	
				315						320					325	
aat	ttt	gct	gcg	gat	ctc	agc	gag	gat	ggc	ttg	ttg	gtg	gtt	cct	ctc	1123
Asn	Phe	Ala	Ala	Asp	Leu	Ser	Glu									

096270-093000



<400> 486															
Met 1	Leu	Leu	Thr	Tyr 5	Ala	Phe	Val	Asp	Val 10	Glu	Gly	Gly	Val	Glu 15	Lys
His	Ser	Leu	Ser 20	Thr	Ala	Asp	Ile	Ala 25	Ala	Arg	Ala	His	Ala 30	His	Met
Lys	Ser	His 35	Asp	Val	Leu	Gly	Arg 40	Gln	Thr	Thr	Pro	Pro 45	Gln	Pro	Glu
Gly	Gly 50	Val	Ala	Ala	Arg	Leu 55	Gly	Gly	Ile	Ala	Trp 60	Thr	Met	Ile	His
Lys 65	Gln	Met	Leu	Ser	Arg 70	Asp	Thr	Lys	Gly	Leu 75	Asp	Ile	Thr	Val	Leu 80
Ser	Thr	Ile	Pro	Glu 85	Gly	Val	Gly	Leu	Gly 90	Glu	Asn	Ser	Ala	Met 95	Asp
Val	Ala	Leu	Ala 100	Leu	Ala	Leu	Tyr	Arg 105	Glu	Asn	Ile	Glu	Glu 110	Ala	Pro
Thr	Lys	Ala 115	Arg	Ile	Ala	Glu	Ile 120	Cys	Ser	Gln	Ser	Ala 125	Phe	Met	Phe
Ser	Glu 130	Thr	Ser	Val	Leu	Arg 135	Ala	Arg	His	Thr	Val 140	Ala	Leu	Arg	Gly
Glu 145	Thr	Gly	Gln	Ile	Ser 150	Val	Val	Asp	Tyr	Ala 155	Asp	Gly	Ser	Val	Thr 160
Gln	Ala	Pro	His	Pro 165	Val	Ser	Arg	Ser	Ala 170	Gly	Leu	Ser	Ala	Phe 175	Val
Val	Ala	Ala	Gln 180	Thr	Glu	Thr	Asp 185	Pro	Ser	Ile	Tyr	Arg 190	Glu	Ile	Tyr
Ala	Arg	His 195	Ala	Phe	Ile	Asp	Glu 200	Ala	Ala	Arg	Ala	Phe 205	Ser	Val	Glu
Ser	Leu 210	Arg	Leu	Leu	Pro	Asp 215	Ala	Ser	Thr	Arg	Val 220	Val	Asp	Trp	Leu
Gln 225	Ala	Val	Ile	Glu	Val 230	Thr	Gly	Arg	Glu	Asp 235	Leu	Pro	Ser	Ile	Glu 240
Gln	Ala	Gln	Arg	Trp 245	Leu	Asn	Leu	Trp	Glu 250	Asn	Glu	Thr	Arg	Arg 255	Ala
Gln	Arg	Thr	Ala 260	Asn	Ala	Leu	Arg	Ser 265	Arg	Arg	Leu	Ser	Glu 270	Phe	Ser
Glu	Leu	Leu 275	Met	Glu	Ser	Gln	Asp 280	Asp	Leu	Ser	Asp	Thr 285	Phe	Asp	Phe



<400> 487															
tagttgtgcc acctaaaacg cgaacagaac cggagtcgag cagcacctcc ccgcaagggt 60															
agagggggctg cttttttgtt tcctaaattc accccatccc atg cat agc cct gaa 115															
Met His Ser Pro Glu 1 5															
agg caa gaa aaa atg agt tct cca gtc tca ctc gaa aac gcg gcg tca 163															
Arg Gln Glu Lys Met Ser Ser Pro Val Ser Leu Glu Asn Ala Ala Ser 10 15 20															
acc agc aac aag cgc gtc gtg gct ttc cac gag ctg cct agc cct aca 211															
Thr Ser Asn Lys Arg Val Val Ala Phe His Glu Leu Pro Ser Pro Thr 25 30 35															
gat ctc atc gcc gca aac cca ctg aca cca aag cag gct tcc aag gtg 259															
Asp Leu Ile Ala Ala Asn Pro Leu Thr Pro Lys Gln Ala Ser Lys Val 40 45 50															
gag cag gat cgc cag gac atc gct gat atc ttc gct ggc gac gat gac 307															
Glu Gln Asp Arg Gln Asp Ile Ala Asp Ile Phe Ala Gly Asp Asp Asp 55 60 65															
cgc ctc gtt gtc gtt gtg gga cct tgc tca gtt cac gat cct gaa gca 355															
Arg Leu Val Val Val Val Gly Pro Cys Ser Val His Asp Pro Glu Ala 70 75 80 85															
gcc atc gat tac gca aac cgc ctg gct ccg ctg gca aag cgc ctt gat 403															
Ala Ile Asp Tyr Ala Asn Arg Leu Ala Pro Leu Ala Lys Arg Leu Asp 90 95 100															
cag gac ctc aag att gtc atg cgc gtg tac ttc gag aag cct cgc acc 451															
Gln Asp Leu Lys Ile Val Met Arg Val Tyr Phe Glu Lys Pro Arg Thr 105 110 115															
atc gtc gga tgg aag gga ttg atc aat gat cct cac ctc aac gaa acc 499															
Ile Val Gly Trp Lys Gly Leu Ile Asn Asp Pro His Leu Asn Glu Thr 120 125 130															

[illegible]



[illegible]



gcc aag taattaaggg cgctagactg tta  
 Ala Lys  
 375

1248

<210> 488  
 <211> 375  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 488  
 Met His Ser Pro Glu Arg Gln Glu Lys Met Ser Ser Pro Val Ser Leu  
 1 5 10 15  
 Glu Asn Ala Ala Ser Thr Ser Asn Lys Arg Val Val Ala Phe His Glu  
 20 25 30  
 Leu Pro Ser Pro Thr Asp Leu Ile Ala Ala Asn Pro Leu Thr Pro Lys  
 35 40 45  
 Gln Ala Ser Lys Val Glu Gln Asp Arg Gln Asp Ile Ala Asp Ile Phe  
 50 55 60  
 Ala Gly Asp Asp Asp Arg Leu Val Val Val Val Gly Pro Cys Ser Val  
 65 70 75 80  
 His Asp Pro Glu Ala Ala Ile Asp Tyr Ala Asn Arg Leu Ala Pro Leu  
 85 90 95  
 Ala Lys Arg Leu Asp Gln Asp Leu Lys Ile Val Met Arg Val Tyr Phe  
 100 105 110  
 Glu Lys Pro Arg Thr Ile Val Gly Trp Lys Gly Leu Ile Asn Asp Pro  
 115 120 125  
 His Leu Asn Glu Thr Tyr Asp Ile Pro Glu Gly Leu Arg Ile Ala Arg  
 130 135 140  
 Lys Val Leu Ile Asp Val Val Asn Leu Asp Leu Pro Val Gly Cys Glu  
 145 150 155 160  
 Phe Leu Glu Pro Asn Ser Pro Gln Tyr Tyr Ala Asp Thr Val Ala Trp  
 165 170 175  
 Gly Ala Ile Gly Ala Arg Thr Thr Glu Ser Gln Val His Arg Gln Leu  
 180 185 190  
 Ala Ser Gly Met Ser Met Pro Ile Gly Phe Lys Asn Gly Thr Asp Gly  
 195 200 205  
 Asn Ile Gln Val Ala Val Asp Ala Val Gln Ala Ala Gln Asn Pro His  
 210 215 220  
 Phe Phe Phe Gly Thr Ser Asp Asp Gly Ala Leu Ser Val Val Glu Thr  
 225 230 235 240  
 Ala Gly Asn Ser Asn Ser His Ile Ile Leu Arg Gly Gly Thr Ser Gly  
 245 250 255  
 Pro Asn His Asp Ala Ala Ser Val Glu Ala Val Val Glu Lys Leu Gly  
 260 265 270

002290-0420960



Glu Asn Ala Arg Leu Met Ile Asp Ala Ser His Ala Asn Ser Gly Lys  
 275 280 285  
 Asp His Ile Arg Gln Val Glu Val Val Arg Glu Ile Ala Glu Gln Ile  
 290 295 300  
 Ser Gly Gly Ser Glu Ala Val Ala Gly Ile Met Ile Glu Ser Phe Leu  
 305 310 315 320  
 Val Gly Gly Ala Gln Asn Leu Asp Pro Ala Lys Leu Arg Ile Asn Gly  
 325 330 335  
 Gly Glu Gly Leu Val Tyr Gly Gln Ser Val Thr Asp Lys Cys Ile Asp  
 340 345 350  
 Ile Asp Thr Thr Ile Asp Leu Leu Ala Glu Leu Ala Ala Ala Val Arg  
 355 360 365  
 Glu Arg Arg Ala Ala Ala Lys  
 370 375

<210> 489  
 <211> 1131  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1108)  
 <223> RXS02574

<400> 489  
 tgtgtctcctt gcgggctgcg cagaagagcc ggaacagcaa aaagcaataa gccgcttattc 60  
 gacgtccccc tccaccctc ccgcaccgac cgcgaggat ttg gcg cgc gcg caa 115  
 Leu Ala Arg Ala Gln  
 1 5  
 atc cct gaa cag caa cgc gac caa gtc gcg tcg ctg atg atg gtt gga 163  
 Ile Pro Glu Gln Gln Arg Asp Gln Val Ala Ser Leu Met Met Val Gly  
 10 15 20  
 gtt gcg aat tat gat cag gca ttg gat gcg ctc aat cag ggg gtg ggt 211  
 Val Ala Asn Tyr Asp Gln Ala Leu Asp Ala Leu Asn Gln Gly Val Gly  
 25 30 35  
 ggc atc ttt att ggt tcc tgg aca gat gaa aat ctg ctc acg gaa cct 259  
 Gly Ile Phe Ile Gly Ser Trp Thr Asp Glu Asn Leu Leu Thr Glu Pro  
 40 45 50  
 ggc cgt aat att gag gcg ctc cgc gaa gcc gtc ggc agg gat ttc tcc 307  
 Gly Arg Asn Ile Glu Ala Leu Arg Glu Ala Val Gly Arg Asp Phe Ser  
 55 60 65  
 gtc agc atc gac ttc gaa ggc ggc cgc gtc cag cgt gcc acc aat att 355  
 Val Ser Ile Asp Phe Glu Gly Gly Arg Val Gln Arg Ala Thr Asn Ile  
 70 75 80 85  
 ctt ggt gat ttc ccc tca ccg cgc gtg atg gcg caa acc atg acg ccg 403

09602740-062300



Leu	Gly	Asp	Phe	Pro 90	Ser	Pro	Arg	Val	Met 95	Ala	Gln	Thr	Met	Thr 100	Pro	
gaa Glu	caa Gln	gta Val	gaa Glu 105	gat Asp	ctc Leu	gca Ala	gaa Glu	atc Ile 110	cta Leu	ggc Gly	act Thr	ggg Gly	tta Leu 115	gct Ala	gca Ala	451
cat His	ggg Gly	gtg Val 120	aca Thr	gtt Val	aac Asn	ttt Phe	gca Ala 125	cct Pro	gtt Val	gta Val	gat Asp	gta Val 130	gat Asp	gct Ala	tgg Trp	499
ggg Gly	ctc Leu 135	ccc Pro	gtc Val	gtt Val	ggc Gly	gat Asp 140	cgt Arg	tcc Ser	ttt Phe	tcc Ser	aac Asn 145	gac Asp	cca Pro	gcc Ala	gta Val	547
gca Ala 150	gct Ala	act Thr	tat Tyr	gcc Ala	aca Thr 155	gct Ala	ttt Phe	gca Ala	aag Lys	ggc Gly 160	tta Leu	agc Ser	aaa Lys	gta Val	gga Gly 165	595
att Ile	acc Thr	cca Pro	gta Val 170	ttc Phe	aaa Lys	cat His	ttc Phe	cca Pro	ggg Gly 175	cac His	ggg Gly	cgt Arg	gca Ala 180	agt Ser	ggc Gly	643
gat Asp	tcg Ser	cac His	acc Thr 185	caa Gln	gat Asp	gtg Val	gtg Val	acc Thr 190	ccc Pro	gca Ala	ctt Leu	gat Asp	gag Glu 195	ctt Leu	aaa Lys	691
act Thr	tac Tyr	gac Asp 200	ctc Leu	atc Ile	cct Pro	tat Tyr	ggg Gly 205	caa Gln	gca Ala	ctt Leu	tct Ser	gaa Glu 210	act Thr	gac Asp	gga Gly	739
gcc Ala 215	gtc Val	atg Met	gtg Val	ggc Gly	cac His	atg Met 220	att Ile	gtt Val	cca Pro	ggg Gly	ctt Leu 225	ggc Gly	acc Thr	gac Asp	gga Gly	787
gtt Val 230	cca Pro	tcc Ser	tct Ser	atc Ile	gac Asp 235	ccc Pro	gcc Ala	acc Thr	tat Tyr	caa Gln 240	ctg Leu	ctc Leu	cgc Arg	agt Ser	ggc Gly 245	835
gat Asp	tac Tyr	cca Pro	ggg Gly 250	ggc Gly	gtg Val	cct Pro	ttc Phe	gat Asp 255	ggc Gly	gtg Val	atc Ile	tac Tyr	acc Thr 260	gac Asp	gat Asp	883
ctc Leu	tct Ser	gga Gly 265	atg Met	agt Ser	gcc Ala	att Ile	tcc Ser	gcc Ala 270	acc Thr	cat His	tca Ser	ccc Pro	gca Ala 275	gaa Glu	gca Ala	931
gtg Val	ctt Leu	gcc Ala 280	tcc Ser	ctc Leu	aaa Lys	gca Ala	ggc Gly 285	gca Ala	gac Asp	caa Gln	gca Ala	cta Leu 290	tgg Trp	atc Ile	gac Asp	979
tat Tyr	ggg Gly 295	tcg Ser	ttg Leu	ggc Gly	tcc Ser	gcg Ala 300	att Ile	gat Asp	cgc Arg	gtt Val	gat Asp 305	gct Ala	gcc Ala	gtt Val	agc Ser	1027
agc Ser 310	ggg Gly	gaa Glu	tac Tyr	cct Pro	caa Gln 315	gaa Glu	caa Gln	atg Met	ctg Leu	gca Ala 320	tct Ser	gcg Ala	tta Leu	aga Arg	gtc Val 325	1075
caa Gln	ttg Leu	ctc Leu	tac Tyr	atc Ile	aca Thr	cgt Arg	ctc Leu	gaa Glu	caa Gln	aag Lys	tgaagttacc	agtc	ccgtaac			1128

[illegible]



330

335

ccc

1131

&lt;210&gt; 490

&lt;211&gt; 336

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 490

Leu Ala Arg Ala Gln Ile Pro Glu Gln Gln Arg Asp Gln Val Ala Ser  
 1 5 10 15

Leu Met Met Val Gly Val Ala Asn Tyr Asp Gln Ala Leu Asp Ala Leu  
 20 25 30

Asn Gln Gly Val Gly Gly Ile Phe Ile Gly Ser Trp Thr Asp Glu Asn  
 35 40 45

Leu Leu Thr Glu Pro Gly Arg Asn Ile Glu Ala Leu Arg Glu Ala Val  
 50 55 60

Gly Arg Asp Phe Ser Val Ser Ile Asp Phe Glu Gly Gly Arg Val Gln  
 65 70 75 80

Arg Ala Thr Asn Ile Leu Gly Asp Phe Pro Ser Pro Arg Val Met Ala  
 85 90 95

Gln Thr Met Thr Pro Glu Gln Val Glu Asp Leu Ala Glu Ile Leu Gly  
 100 105 110

Thr Gly Leu Ala Ala His Gly Val Thr Val Asn Phe Ala Pro Val Val  
 115 120 125

Asp Val Asp Ala Trp Gly Leu Pro Val Val Gly Asp Arg Ser Phe Ser  
 130 135 140

Asn Asp Pro Ala Val Ala Ala Thr Tyr Ala Thr Ala Phe Ala Lys Gly  
 145 150 155 160

Leu Ser Lys Val Gly Ile Thr Pro Val Phe Lys His Phe Pro Gly His  
 165 170 175

Gly Arg Ala Ser Gly Asp Ser His Thr Gln Asp Val Val Thr Pro Ala  
 180 185 190

Leu Asp Glu Leu Lys Thr Tyr Asp Leu Ile Pro Tyr Gly Gln Ala Leu  
 195 200 205

Ser Glu Thr Asp Gly Ala Val Met Val Gly His Met Ile Val Pro Gly  
 210 215 220

Leu Gly Thr Asp Gly Val Pro Ser Ser Ile Asp Pro Ala Thr Tyr Gln  
 225 230 235 240

Leu Leu Arg Ser Gly Asp Tyr Pro Gly Gly Val Pro Phe Asp Gly Val  
 245 250 255

Ile Tyr Thr Asp Asp Leu Ser Gly Met Ser Ala Ile Ser Ala Thr His  
 260 265 270

003290"0420950



```
<210> 491
<211> 1038
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (1)..(1008)
<223> RXS03215
```

<400> 491																
atc	gat	gtt	gtc	agc	gtc	gtg	gtg	gct	aac	ttc	ctg	cac	cgc	gaa	atc	48
Ile	Asp	Val	Val	Ser	Val	Val	Val	Ala	Asn	Phe	Leu	His	Arg	Glu	Ile	
1				5				10				15				
gtg	gaa	gca	ctt	ctg	gca	tcc	ggc	aag	cat	gtg	ctg	tgc	gag	aag	cca	96
Val	Glu	Ala	Leu	Leu	Ala	Ser	Gly	Lys	His	Val	Leu	Cys	Glu	Lys	Pro	
20				25				30								
ctg	tca	gac	acc	atc	gaa	gat	gca	gaa	gcc	atg	att	gag	gca	gcc	ggc	144
Leu	Ser	Asp	Thr	Ile	Glu	Asp	Ala	Glu	Ala	Met	Ile	Glu	Ala	Ala	Gly	
35				40				45								
cgt	gca	gca	aca	aat	ggc	acc	atc	gcc	cgc	atc	gga	ctg	acc	tac	cgc	192
Arg	Ala	Ala	Thr	Asn	Gly	Thr	Ile	Ala	Arg	Ile	Gly	Leu	Thr	Tyr	Arg	
50				55				60								
cgt	tcc	cca	ggc	gtg	gca	cac	atc	cgt	gat	ctc	gtg	cag	tcc	ggc	gag	240
Arg	Ser	Pro	Gly	Val	Ala	His	Ile	Arg	Asp	Leu	Val	Gln	Ser	Gly	Glu	
65				70				75				80				
ctt	ggc	aag	gtt	cta	cac	gtc	acc	ggc	cac	tac	tgg	acc	gac	tac	gga	288
Leu	Gly	Lys	Val	Leu	His	Val	Thr	Gly	His	Tyr	Trp	Thr	Asp	Tyr	Gly	
85				90				95								
tcc	aat	gca	cag	gca	cca	atc	agc	tgg	cgt	tac	aag	ggg	cca	aac	ggc	336
Ser	Asn	Ala	Gln	Ala	Pro	Ile	Ser	Trp	Arg	Tyr	Lys	Gly	Pro	Asn	Gly	
100				105				110								
tcc	ggc	gca	ctg	gca	gat	gtg	gga	agc	cac	ctc	acc	tac	ctg	gca	gaa	384
Ser	Gly	Ala	Leu	Ala	Asp	Val	Gly	Ser	His	Leu	Thr	Tyr	Leu	Ala	Glu	
115				120				125								
ttc	gtt	gca	gga	tct	gac	ttc	gcc	gcc	gtc	cgt	ggt	ggc	cag	ttg	tcc	432



<400> 492  
Ile Asp Val Val Ser Val Val Val Ala Asn Phe Leu His Arg Glu Ile

[illegible]



[illegible]



<210> 493  
 <211> 1031  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(1008)  
 <223> FRXA01915

<400> 493  
 atc gat gtt gtc agc gtc gtg gtg gct aac ttc ctg cac cgc gaa atc 48  
 Ile Asp Val Val Ser Val Val Val Ala Asn Phe Leu His Arg Glu Ile  
     1                    5                    10                    15

gtg gaa gca ctt ctg gca tcc ggc aag cat gtg ctg tgc gag aag cca 96  
 Val Glu Ala Leu Leu Ala Ser Gly Lys His Val Leu Cys Glu Lys Pro  
                     20                    25                    30

ctg tca gac acc atc gaa gat gca gaa gcc atg att gag gca gcc ggc 144  
 Leu Ser Asp Thr Ile Glu Asp Ala Glu Ala Met Ile Glu Ala Ala Gly  
                     35                    40                    45

cgt gca gca aca aat ggc acc atc gcc cgc atc gga ctg acc tac cgc 192  
 Arg Ala Ala Thr Asn Gly Thr Ile Ala Arg Ile Gly Leu Thr Tyr Arg  
                     50                    55                    60

cgt tcc cca ggc gtg gca cac atc cgt gat ctc gtg cag tcc ggc gag 240  
 Arg Ser Pro Gly Val Ala His Ile Arg Asp Leu Val Gln Ser Gly Glu  
                     65                    70                    75                    80

ctt ggc aag gtt cta cac gtc acc ggc cac tac tgg acc gac tac gga 288  
 Leu Gly Lys Val Leu His Val Thr Gly His Tyr Trp Thr Asp Tyr Gly  
                     85                    90                    95

tcc aat gca cag gca cca atc agc tgg cgt tac aag ggg cca aac ggc 336  
 Ser Asn Ala Gln Ala Pro Ile Ser Trp Arg Tyr Lys Gly Pro Asn Gly  
                     100                    105                    110

tcc ggc gca ctg gca gat gtg gga agc cac ctc acc tac ctg gca gaa 384  
 Ser Gly Ala Leu Ala Asp Val Gly Ser His Leu Thr Tyr Leu Ala Glu  
                     115                    120                    125

ttc gtt gca gga tct gac ttc gcc gcc gtc cgt ggt ggc cag ttg tcc 432  
 Phe Val Ala Gly Ser Asp Phe Ala Ala Val Arg Gly Gly Gln Leu Ser  
                     130                    135                    140

acc gtg atc acc gag cgc ccc aag cca ctc ggc gcg att gtc ggc cac 480  
 Thr Val Ile Thr Glu Arg Pro Lys Pro Leu Gly Ala Ile Val Gly His  
                     145                    150                    155                    160

gaa ggc ggc gca gtt tcc gat gaa tac gaa gca gtg gaa aat gat gac 528  
 Glu Gly Gly Ala Val Ser Asp Glu Tyr Glu Ala Val Glu Asn Asp Asp  
                     165                    170                    175

att gca tca ttc tcc gga tcc ttc atc ggt ggc gga acc gca acc ctc 576

09602740 "062300



Ile Ala Ser Phe Ser Gly Ser Phe Ile Gly Gly Gly Thr Ala Thr Leu  
180 185 190

cag gtc agc cgc att tcc cag gga cac cca aac acc cta ggt ttt gaa 624  
Gln Val Ser Arg Ile Ser Gln Gly His Pro Asn Thr Leu Gly Phe Glu  
195 200 205

gtg ttc tgt gaa aag ggc tcc gtg ctc ttt gat ttc cgc aac tca ggc 672  
Val Phe Cys Glu Lys Gly Ser Val Leu Phe Asp Phe Arg Asn Ser Gly  
210 215 220

gaa ttc aaa atc ttc acc cca gca acc tcc ggt gac atc agc caa gaa 720  
Glu Phe Lys Ile Phe Thr Pro Ala Thr Ser Gly Asp Ile Ser Gln Glu  
225 230 235 240

gcc ggc tac cgc acc atc acc atc gga cca aag cac cca tac tgg cgc 768  
Ala Gly Tyr Arg Thr Ile Thr Ile Gly Pro Lys His Pro Tyr Trp Arg  
245 250 255

ggc ggc ctt gca atg gat gca cca ggc gtg gga att ggc caa aac gaa 816  
Gly Gly Leu Ala Met Asp Ala Pro Gly Val Gly Ile Gly Gln Asn Glu  
260 265 270

ggc ttc gtt ttc cag gcg cgc gca ttc ctc gaa gaa atc gca gga atc 864  
Gly Phe Val Phe Gln Ala Arg Ala Phe Leu Glu Glu Ile Ala Gly Ile  
275 280 285

tcc gaa gct gaa agc ctg cca cgc tgc gca act ttg gaa gaa ggg cta 912  
Ser Glu Ala Glu Ser Leu Pro Arg Cys Ala Thr Leu Glu Glu Gly Leu  
290 295 300

cac aat atg cag ctc att gat gct gta tca cag tca gct gca gca ggt 960  
His Asn Met Gln Leu Ile Asp Ala Val Ser Gln Ser Ala Ala Ala Gly  
305 310 315 320

ggc gaa acc gtt gcg gtc cca gcg gct gct ctg atc cct gca aac aac 1008  
Gly Glu Thr Val Ala Val Pro Ala Ala Leu Ile Pro Ala Asn Asn  
325 330 335

tagaaactat tcagaaagca tca 1031

&lt;210&gt; 494

&lt;211&gt; 336

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 494

Ile Asp Val Val Ser Val Val Val Ala Asn Phe Leu His Arg Glu Ile  
1 5 10 15

Val Glu Ala Leu Leu Ala Ser Gly Lys His Val Leu Cys Glu Lys Pro  
20 25 30

Leu Ser Asp Thr Ile Glu Asp Ala Glu Ala Met Ile Glu Ala Ala Gly  
35 40 45

Arg Ala Ala Thr Asn Gly Thr Ile Ala Arg Ile Gly Leu Thr Tyr Arg  
50 55 60

Arg Ser Pro Gly Val Ala His Ile Arg Asp Leu Val Gln Ser Gly Glu

09602740-062300



<220>  
<221> CDS

[illegible]



&lt;222&gt; (101)..(1258)

&lt;223&gt; RXS03224

&lt;400&gt; 495

```

acgattgtgc tgtcgtttgc gttggtgaat agttctggac cgggtatttt gcggcgcaca 60

tggaactcat tgaacgccgc gcccggtctaa ggtgggagggc atg agt ttt gct gaa 115
                                         Met Ser Phe Ala Glu
                                         1                               5

cat gcg atc atc tgg cac gtc tac ccc ctg ggc gct ttg ggt gct ccc 163
His Ala Ile Ile Trp His Val Tyr Pro Leu Gly Ala Leu Gly Ala Pro
                        10                        15                        20

atc cgg cct gaa gcc ccc gca cct gtc aca cat cgg ctc ccc aat cta 211
Ile Arg Pro Glu Ala Pro Ala Pro Val Thr His Arg Leu Pro Asn Leu
                        25                        30                        35

att ggg tgg ctg gat tat gtt gtc gaa cta ggc tgc aac gcc ctc atg 259
Ile Gly Trp Leu Asp Tyr Val Val Glu Leu Gly Cys Asn Ala Leu Met
                        40                        45                        50

ctg gga ccg gta ttc gag tcc gtc agc cac ggc tac gac acc ctc gat 307
Leu Gly Pro Val Phe Glu Ser Val Ser His Gly Tyr Asp Thr Leu Asp
                        55                        60                        65

ttc tac cgc atc gac ccg cgc ctc ggc acc gag gaa gac atg gac gcg 355
Phe Tyr Arg Ile Asp Pro Arg Leu Gly Thr Glu Glu Asp Met Asp Ala
                        70                        75                        80                        85

ctg ctg gag gct gcg aat cag cgg ggc att gga gtg ctt ttc gac ggc 403
Leu Leu Glu Ala Ala Asn Gln Arg Gly Ile Gly Val Leu Phe Asp Gly
                        90                        95                        100

gtc ttc aat cat gtt tcc agt tcc tct aaa tat ctc gac ctg acc acc 451
Val Phe Asn His Val Ser Ser Ser Ser Lys Tyr Leu Asp Leu Thr Thr
                        105                        110                        115

ggg gcg tca ttt gaa ggc cac gac atc ctg gcg gaa ctc gac cac acg 499
Gly Ala Ser Phe Glu Gly His Asp Ile Leu Ala Glu Leu Asp His Thr
                        120                        125                        130

aat ccc gcc gta gtg gat ctg gtt gtc gat gtc atg aac cac tgg ctc 547
Asn Pro Ala Val Val Asp Leu Val Val Asp Val Met Asn His Trp Leu
                        135                        140                        145

gac cgc gga atc gca ggc tgg cga ctc gac gct gtc tac gcc atc gcc 595
Asp Arg Gly Ile Ala Gly Trp Arg Leu Asp Ala Val Tyr Ala Ile Ala
                        150                        155                        160                        165

cct gaa ttt tgg gaa aaa gtc ctg cca gaa gtg cga cga aaa cac cca 643
Pro Glu Phe Trp Glu Lys Val Leu Pro Glu Val Arg Arg Lys His Pro
                        170                        175                        180

cac gca tgg atc gtg ggg gag atg atc cat gga gat tac tcc gac tac 691
His Ala Trp Ile Val Gly Glu Met Ile His Gly Asp Tyr Ser Asp Tyr
                        185                        190                        195

gtg aaa agc tcc ggc att gat tcc gtt acc gaa tac gaa ctg tgg aaa 739
Val Lys Ser Ser Gly Ile Asp Ser Val Thr Glu Tyr Glu Leu Trp Lys
                        200                        205                        210

```

09602740 062300



gcc Ala	att Ile	tgg Trp	agc Ser	agc Ser	atc Ile	aaa Lys	gag Glu	cgc Arg	aat Asn	ttc Phe	ttt Phe	gaa Glu	ctc Leu	gaa Glu	tgg Trp	787	
215220225																	
act Thr	ttg Leu	agt Ser	cgc Arg	cac His	aat Asn	gaa Glu	ttc Phe	ctc Leu	gat Asp	act Thr	ttc Phe	gta Val	ccg Pro	cag Gln	aca Thr	835	
230235240245																	
ttc Phe	att Ile	ggt Gly	aac Asn	cat His	gac Asp	gtc Val	acc Thr	cgc Arg	att Ile	gcc Ala	acc Thr	cga Arg	atc Ile	ggt Gly	caa Gln	883	
250255260																	
tca Ser	aat Asn	gcg Ala	atc Ile	ctg Leu	gcc Ala	gca Ala	gcg Ala	atc Ile	ctc Leu	ttc Phe	acg Thr	gtc Val	gga Gly	gga Gly	acc Thr	931	
265270275																	
cca Pro	agc Ser	att Ile	tac Tyr	tac Tyr	ggc Gly	gat Asp	gag Glu	cag Gln	ggc Gly	ttt Phe	acg Thr	gga Gly	ttg Leu	aaa Lys	gag Glu	979	
280285290																	
gat Asp	aac Asn	gtt Val	ttc Phe	ggt Gly	gac Asp	gat Asp	gcc Ala	att Ile	agg Arg	cca Pro	cct Pro	ctt Leu	cct Pro	gcc Ala	gag Glu	1027	
295300305																	
ttt Phe	tct Ser	cca Pro	ctg Leu	ggc Gly	acc Thr	tgg Trp	att Ile	gaa Glu	aac Asn	att Ile	tat Tyr	aag Lys	gct Ala	ctg Leu	atc Ile	1075	
310315320325																	
gcg Ala	ctg Leu	cgc Arg	agg Arg	caa Gln	cac His	ccg Pro	tgg Trp	ttg Leu	tat Tyr	cag Gln	gcg Ala	cac His	acc Thr	gaa Glu	gtc Val	1123	
330335340																	
ctt Leu	gag Glu	att Ile	gct Ala	aat Asn	gaa Glu	gcg Ala	atg Met	acc Thr	tat Tyr	aag Lys	tcc Ser	gtc Val	ggt Gly	ctt Leu	gga Gly	1171	
345350355																	
ggt Gly	gaa Glu	gag Glu	ctg Leu	aca Thr	gtg Val	cat His	ctt Leu	gat Asp	ttg Leu	gaa Glu	gag Glu	gtg Val	tct Ser	gtt Val	cgg Arg	1219	
360365370																	
atc Ile	ctt Leu	gat Asp	ggc Gly	gag Glu	aag Lys	gtg Val	ctg Leu	ttt Phe	cag Gln	tac Tyr	agc Ser	gct Ala	tag	ttg	gtc	cg	1268
375380385																	
ttcaagggta ggggaacaaa																	
1288																	

```
<210> 496
<211> 386
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 496  
Met Ser Phe Ala Glu His Ala Ile Ile Trp His Val Tyr Pro Leu Gly  
1 5 10 15  
Ala Leu Gly Ala Pro Ile Arg Pro Glu Ala Pro Ala Pro Val Thr His  
20 25 30  
Arg Leu Pro Asn Leu Ile Gly Trp Leu Asp Tyr Val Val Glu Leu Gly



35					40					45					
Cys	Asn	Ala	Leu	Met	Leu	Gly	Pro	Val	Phe	Glu	Ser	Val	Ser	His	Gly
50						55					60				
Tyr	Asp	Thr	Leu	Asp	Phe	Tyr	Arg	Ile	Asp	Pro	Arg	Leu	Gly	Thr	Glu
65					70					75					80
Glu	Asp	Met	Asp	Ala	Leu	Leu	Glu	Ala	Ala	Asn	Gln	Arg	Gly	Ile	Gly
				85					90					95	
Val	Leu	Phe	Asp	Gly	Val	Phe	Asn	His	Val	Ser	Ser	Ser	Ser	Lys	Tyr
			100					105						110	
Leu	Asp	Leu	Thr	Thr	Gly	Ala	Ser	Phe	Glu	Gly	His	Asp	Ile	Leu	Ala
		115					120					125			
Glu	Leu	Asp	His	Thr	Asn	Pro	Ala	Val	Val	Asp	Leu	Val	Val	Asp	Val
		130					135					140			
Met	Asn	His	Trp	Leu	Asp	Arg	Gly	Ile	Ala	Gly	Trp	Arg	Leu	Asp	Ala
145						150					155				160
Val	Tyr	Ala	Ile	Ala	Pro	Glu	Phe	Trp	Glu	Lys	Val	Leu	Pro	Glu	Val
				165					170					175	
Arg	Arg	Lys	His	Pro	His	Ala	Trp	Ile	Val	Gly	Glu	Met	Ile	His	Gly
			180					185					190		
Asp	Tyr	Ser	Asp	Tyr	Val	Lys	Ser	Ser	Gly	Ile	Asp	Ser	Val	Thr	Glu
		195					200					205			
Tyr	Glu	Leu	Trp	Lys	Ala	Ile	Trp	Ser	Ser	Ile	Lys	Glu	Arg	Asn	Phe
		210				215					220				
Phe	Glu	Leu	Glu	Trp	Thr	Leu	Ser	Arg	His	Asn	Glu	Phe	Leu	Asp	Thr
225						230					235				240
Phe	Val	Pro	Gln	Thr	Phe	Ile	Gly	Asn	His	Asp	Val	Thr	Arg	Ile	Ala
				245					250					255	
Thr	Arg	Ile	Gly	Gln	Ser	Asn	Ala	Ile	Leu	Ala	Ala	Ala	Ile	Leu	Phe
			260					265					270		
Thr	Val	Gly	Gly	Thr	Pro	Ser	Ile	Tyr	Tyr	Gly	Asp	Glu	Gln	Gly	Phe
		275					280					285			
Thr	Gly	Leu	Lys	Glu	Asp	Asn	Val	Phe	Gly	Asp	Asp	Ala	Ile	Arg	Pro
		290				295						300			
Pro	Leu	Pro	Ala	Glu	Phe	Ser	Pro	Leu	Gly	Thr	Trp	Ile	Glu	Asn	Ile
305						310					315				320
Tyr	Lys	Ala	Leu	Ile	Ala	Leu	Arg	Arg	Gln	His	Pro	Trp	Leu	Tyr	Gln
				325					330					335	
Ala	His	Thr	Glu	Val	Leu	Glu	Ile	Ala	Asn	Glu	Ala	Met	Thr	Tyr	Lys
			340					345					350		
Ser	Val	Gly	Leu	Gly	Gly	Glu	Glu	Leu	Thr	Val	His	Leu	Asp	Leu	Glu
		355					360					365			

002290"0420960



Glu Val Ser Val Arg Ile Leu Asp Gly Glu Lys Val Leu Phe Gln Tyr  
 370 375 380

Ser Ala  
 385

<210> 497  
 <211> 1281  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1258)  
 <223> FRXA00038

<400> 497  
 acgattgtgc tgtcgtttgc gttggtgaat agttctggac cgggtatttt gcggcgacaca 60  
 tggaactcat tgaacgccgc gcccggtctaa ggtgggaggc atg agt ttt gct gaa 115  
 Met Ser Phe Ala Glu  
 1 5  
 cat gcg atc atc tgg cac gtc tac ccc ctg ggc gct ttg ggt gct ccc 163  
 His Ala Ile Ile Trp His Val Tyr Pro Leu Gly Ala Leu Gly Ala Pro  
 10 15 20  
 atc cgg cct gaa gcc ccc gca cct gtc aca cat cgg ctc ccc aat cta 211  
 Ile Arg Pro Glu Ala Pro Ala Pro Val Thr His Arg Leu Pro Asn Leu  
 25 30 35  
 att ggg tgg ctg gat tat gtt gtc gaa cta ggc tgc aac gcc ctc atg 259  
 Ile Gly Trp Leu Asp Tyr Val Val Glu Leu Gly Cys Asn Ala Leu Met  
 40 45 50  
 ctg gga ccg gta ttc gag tcc gtc agc cac ggc tac gac acc ctc gat 307  
 Leu Gly Pro Val Phe Glu Ser Val Ser His Gly Tyr Asp Thr Leu Asp  
 55 60 65  
 ttc tac cgc atc gac ccg cgc ctc ggc acc gag gaa gac atg gac gcg 355  
 Phe Tyr Arg Ile Asp Pro Arg Leu Gly Thr Glu Glu Asp Met Asp Ala  
 70 75 80 85  
 ctg ctg gag gct gcg aat cag cgg ggc att gga gtg ctt ttc gac ggc 403  
 Leu Leu Glu Ala Ala Asn Gln Arg Gly Ile Gly Val Leu Phe Asp Gly  
 90 95 100  
 gtc ttc aat cat gtt tcc agt tcc tct aaa tat ctc gac ctg acc acc 451  
 Val Phe Asn His Val Ser Ser Ser Lys Tyr Leu Asp Leu Thr Thr  
 105 110 115  
 ggg gcg tca ttt gaa ggc cac gac atc ctg gcg gaa ctc gac cac acg 499  
 Gly Ala Ser Phe Glu Gly His Asp Ile Leu Ala Glu Leu Asp His Thr  
 120 125 130  
 aat ccc gcc gta gtg gat ctg gtt gtc gat gtc atg aac cac tgg ctc 547  
 Asn Pro Ala Val Val Asp Leu Val Val Asp Val Met Asn His Trp Leu  
 135 140 145

00602740-062300



gac cgc gga atc gca ggc tgg cga ctc gac gct gtc tac gcc atc gcc 595  
 Asp Arg Gly Ile Ala Gly Trp Arg Leu Asp Ala Val Tyr Ala Ile Ala  
 150 155 160 165

cct gaa ttt tgg gaa aaa gtc ctg cca gaa gtg cga cga aaa cac cca 643  
 Pro Glu Phe Trp Glu Lys Val Leu Pro Glu Val Arg Arg Lys His Pro  
 170 175 180

cac gca tgg atc gtg ggg gag atg atc cat gga gat tac tcc gac tac 691  
 His Ala Trp Ile Val Gly Glu Met Ile His Gly Asp Tyr Ser Asp Tyr  
 185 190 195

gtg aaa agc tcc ggc att gat tcc gtt acc gaa tac gaa ctg tgg aaa 739  
 Val Lys Ser Ser Gly Ile Asp Ser Val Thr Glu Tyr Glu Leu Trp Lys  
 200 205 210

gcc att tgg agc agc atc aaa gag cgc aat ttc ttt gaa ctc gaa tgg 787  
 Ala Ile Trp Ser Ser Ile Lys Glu Arg Asn Phe Phe Glu Leu Glu Trp  
 215 220 225

act ttg agt cgc cac aat gaa ttc ctc gat act ttc gta ccg cag aca 835  
 Thr Leu Ser Arg His Asn Glu Phe Leu Asp Thr Phe Val Pro Gln Thr  
 230 235 240 245

ttc att ggt aac cat gac gtc acc cgc att gcc acc cga atc ggt caa 883  
 Phe Ile Gly Asn His Asp Val Thr Arg Ile Ala Thr Arg Ile Gly Gln  
 250 255 260

tca aat gcg atc ctg gcc gca gcg atc ctc ttc acg gtc gga gga acc 931  
 Ser Asn Ala Ile Leu Ala Ala Ala Ile Leu Phe Thr Val Gly Gly Thr  
 265 270 275

cca agc att tac tac ggc gat gag cag ggc ttt acg gga ttg aaa gag 979  
 Pro Ser Ile Tyr Tyr Gly Asp Glu Gln Gly Phe Thr Gly Leu Lys Glu  
 280 285 290

gat aac gtt ttc ggt gac gat gcc att agg cca cct ctt cct gcc gag 1027  
 Asp Asn Val Phe Gly Asp Asp Ala Ile Arg Pro Pro Leu Pro Ala Glu  
 295 300 305

ttt tct cca ctg ggc acc tgg att gaa aac att tat aag gct ctg atc 1075  
 Phe Ser Pro Leu Gly Thr Trp Ile Glu Asn Ile Tyr Lys Ala Leu Ile  
 310 315 320 325

gcg ctg cgc agg caa cac ccg tgg ttg tat cag gcg cac acc gaa gtc 1123  
 Ala Leu Arg Arg Gln His Pro Trp Leu Tyr Gln Ala His Thr Glu Val  
 330 335 340

ctt gag att gct aat gaa gcg atg acc tat aag tcc gtc ggt ctt gga 1171  
 Leu Glu Ile Ala Asn Glu Ala Met Thr Tyr Lys Ser Val Gly Leu Gly  
 345 350 355

ggt gaa gag ctg aca gtg cat ctt gat ttg gaa gag gtg tct gtt cgg 1219  
 Gly Glu Glu Leu Thr Val His Leu Asp Leu Glu Glu Val Ser Val Arg  
 360 365 370

atc ctt gat ggc gag aag gtg ctg ttt cag tac agc gct tagttgtcgg 1268  
 Ile Leu Asp Gly Glu Lys Val Leu Phe Gln Tyr Ser Ala  
 375 380 385

ttcaagggta ggg 1281

005290"0420960



<400> 498															
Met 1	Ser	Phe	Ala	Glu 5	His	Ala	Ile	Ile	Trp 10	His	Val	Tyr	Pro	Leu 15	Gly
Ala	Leu	Gly	Ala 20	Pro	Ile	Arg	Pro	Glu 25	Ala	Pro	Ala	Pro	Val 30	Thr	His
Arg	Leu	Pro 35	Asn	Leu	Ile	Gly	Trp 40	Leu	Asp	Tyr	Val	Val 45	Glu	Leu	Gly
Cys 50	Asn	Ala	Leu	Met	Leu	Gly 55	Pro	Val	Phe	Glu	Ser 60	Val	Ser	His	Gly
Tyr 65	Asp	Thr	Leu	Asp	Phe 70	Tyr	Arg	Ile	Asp	Pro 75	Arg	Leu	Gly	Thr	Glu 80
Glu	Asp	Met	Asp	Ala 85	Leu	Leu	Glu	Ala	Ala 90	Asn	Gln	Arg	Gly	Ile 95	Gly
Val	Leu	Phe	Asp 100	Gly	Val	Phe	Asn	His 105	Val	Ser	Ser	Ser	Ser 110	Lys	Tyr
Leu	Asp	Leu 115	Thr	Thr	Gly	Ala	Ser 120	Phe	Glu	Gly	His	Asp 125	Ile	Leu	Ala
Glu 130	Leu	Asp	His	Thr	Asn	Pro 135	Ala	Val	Val	Asp	Leu 140	Val	Val	Asp	Val
Met 145	Asn	His	Trp	Leu	Asp 150	Arg	Gly	Ile	Ala	Gly 155	Trp	Arg	Leu	Asp	Ala 160
Val	Tyr	Ala	Ile	Ala 165	Pro	Glu	Phe	Trp	Glu 170	Lys	Val	Leu	Pro	Glu 175	Val
Arg	Arg	Lys	His 180	Pro	His	Ala	Trp	Ile 185	Val	Gly	Glu	Met	Ile 190	His	Gly
Asp	Tyr	Ser 195	Asp	Tyr	Val	Lys	Ser 200	Ser	Gly	Ile	Asp	Ser 205	Val	Thr	Glu
Tyr 210	Glu	Leu	Trp	Lys	Ala	Ile 215	Trp	Ser	Ser	Ile	Lys 220	Glu	Arg	Asn	Phe
Phe 225	Glu	Leu	Glu	Trp	Thr 230	Leu	Ser	Arg	His	Asn 235	Glu	Phe	Leu	Asp	Thr 240
Phe	Val	Pro	Gln	Thr 245	Phe	Ile	Gly	Asn	His 250	Asp	Val	Thr	Arg	Ile 255	Ala
Thr	Arg	Ile	Gly 260	Gln	Ser	Asn	Ala	Ile 265	Leu	Ala	Ala	Ala	Ile 270	Leu	Phe
Thr	Val	Gly 275	Gly	Thr	Pro	Ser	Ile 280	Tyr	Tyr	Gly	Asp 285	Glu	Gln	Gly	Phe



Thr Gly Leu Lys Glu Asp Asn Val Phe Gly Asp Asp Ala Ile Arg Pro  
 290 295 300

Pro Leu Pro Ala Glu Phe Ser Pro Leu Gly Thr Trp Ile Glu Asn Ile  
 305 310 315 320

Tyr Lys Ala Leu Ile Ala Leu Arg Arg Gln His Pro Trp Leu Tyr Gln  
 325 330 335

Ala His Thr Glu Val Leu Glu Ile Ala Asn Glu Ala Met Thr Tyr Lys  
 340 345 350

Ser Val Gly Leu Gly Gly Glu Glu Leu Thr Val His Leu Asp Leu Glu  
 355 360 365

Glu Val Ser Val Arg Ile Leu Asp Gly Glu Lys Val Leu Phe Gln Tyr  
 370 375 380

Ser Ala  
 385

<210> 499  
 <211> 517  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(517)  
 <223> RXC00233

<400> 499  
 cgctccagc agttgagggga gaagttccaa cacttgacc aactgaggaa gcaactgtgc 60

aatagcgctt tagacacaga ctcatgacag aatagaagac atg agt gtg aat gaa 115  
 Met Ser Val Asn Glu  
 1 5

gca gat ctg aac gct gtc gaa gag caa ttg gga agg gcc cca cga ggt 163  
 Ala Asp Leu Asn Ala Val Glu Glu Gln Leu Gly Arg Ala Pro Arg Gly  
 10 15 20

gtc ctc gat att tct tac cgc agc cct gat gga gta ccc ggt gtg gtg 211  
 Val Leu Asp Ile Ser Tyr Arg Ser Pro Asp Gly Val Pro Gly Val Val  
 25 30 35

atg acc gca cca aaa ctg gat gac gga acc cca ttc cca acc ctg tac 259  
 Met Thr Ala Pro Lys Leu Asp Asp Gly Thr Pro Phe Pro Thr Leu Tyr  
 40 45 50

tac ttg aca gat cca cgc ctg acc acc gag gca tcc cgc ctc gag gtc 307  
 Tyr Leu Thr Asp Pro Arg Leu Thr Thr Glu Ala Ser Arg Leu Glu Val  
 55 60 65

gca ttg gta atg aag tgg atg act gat cgc ctt tcc acc gac gaa gag 355  
 Ala Leu Val Met Lys Trp Met Thr Asp Arg Leu Ser Thr Asp Glu Glu  
 70 75 80 85

ctt cgt gcc gac tac cag cgc gcc cac gag cac ttc ctg gca aag cgc 403

002290"0420950



Leu Arg Ala Asp Tyr Gln Arg Ala His Glu His Phe Leu Ala Lys Arg  
                     90                    95                    100  
 aac gca att gaa gat ctc ggc acg gat ttt tcc ggc ggt ggc atg cct 451  
 Asn Ala Ile Glu Asp Leu Gly Thr Asp Phe Ser Gly Gly Gly Met Pro  
                     105                    110                    115  
 gac cga gtg aag tgc ctt cac gtc ctc att gac tat gca ctg gca gaa 499  
 Asp Arg Val Lys Cys Leu His Val Leu Ile Asp Tyr Ala Leu Ala Glu  
                     120                    125                    130  
 ggc cca cac cat ttc ctt 517  
 Gly Pro His His Phe Leu  
                     135

<210> 500  
 <211> 139  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 500  
 Met Ser Val Asn Glu Ala Asp Leu Asn Ala Val Glu Glu Gln Leu Gly  
           1                    5                    10                    15  
 Arg Ala Pro Arg Gly Val Leu Asp Ile Ser Tyr Arg Ser Pro Asp Gly  
                     20                    25                    30  
 Val Pro Gly Val Val Met Thr Ala Pro Lys Leu Asp Asp Gly Thr Pro  
                     35                    40                    45  
 Phe Pro Thr Leu Tyr Tyr Leu Thr Asp Pro Arg Leu Thr Thr Glu Ala  
           50                    55                    60  
 Ser Arg Leu Glu Val Ala Leu Val Met Lys Trp Met Thr Asp Arg Leu  
           65                    70                    75                    80  
 Ser Thr Asp Glu Glu Leu Arg Ala Asp Tyr Gln Arg Ala His Glu His  
                     85                    90                    95  
 Phe Leu Ala Lys Arg Asn Ala Ile Glu Asp Leu Gly Thr Asp Phe Ser  
                     100                    105                    110  
 Gly Gly Gly Met Pro Asp Arg Val Lys Cys Leu His Val Leu Ile Asp  
           115                    120                    125  
 Tyr Ala Leu Ala Glu Gly Pro His His Phe Leu  
           130                    135

<210> 501  
 <211> 849  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(826)  
 <223> RXC00236

<400> 501

09602740.062300



```

aatgcgagag ttctaaaacg agccggtaac atcgaccccc atgagttcag gggttagaaa 60
agcaatggga tttggatgcg gttcgggtttt ggccgtcatc atg gtg atc tca ttt 115
                                         Met Val Ile Ser Phe
                                         1           5
gtt gga tgg gcg ctc agc ttc atg gat gga acg gca cct att cgc caa 163
Val Gly Trp Ala Leu Ser Phe Met Asp Gly Thr Ala Pro Ile Arg Gln
                        10                15                20
ctc cag caa atc cct gaa gat gtt ccg ccg gcg cgt ggt gta gaa gtt 211
Leu Gln Gln Ile Pro Glu Asp Val Pro Pro Ala Arg Gly Val Glu Val
                        25                30                35
ccg caa att gat aca gag gca gat gga cgc aca tcc aac cat ttg cgt 259
Pro Gln Ile Asp Thr Glu Ala Asp Gly Arg Thr Ser Asn His Leu Arg
                        40                45                50
ttt tgg gcg gaa cca att gct caa gat act ggt gtg tcc gct caa gcg 307
Phe Trp Ala Glu Pro Ile Ala Gln Asp Thr Gly Val Ser Ala Gln Ala
                        55                60                65
att gcg gct tat gga aac gca gag ctc atc gcg agt act gcg tgg cct 355
Ile Ala Ala Tyr Gly Asn Ala Glu Leu Ile Ala Ser Thr Ala Trp Pro
                        70                75                80                85
ggc tgc aat ctg ggg tgg aat acc ttg gca ggt atc ggc cag gtg gaa 403
Gly Cys Asn Leu Gly Trp Asn Thr Leu Ala Gly Ile Gly Gln Val Glu
                        90                95                100
acc cgt cac ggt acc tac aac ggc aaa atg ttc ggg ggc agt tcc ctg 451
Thr Arg His Gly Thr Tyr Asn Gly Lys Met Phe Gly Gly Ser Ser Leu
                        105                110                115
gat gaa aat gga gtt gca acc cct cca atc atc ggc gtt cca ctt gat 499
Asp Glu Asn Gly Val Ala Thr Pro Pro Ile Ile Gly Val Pro Leu Asp
                        120                125                130
ggt tca ccg ggg ttt gcg gaa att ccc gac act gat ggt ggg gaa tta 547
Gly Ser Pro Gly Phe Ala Glu Ile Pro Asp Thr Asp Gly Gly Glu Leu
                        135                140                145
gat ggc gat act gaa tat gat cgc gcg gta ggt ccc atg cag ttc att 595
Asp Gly Asp Thr Glu Tyr Asp Arg Ala Val Gly Pro Met Gln Phe Ile
                        150                155                160                165
ccg gaa acg tgg cga ctt atg gga ttg gat gca aac ggt gat ggg gta 643
Pro Glu Thr Trp Arg Leu Met Gly Leu Asp Ala Asn Gly Asp Gly Val
                        170                175                180
gcg gac ccc aac caa att gat gac gca gca ttg agt gcc gca aac ctg 691
Ala Asp Pro Asn Gln Ile Asp Asp Ala Ala Leu Ser Ala Ala Asn Leu
                        185                190                195
ttg tgt tcc aac gat cgt gac ttg tcc act cct gaa gga tgg acc gca 739
Leu Cys Ser Asn Asp Arg Asp Leu Ser Thr Pro Glu Gly Trp Thr Ala
                        200                205                210
gct gtt cat tct tac aac atg tct aat cag tat ttg atg gac gtt cga 787
Ala Val His Ser Tyr Asn Met Ser Asn Gln Tyr Leu Met Asp Val Arg
                        215                220                225

```

09602740-062300



caaqcqaac ccc 849

<400> 502															
Met 1	Val	Ile	Ser	Phe 5	Val	Gly	Trp	Ala	Leu 10	Ser	Phe	Met	Asp	Gly 15	Thr
Ala	Pro	Ile	Arg 20	Gln	Leu	Gln	Gln	Ile 25	Pro	Glu	Asp	Val	Pro 30	Pro	Ala
Arg	Gly	Val 35	Glu	Val	Pro	Gln	Ile 40	Asp	Thr	Glu	Ala	Asp 45	Gly	Arg	Thr
Ser	Asn 50	His	Leu	Arg	Phe	Trp 55	Ala	Glu	Pro	Ile	Ala 60	Gln	Asp	Thr	Gly
Val 65	Ser	Ala	Gln	Ala	Ile 70	Ala	Ala	Tyr	Gly	Asn 75	Ala	Glu	Leu	Ile	Ala 80
Ser	Thr	Ala	Trp	Pro 85	Gly	Cys	Asn	Leu	Gly 90	Trp	Asn	Thr	Leu	Ala 95	Gly
Ile	Gly	Gln	Val 100	Glu	Thr	Arg	His	Gly 105	Thr	Tyr	Asn	Gly	Lys 110	Met	Phe
Gly	Gly	Ser 115	Ser	Leu	Asp	Glu	Asn 120	Gly	Val	Ala	Thr	Pro 125	Pro	Ile	Ile
Gly	Val 130	Pro	Leu	Asp	Gly	Ser 135	Pro	Gly	Phe	Ala	Glu 140	Ile	Pro	Asp	Thr
Asp 145	Gly	Gly	Glu	Leu	Asp 150	Gly	Asp	Thr	Glu	Tyr 155	Asp	Arg	Ala	Val	Gly 160
Pro	Met	Gln	Phe	Ile 165	Pro	Glu	Thr	Trp	Arg 170	Leu	Met	Gly	Leu	Asp 175	Ala
Asn	Gly	Asp	Gly 180	Val	Ala	Asp	Pro	Asn 185	Gln	Ile	Asp	Asp	Ala 190	Ala	Leu
Ser	Ala 195	Ala	Asn	Leu	Leu	Cys	Ser 200	Asn	Asp	Arg	Asp	Leu 205	Ser	Thr	Pro
Glu	Gly 210	Trp	Thr	Ala	Ala	Val 215	His	Ser	Tyr	Asn	Met 220	Ser	Asn	Gln	Tyr
Leu 225	Met	Asp	Val	Arg	Asp 230	Ala	Ala	Ala	Ser	Tyr 235	Ala	Leu	Arg	Gln	Pro 240
Ala Ile															



```
<220>  
<221> CDS  
<222> (101)..(1090)  
<223> RXC00271
```

0960340-0960300



```
<210> 504
<211> 330
<212> PRT
<213> Corynebacterium glutamicum
```

Leu Val Gln His Pro Ala Leu Asp Ala Ala Thr Thr Gly Phe Lys Glu  
50 55 60

Overall		Non-Black		Black	
Age	Gender	Age	Gender	Age	Gender
18-24	Male	18-24	Male	18-24	Male
25-34	Female	25-34	Female	25-34	Female
35-44	Male	35-44	Male	35-44	Male
45-54	Female	45-54	Female	45-54	Female
55-64	Male	55-64	Male	55-64	Male
65-74	Female	65-74	Female	65-74	Female
75-84	Male	75-84	Male	75-84	Male
85-94	Female	85-94	Female	85-94	Female
95-104	Male	95-104	Male	95-104	Male
105-114	Female	105-114	Female	105-114	Female
115-124	Male	115-124	Male	115-124	Male
125-134	Female	125-134	Female	125-134	Female
135-144	Male	135-144	Male	135-144	Male
145-154	Female	145-154	Female	145-154	Female
155-164	Male	155-164	Male	155-164	Male
165-174	Female	165-174	Female	165-174	Female
175-184	Male	175-184	Male	175-184	Male
185-194	Female	185-194	Female	185-194	Female
195-204	Male	195-204	Male	195-204	Male
205-214	Female	205-214	Female	205-214	Female
215-224	Male	215-224	Male	215-224	Male
225-234	Female	225-234	Female	225-234	Female
235-244	Male	235-244	Male	235-244	Male
245-254	Female	245-254	Female	245-254	Female
255-264	Male	255-264	Male	255-264	Male
265-274	Female	265-274	Female	265-274	Female
275-284	Male	275-284	Male	275-284	Male
285-294	Female	285-294	Female	285-294	Female
295-304	Male	295-304	Male	295-304	Male
305-314	Female	305-314	Female	305-314	Female
315-324	Male	315-324	Male	315-324	Male
325-334	Female	325-334	Female	325-334	Female
335-344	Male	335-344	Male	335-344	Male
345-354	Female	345-354	Female	345-354	Female
355-364	Male	355-364	Male	355-364	Male
365-374	Female	365-374	Female	365-374	Female
375-384	Male	375-384	Male	375-384	Male
385-394	Female	385-394	Female	385-394	Female
395-404	Male	395-404	Male	395-404	Male
405-414	Female	405-414	Female	405-414	Female
415-424	Male	415-424	Male	415-424	Male
425-434	Female	425-434	Female	425-434	Female
435-444	Male	435-444	Male	435-444	Male
445-454	Female	445-454	Female	445-454	Female
455-464	Male	455-464	Male	455-464	Male
465-474	Female	465-474	Female	465-474	Female
475-484	Male	475-484	Male	475-484	Male
485-494	Female	485-494	Female	485-494	Female
495-504	Male	495-504	Male	495-504	Male
505-514	Female	505-514	Female	505-514	Female
515-524	Male	515-524	Male	515-524	Male
525-534	Female	525-534	Female	525-534	Female
535-544	Male	535-544	Male	535-544	Male
545-554	Female	545-554	Female	545-554	Female
555-564	Male	555-564	Male	555-564	Male
565-574	Female	565-574	Female	565-574	Female
575-584	Male	575-584	Male	575-584	Male
585-594	Female	585-594	Female	585-594	Female
595-604	Male	595-604	Male	595-604	Male
605-614	Female	605-614	Female	605-614	Female
615-624	Male				



```
<210> 505
<211> 1263
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1240)
<223> RXC00338
```

```
<220>
<221> CDS
<222> (101) .. (1240)
<223> BXC00338
```



tcttagaagg cgtagtcaca ccattaacct tgccagaatt tttcaaggct tggctagact																60
tgggaaacga acatgcggta ccaaccaggg gagttaatgc																115
Val Ser Asp Val Thr																
gtg agt gat gta acc																163
1 5																
gtt ggc gat att cgc cgc att ttg gat gag gct tat ccg ccg gcg ttg																211
Val Gly Asp Ile Arg Arg Ile Leu Asp Glu Ala Tyr Pro Pro Ala Leu																
gcg gaa agc tgg gac aaa gtg ggg ctg atc tgc ggt gat cca aca gag																259
Ala Glu Ser Trp Asp Lys Val Gly Leu Ile Cys Gly Asp Pro Thr Glu																
tcg gtg aag cgt gtc ggt tta gca ctc gat tgc acc cag gca gtg gcc																307
Ser Val Lys Arg Val Gly Leu Ala Leu Asp Cys Thr Gln Ala Val Ala																
gac aag gct gtg gac atg ggt ttg gac atg ctg atc att cac cac cca																355
Asp Lys Ala Val Asp Met Gly Leu Asp Met Leu Ile Ile His His Pro																
ttg ctg ctg cgt ggg gtg acg tct gtt gct gcg gat gag cca aaa ggc																403
Leu Leu Leu Arg Gly Val Thr Ser Val Ala Ala Asp Glu Pro Lys Gly																
aag gtc att cac acc cta att cgc ggc ggg gtg gca ctg ttt tcc gcg																451
Lys Val Ile His Thr Leu Ile Arg Gly Gly Val Ala Leu Phe Ser Ala																
cac act aat gcg gat tcc gcg cgc cca ggt gtc aac gat aaa ctc gcc																499
His Thr Asn Ala Asp Ser Ala Arg Pro Gly Val Asn Asp Lys Leu Ala																
gag ctc gtc ggc atc acg gcc ggg cga ccc atc gcg aca cgg ctt tta																547
Glu Leu Val Gly Ile Thr Ala Gly Arg Pro Ile Ala Thr Arg Leu Leu																
ggc ggc atg gac aaa tgg ggc gtg cac gtt ctg ccc aag gat gca gcg																595
Gly Gly Met Asp Lys Trp Gly Val His Val Leu Pro Lys Asp Ala Ala																
tac cta aag aag atg ctt ttc gac gca ggt gcc ggt gcg atc ggc gac																643
Tyr Leu Lys Lys Met Leu Phe Asp Ala Gly Gly Ala Gly Ile Gly Asp																
tac cga gag tgt gcc ttt gag atc gaa gga acc ggg cag ttt agg ccc																691
Tyr Arg Glu Cys Ala Phe Glu Ile Glu Gly Thr Gly Gln Phe Arg Pro																
gtg gag ggg gcg aat ccg gca gag ggg gac gtc gat aag ctt ttt aaa																739
Val Glu Gly Ala Asn Pro Ala Glu Gly Asp Val Asp Lys Leu Phe Lys																
tcc ctt gag ctg cgc atc gag ttt gtt gca ccg gcg aac ctg cgc gcc																787
Ser Leu Glu Leu Arg Ile Glu Phe Val Ala Pro Arg Asn Leu Arg Ala																
cgg ctc acg tcg qtq ctq cqq qaq qct cat ccg tat qaq qaq cct qcc																

Parameter	Unit	Value
Initial concentration	g/L	1.0
Initial pH	-	7.0
Temperature	°C	25
Time	h	0, 1, 2, 4, 8, 16, 32, 64, 128, 256, 512, 1024, 2048, 4096, 8192, 16384, 32768, 65536, 131072, 262144, 524288, 1048576, 2097152, 4194304, 8388608, 16777216, 33554432, 67108864, 134217728, 268435456, 536870912, 1073741824, 2147483648, 4294967296, 8589934592, 17179869184, 34359738368, 68719476736, 137438953472, 274877906944, 549755813888, 1099511627776, 2199023255552, 4398046511104, 8796093022208, 17592186044416, 35184372088832, 70368744177664, 140737488355328, 281474976710656, 562949953421312, 1125899906842624, 2251799813685248, 4503599627370496, 9007199254740992, 18014398509481984, 36028797018963968, 72057594037927936, 144115188075855872, 288230376151711744, 576460752303423488, 1152921504606846976, 2305843009213693952, 4611686018427387904, 9223372036854775808, 18446744073709551616, 36893488147419103232, 73786976294838206464, 147573952589676412928, 295147905179352825856, 590295810358705651712, 1180591620717411303424, 2361183241434822606848, 4722366482869645213696, 9444732965739290427392, 18889465931478580854784, 37778931862957161709568, 75557863725914323419136, 151115727451828646838272, 302231454903657293676544, 604462909807314587353088, 1208925819614629174706176, 2417851639229258349412352, 4835703278458516698824704, 9671406556917033397649408, 19342813113834066795298816, 38685626227668133590597632, 77371252455336267181195264, 154742504910672534362390528, 309485009821345068724781056, 618970019642690137449562112, 1237940039285380274899124224, 2475880078570760549798248448, 4951760157141521099596496896, 9903520314283042199192993792, 19807040628566084398385987584, 39614081257132168796771975168, 79228162514264337593543950336, 158456325028528675187087900672, 316912650057057350374175801344, 633825300114114700748351602688, 1267650600228229401496703205376, 2535301200456458802993406410752, 5070602400912917605986812821504, 10141204801825835211973625643008, 20282409603651670423947251286016, 40564819207303340847894502572032, 81129638414606681695789005144064, 162259276829213363391578010288128, 324518553658426726783156020576256, 649037107316853453566312041152512, 1298074214633706907132624082305024, 2596148429267413814265248164610048, 5192296858534827628530496329220096, 10384593717069655257060992658440192, 20769187434139310514121985316880384, 41538374868278621028243970633760768, 83076749736557242056487941267521536, 166153499473114484112975882535043072, 332306998946228968225951765070086144, 664613997892457936451903530140172288, 1329227995784915872903807060280344576, 2658455991569831745807614120560689152, 5316911983139663491615228241121378304, 10633823966279326983230456482242756608, 21267647932558653966460912964485513216, 42535295865117307932921825928971026432, 85070591730234615865843651857942052864, 170141183460469231731687303715884105728, 340282366920938463463374607431768211456, 680564733841876926926749214863536422912, 1361129467683753853853498429727072845824, 2722258935367507707706996859454145691648, 5444517870735015415413993718908291383296, 10889035741470030830827987437816582766592, 21778071482940061661655974875633165533184, 43556142965880123323311949751266331066368, 87112285931760246646623899502532662132736, 174224571863520493293247799005065324265472, 348449143727040986586495598010130648530944, 696898287454081973172991196020261297061888, 1393796574908163946345982392040522594123776, 2787593149816327892691964784081045188247552, 5575186299632655785383929568162090376495104, 11150372599265311570767859136324180752990208, 22300745198530623141535718272648361505980416, 44601490397061246283071436545296723011960832, 89202980794122492566142873090593446023921664, 178405961588244985132285746181186892047843328, 356811923176489970264571492362373784095686656, 713623846352979940529142984724747568191373312, 1427247692705959881058285969449495136382746624, 2854495385411919762116571938898990272765493248, 5708990770823839524233143877797980545530986496, 11417981541647679048466287755595961091061972992, 22835



```

Arg Leu Thr Ser Val Leu Arg Glu Ala His Pro Tyr Glu Glu Pro Ala
215                220                225

ttc gat att gtt gaa atg cac agc gct gag agt tta gaa aat gcg acc 835
Phe Asp Ile Val Glu Met His Ser Ala Glu Ser Leu Glu Asn Ala Thr
230                235                240                245

gga ttg ggt cgt gtg ggt gaa ttg ccg gag ccg atg cgc ctc gcg gat 883
Gly Leu Gly Arg Val Gly Glu Leu Pro Glu Pro Met Arg Leu Ala Asp
                250                255                260

ttc gtg caa caa gtg gcc aac aac ctg cct gtc acc gaa tgg ggc gtg 931
Phe Val Gln Gln Val Ala Asn Asn Leu Pro Val Thr Glu Trp Gly Val
                265                270                275

cgc gct acc ggc gat cct gaa caa atg gtg tcc cgt gtg gcg gtt tca 979
Arg Ala Thr Gly Asp Pro Glu Gln Met Val Ser Arg Val Ala Val Ser
                280                285                290

tca ggg tcg ggt gac agt ttc tta aac gat gtg att aag ctc gga gtg 1027
Ser Gly Ser Gly Asp Ser Phe Leu Asn Asp Val Ile Lys Leu Gly Val
                295                300                305

gac gtt tat gtc act tct gat ctg cgc cac cat cca gtt gat gaa tat 1075
Asp Val Tyr Val Thr Ser Asp Leu Arg His His Pro Val Asp Glu Tyr
310                315                320                325

ctc cga gaa ggt ggc cct gca gta atc gat act gca cac tgg gcc agc 1123
Leu Arg Glu Gly Gly Pro Ala Val Ile Asp Thr Ala His Trp Ala Ser
                330                335                340

gaa ttt cca tgg act tcc caa gcc caa gaa att ttg cag gac aaa gcc 1171
Glu Phe Pro Trp Thr Ser Gln Ala Gln Glu Ile Leu Gln Asp Lys Ala
                345                350                355

cca cag gtt gaa gtt gat gtg att tcg atc cgc aca gac ccc tgg acc 1219
Pro Gln Val Glu Val Asp Val Ile Ser Ile Arg Thr Asp Pro Trp Thr
                360                365                370

atg tct gcg cga gca gtg aac taaattcttg agaactaaaa aag 1263
Met Ser Ala Arg Ala Val Asn
375                380

```

&lt;210&gt; 506

&lt;211&gt; 380

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 506

```

Val Ser Asp Val Thr Val Gly Asp Ile Arg Arg Ile Leu Asp Glu Ala
1                5                10                15

Tyr Pro Pro Ala Leu Ala Glu Ser Trp Asp Lys Val Gly Leu Ile Cys
                20                25                30

Gly Asp Pro Thr Glu Ser Val Lys Arg Val Gly Leu Ala Leu Asp Cys
35                40                45

Thr Gln Ala Val Ala Asp Lys Ala Val Asp Met Gly Leu Asp Met Leu
50                55                60

```

09602740.062300



Ile Ile His His Pro Leu Leu Leu Arg Gly Val Thr Ser Val Ala Ala  
 65 70 75 80  
 Asp Glu Pro Lys Gly Lys Val Ile His Thr Leu Ile Arg Gly Gly Val  
 85 90 95  
 Ala Leu Phe Ser Ala His Thr Asn Ala Asp Ser Ala Arg Pro Gly Val  
 100 105 110  
 Asn Asp Lys Leu Ala Glu Leu Val Gly Ile Thr Ala Gly Arg Pro Ile  
 115 120 125  
 Ala Thr Arg Leu Leu Gly Gly Met Asp Lys Trp Gly Val His Val Leu  
 130 135 140  
 Pro Lys Asp Ala Ala Tyr Leu Lys Lys Met Leu Phe Asp Ala Gly Ala  
 145 150 155 160  
 Gly Ala Ile Gly Asp Tyr Arg Glu Cys Ala Phe Glu Ile Glu Gly Thr  
 165 170 175  
 Gly Gln Phe Arg Pro Val Glu Gly Ala Asn Pro Ala Glu Gly Asp Val  
 180 185 190  
 Asp Lys Leu Phe Lys Ser Leu Glu Leu Arg Ile Glu Phe Val Ala Pro  
 195 200 205  
 Arg Asn Leu Arg Ala Arg Leu Thr Ser Val Leu Arg Glu Ala His Pro  
 210 215 220  
 Tyr Glu Glu Pro Ala Phe Asp Ile Val Glu Met His Ser Ala Glu Ser  
 225 230 235 240  
 Leu Glu Asn Ala Thr Gly Leu Gly Arg Val Gly Glu Leu Pro Glu Pro  
 245 250 255  
 Met Arg Leu Ala Asp Phe Val Gln Gln Val Ala Asn Asn Leu Pro Val  
 260 265 270  
 Thr Glu Trp Gly Val Arg Ala Thr Gly Asp Pro Glu Gln Met Val Ser  
 275 280 285  
 Arg Val Ala Val Ser Ser Gly Ser Gly Asp Ser Phe Leu Asn Asp Val  
 290 295 300  
 Ile Lys Leu Gly Val Asp Val Tyr Val Thr Ser Asp Leu Arg His His  
 305 310 315 320  
 Pro Val Asp Glu Tyr Leu Arg Glu Gly Gly Pro Ala Val Ile Asp Thr  
 325 330 335  
 Ala His Trp Ala Ser Glu Phe Pro Trp Thr Ser Gln Ala Gln Glu Ile  
 340 345 350  
 Leu Gln Asp Lys Ala Pro Gln Val Glu Val Asp Val Ile Ser Ile Arg  
 355 360 365  
 Thr Asp Pro Trp Thr Met Ser Ala Arg Ala Val Asn  
 370 375 380

002290" 0420960



<210> 507  
 <211> 1470  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1447)  
 <223> RXC00362

<400> 507

```

cacttttttgg gtgaaaattc cacgaagtta atgccgcttt aagtcaattc aatcacatgt 60

aacatgctac ggtttttttcg gtcacttaaa ggaggcgctt atg gga atc att gct 115
                                         Met Gly Ile Ile Ala
                                         1           5

ctg ctc gtt ttt atc gca att gcc gtg ata ttg aat gtg ttt ttg aaa 163
Leu Leu Val Phe Ile Ala Ile Ala Val Ile Leu Asn Val Phe Leu Lys
                        10                        15                        20

cga gat att tca gaa gca ttg cta gtt gga tta gta gga act gcg ctt 211
Arg Asp Ile Ser Glu Ala Leu Leu Val Gly Leu Val Gly Thr Ala Leu
                        25                        30                        35

gtc ggc ggt gta aat gca ccg aca tta ctg att gat gct gta gtg gat 259
Val Gly Gly Val Asn Ala Pro Thr Leu Leu Ile Asp Ala Val Val Asp
                        40                        45                        50

gct gct cag tcg gaa gtt act ttc gca ggt atg gcc ttt gtt ttc atg 307
Ala Ala Gln Ser Glu Val Thr Phe Ala Gly Met Ala Phe Val Phe Met
                        55                        60                        65

ggc atc gtt gtg caa tca act gga ttg att gat cga tta atc gca atc 355
Gly Ile Val Val Gln Ser Thr Gly Leu Ile Asp Arg Leu Ile Ala Ile
                        70                        75                        80                        85

ctt aac tcg att ttt ggt cgg ctt cga ggt ggc gca ggt tat gtt tcc 403
Leu Asn Ser Ile Phe Gly Arg Leu Arg Gly Gly Ala Gly Tyr Val Ser
                        90                        95                        100

act ctt gga tct gcg ctc att gga ctc atc gct gga tca acg gct gga 451
Thr Leu Gly Ser Ala Leu Ile Gly Leu Ile Ala Gly Ser Thr Ala Gly
                        105                        110                        115

aac tcc gcg acg gtt ggc tca gtg acg atc cct tgg atg aaa aag acg 499
Asn Ser Ala Thr Val Gly Ser Val Thr Ile Pro Trp Met Lys Lys Thr
                        120                        125                        130

gga tgg act gct gaa agg tcc gca acg tta gtc gcg ggc aac tct ggc 547
Gly Trp Thr Ala Glu Arg Ser Ala Thr Leu Val Ala Gly Asn Ser Gly
                        135                        140                        145

ctt ggt gtt gcg ttg cct ccc aat tca aca atg ttc atc att ttg gca 595
Leu Gly Val Ala Leu Pro Pro Asn Ser Thr Met Phe Ile Ile Leu Ala
                        150                        155                        160                        165

ttg cca gct gca gca gct tct tcg gcc tct cag gtg tac att gct ttg 643
Leu Pro Ala Ala Ala Ala Ser Ser Ala Ser Gln Val Tyr Ile Ala Leu
                        170                        175                        180

```

09602740.062360



gct tgt ggt ggt gcg tat gca gtg ctc tac cgc tta gcg gtc gtc ttt 691  
 Ala Cys Gly Gly Ala Tyr Ala Val Leu Tyr Arg Leu Ala Val Val Phe  
 185 190 195

tac tgg aca cgt aaa gat aaa att cct gcc acc cct gat gat caa cgg 739  
 Tyr Trp Thr Arg Lys Asp Lys Ile Pro Ala Thr Pro Asp Asp Gln Arg  
 200 205 210

gtg tca ttc ggt gag gca atg aag act gga tgg cgt tca ccg ttg atc 787  
 Val Ser Phe Gly Glu Ala Met Lys Thr Gly Trp Arg Ser Pro Leu Ile  
 215 220 225

ttc ctt gga att ttg atc ccc gta atc ctc aca atc ggc cca ttg tct 835  
 Phe Leu Gly Ile Leu Ile Pro Val Ile Leu Thr Ile Gly Pro Leu Ser  
 230 235 240 245

gaa tgg tta aag aca cat gga gtt ggg gag tct ggt gtt aaa tcg atg 883  
 Glu Trp Leu Lys Thr His Gly Val Gly Glu Ser Gly Val Lys Ser Met  
 250 255 260

tcg atc atc gtg tgg gtg cca att ctg att acg gca att gct ctg att 931  
 Ser Ile Ile Val Trp Val Pro Ile Leu Ile Thr Ala Ile Ala Leu Ile  
 265 270 275

gaa ggg cgt aaa cga att gct aac aac atg gca cac ttt agg gtt cag 979  
 Glu Gly Arg Lys Arg Ile Ala Asn Asn Met Ala His Phe Arg Val Gln  
 280 285 290

atc tcc aag gac ttg cca caa ttt gcc acc gta gga att tcg ttg ttt 1027  
 Ile Ser Lys Asp Leu Pro Gln Phe Ala Thr Val Gly Ile Ser Leu Phe  
 295 300 305

tct gcg ctt gca gca gcg aac atc atg gaa gaa ctg ggt gtt ggc ccg 1075  
 Ser Ala Leu Ala Ala Ala Asn Ile Met Glu Glu Leu Gly Val Gly Pro  
 310 315 320 325

cag ttg tct aac tgg ctt gat tcc atg gac cta cct aag tct gtc atg 1123  
 Gln Leu Ser Asn Trp Leu Asp Ser Met Asp Leu Pro Lys Ser Val Met  
 330 335 340

gtg atc att gtc tgc atc atg tgc att gtg gtg gca acg cca ctg tcg 1171  
 Val Ile Ile Val Cys Ile Met Cys Ile Val Val Ala Thr Pro Leu Ser  
 345 350 355

tca aca gca acc gcg gct gcg att ggt gct ccc gct gtc gct gcg ttg 1219  
 Ser Thr Ala Thr Ala Ala Ala Ile Gly Ala Pro Ala Val Ala Ala Leu  
 360 365 370

gct gcg gta ggt att gat cca act gtg gcg atc gta gtg atc ttg ctg 1267  
 Ala Ala Val Gly Ile Asp Pro Thr Val Ala Ile Val Val Ile Leu Leu  
 375 380 385

tgc act tcc act gaa ggt gca tcc ccg ccg gtg ggc gcg ccg att tac 1315  
 Cys Thr Ser Thr Glu Gly Ala Ser Pro Pro Val Gly Ala Pro Ile Tyr  
 390 395 400 405

ctt tct gct gcg atc gcc gat gca aac cca acg aaa atg ttc gta cca 1363  
 Leu Ser Ala Ala Ile Ala Asp Ala Asn Pro Thr Lys Met Phe Val Pro  
 410 415 420

09602740-062900



ctg att acg tac ttt gtt gtc ccc atg att ctg ctt gct tgg cta gtt 1411  
 Leu Ile Thr Tyr Phe Val Val Pro Met Ile Leu Leu Ala Trp Leu Val  
                   425                                  430                                  435

gga atg gga ttc tta cca gtg att gtt cct acg ggt taaaggggta 1457  
 Gly Met Gly Phe Leu Pro Val Ile Val Pro Thr Gly  
                   440                                  445

aaaatgaact caa 1470

<210> 508

<211> 449

<212> PRT

<213> Corynebacterium glutamicum

<400> 508

Met Gly Ile Ile Ala Leu Leu Val Phe Ile Ala Ile Ala Val Ile Leu  
   1                                  5                                  10                                  15

Asn Val Phe Leu Lys Arg Asp Ile Ser Glu Ala Leu Leu Val Gly Leu  
                   20                                  25                                  30

Val Gly Thr Ala Leu Val Gly Gly Val Asn Ala Pro Thr Leu Leu Ile  
                   35                                  40                                  45

Asp Ala Val Val Asp Ala Ala Gln Ser Glu Val Thr Phe Ala Gly Met  
                   50                                  55                                  60

Ala Phe Val Phe Met Gly Ile Val Val Gln Ser Thr Gly Leu Ile Asp  
                   65                                  70                                  75                                  80

Arg Leu Ile Ala Ile Leu Asn Ser Ile Phe Gly Arg Leu Arg Gly Gly  
                   85                                  90                                  95

Ala Gly Tyr Val Ser Thr Leu Gly Ser Ala Leu Ile Gly Leu Ile Ala  
                   100                                  105                                  110

Gly Ser Thr Ala Gly Asn Ser Ala Thr Val Gly Ser Val Thr Ile Pro  
                   115                                  120                                  125

Trp Met Lys Lys Thr Gly Trp Thr Ala Glu Arg Ser Ala Thr Leu Val  
                   130                                  135                                  140

Ala Gly Asn Ser Gly Leu Gly Val Ala Leu Pro Pro Asn Ser Thr Met  
                   145                                  150                                  155                                  160

Phe Ile Ile Leu Ala Leu Pro Ala Ala Ala Ser Ser Ala Ser Gln  
                   165                                  170                                  175

Val Tyr Ile Ala Leu Ala Cys Gly Gly Ala Tyr Ala Val Leu Tyr Arg  
                   180                                  185                                  190

Leu Ala Val Val Phe Tyr Trp Thr Arg Lys Asp Lys Ile Pro Ala Thr  
                   195                                  200                                  205

Pro Asp Asp Gln Arg Val Ser Phe Gly Glu Ala Met Lys Thr Gly Trp  
                   210                                  215                                  220

Arg Ser Pro Leu Ile Phe Leu Gly Ile Leu Ile Pro Val Ile Leu Thr  
                   225                                  230                                  235                                  240

00602740-062300



cttttgtccc ccgacttttg tacgaatcga ggacaccgtc gtg tca cac acc gcg 115  
Val Ser His Thr Ala  
1 5

[illegible]



09602740-062300



Tyr Gly Ser Val Tyr Glu Val Phe Ser Asn Pro Gln Thr Gln Val Ala  
 250 255 260

caa aag ttc gtg gcc acc gcg ctg cgt aac acc cca gac caa gtg gaa 931  
 Gln Lys Phe Val Ala Thr Ala Leu Arg Asn Thr Pro Asp Gln Val Glu  
 265 270 275

tcg gaa gat ctg ctt agc cat gag gga cgt ctg ttc acc att gat ctg 979  
 Ser Glu Asp Leu Leu Ser His Glu Gly Arg Leu Phe Thr Ile Asp Leu  
 280 285 290

act gaa acg tcc ggc ttc ttt gca gca acc gct cgt gct gcc gaa caa 1027  
 Thr Glu Thr Ser Gly Phe Phe Ala Ala Thr Ala Arg Ala Ala Glu Gln  
 295 300 305

ggt gct ttt gtc aac atc gtt cac ggt ggc gtg acc acc ttg caa cgc 1075  
 Gly Ala Phe Val Asn Ile Val His Gly Gly Val Thr Thr Leu Gln Arg  
 310 315 320 325

caa tca ttt ggc aaa atg act gtt cga ctc acc ggc aac acc gct gcg 1123  
 Gln Ser Phe Gly Lys Met Thr Val Arg Leu Thr Gly Asn Thr Ala Ala  
 330 335 340

att gaa gag ttc tat caa acc ttg acc aag acc acg acc atc aag gag 1171  
 Ile Glu Glu Phe Tyr Gln Thr Leu Thr Lys Thr Thr Ile Lys Glu  
 345 350 355

atc acc cga tgaacgagat gatcctcgca gct 1203  
 Ile Thr Arg  
 360

<210> 510  
 <211> 360  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 510  
 Val Ser His Thr Ala Ser Thr Pro Thr Pro Glu Glu Tyr Ser Ala Gln  
 1 5 10 15

Gln Pro Ser Thr Gln Gly Thr Arg Val Glu Phe Arg Gly Ile Thr Lys  
 20 25 30

Val Phe Ser Asn Asn Lys Ser Ala Lys Thr Thr Ala Leu Asp Asn Val  
 35 40 45

Thr Leu Thr Val Glu Pro Gly Glu Val Ile Gly Ile Ile Gly Tyr Ser  
 50 55 60

Gly Ala Gly Lys Ser Thr Leu Val Arg Leu Ile Asn Gly Leu Asp Ser  
 65 70 75 80

Pro Thr Ser Gly Ser Leu Leu Leu Asn Gly Thr Asp Ile Val Gly Met  
 85 90 95

Pro Glu Ser Lys Leu Arg Lys Leu Arg Ser Asn Ile Gly Met Ile Phe  
 100 105 110

Gln Gln Phe Asn Leu Phe Gln Ser Arg Thr Ala Ala Gly Asn Val Glu  
 115 120 125

0062290" 0420960



06290-062740

06290-062740

06290-062740

062300-090740-090900



[illegible]



```
<210> 512
<211> 230
<212> PRT
<213> Corynebacterium glutamicum
```

```
<210> 513
<211> 1185
<212> DNA
<213> Corynebacterium glutamicum
```

 $\langle 220 \rangle$



<400> 513

0960240-096000



200	205	210	
cag cgt tcc atc aag gaa ctg gtg att aag gat gag gac gtg cgc acg Gln Arg Ser Ile Lys Glu Leu Val Ile Lys Asp Glu Asp Val Arg Thr 215 220 225			787
ctg gcg ttc ggt aaa tct ggc ccg acc ttg cac cag ttg gag gaa gca Leu Ala Phe Gly Lys Ser Gly Pro Thr Leu His Gln Leu Glu Glu Ala 230 235 240 245			835
gtc cgc gag acc ggt ttc tcc cgc ttc cct gtc acc ggc cgc gat gga Val Arg Glu Thr Gly Phe Ser Arg Phe Pro Val Thr Gly Arg Asp Gly 250 255 260			883
tcc tac ttg ggt tat atc cac atc aag gat att ttg cct cgt ctg gct Ser Tyr Leu Gly Tyr Ile His Ile Lys Asp Ile Leu Pro Arg Leu Ala 265 270 275			931
gat cct gag atg gat ccc tcc gag acc att ccg cgt tct gca ctg cgc Asp Pro Glu Met Asp Pro Ser Glu Thr Ile Pro Arg Ser Ala Leu Arg 280 285 290			979
cct ttg agc aat gtg gat gcc gac ggc ctc atg gat gac gtc ttg gat Pro Leu Ser Asn Val Asp Ala Asp Gly Leu Met Asp Asp Val Leu Asp 295 300 305			1027
ttt atg cac tac cgc tcc gcg cac atg gct cag gtt cgc ctc aaa ggt Phe Met His Tyr Arg Ser Ala His Met Ala Gln Val Arg Leu Lys Gly 310 315 320 325			1075
gag ctt ctc ggc gtg att acg ctg gag gat ctc atc gaa gaa tac gtg Glu Leu Leu Gly Val Ile Thr Leu Glu Asp Leu Ile Glu Glu Tyr Val 330 335 340			1123
ggc acc gtc aac gat tgg act cac gaa agc tcc gac gac tagaaatagt Gly Thr Val Asn Asp Trp Thr His Glu Ser Ser Asp Asp 345 350			1172
aactgtgttg gac			1185
 <210> 514 <211> 354 <212> PRT <213> Corynebacterium glutamicum			
 <400> 514 Val Ser Ile Trp Ala Thr Val Leu Leu Ile Ile Val Leu Leu Ser Ala 1 5 10 15 Asn Ala Phe Phe Val Ala Ala Glu Phe Ala Leu Ile Ser Ser Arg Arg 20 25 30 Asp Arg Leu Asp Ser Leu Val Ser Gln Gly Lys Lys Gly Ala Glu Lys 35 40 45 Val Leu Tyr Ala Thr Glu His Leu Ser Ile Met Leu Ala Gly Ala Gln 50 55 60 Phe Gly Ile Thr Val Cys Ser Leu Ile Leu Gly Lys Val Ala Glu Pro 65 70 75 80			

002290-0420960







<400> 515

```

agtgtggatt gctagaaaac tttaagaaag aggaaataat atg gct caa aaa gta    115
              Met Ala Gln Lys Val
              1                      5

```

acc ttc tgg ttc gat acc acc tgc cca ttc tgc tgg gtc acc tcc cgc 163  
Thr Phe Trp Phe Asp Thr Thr Cys Pro Phe Cys Trp Val Thr Ser Arg  
10 15 20

tgg	att	aag	gaa	gtc	gaa	caa	gtc	cgc	gat	att	gaa	atc	cag	tgg	gtt	211
Trp	Ile	Lys	Glu	Val	Glu	Gln	Val	Arg	Asp	Ile	Glu	Ile	Gln	Trp	Val	
			25					30					35			

cca atg agc ctc gct gtc cta aac gaa ggc cgt gat ctc cca gag gat 259  
Pro Met Ser Leu Ala Val Leu Asn Glu Gly Arg Asp Leu Pro Glu Asp  
40 45 50

tac aag gag cgc atg aag gct gca tgg gga cca gca cgc gtt ttc gca 307  
 Tyr Lys Glu Arg Met Lys Ala Ala Trp Gly Pro Ala Arg Val Phe Ala  
 55 60 65

gct gtc gcc acc gac cat gct gac aag ctc ggc gac ctg tac acc gca 355  
Ala Val Ala Thr Asp His Ala Asp Lys Leu Gly Asp Leu Tyr Thr Ala  
70 75 80 85

atg ggt acc cgc atc cac aac gac ggt cgc gga cca atc gaa ggt tcc 403  
Met Gly Thr Arg Ile His Asn Asp Gly Arg Gly Pro Ile Glu Gly Ser  
90 95 100

ttc aat gat gtc atc gca gag gca ctt gaa gag gtc ggc cta gac gct 451  
Phe Asn Asp Val Ile Ala Glu Ala Leu Glu Glu Val Gly Leu Asp Ala  
105 110 115

gca ctt ggt gaa gtt gca gac acc acc gaa tgg gac gac gca ctt cgc 499  
Ala Leu Gly Glu Val Ala Asp Thr Thr Glu Trp Asp Asp Ala Leu Arg  
120 125 130

gca ttc cac cag acc gca atg gac gag gtc ggc aac gat gtc gga acc 547  
Ala Phe His Gln Thr Ala Met Asp Glu Val Gly Asn Asp Val Gly Thr  
135 140 145

cca gtg gtc aag ctc ggc gac acc gct ttc ttc ggc cca gtg ctc acc 595  
Pro Val Val Lys Leu Gly Asp Thr Ala Phe Phe Gly Pro Val Leu Thr  
150 155 160 165

cgc atc cca cgc ggc gag gaa gca gga gag atc ttc gac gct tcc ttc 643  
 Arg Ile Pro Arg Gly Glu Glu Ala Gly Glu Ile Phe Asp Ala Ser Phe  
 170 175 180

aag ctc gca agc tat ccc cac ttc ttt gaa atc aag cgc agc cgc act 691  
Lys Leu Ala Ser Tyr Pro His Phe Phe Glu Ile Lys Arg Ser Arg Thr  
185 190 195

qag aac cca caq ttc qac taattaacgc tgtctctgct tat 732

**00000000000000000000**



<400> 517

[illegible]



cgagaggcctt ttttggtctt aagcctttta gtcgtgcgaa cgaaatctta agcagcctcg 60

gtgccaccga gatcgattgg tcgctgtaag gtatctgatt atg tcc agt tcc gaa 115  
Met Ser Ser Ser Glu  
1 5

agc tcg cgt tcc gaa ggc tcg cag cca gca ccg tct gta cag cct gaa 163  
Ser Ser Arg Ser Glu Gly Ser Gln Pro Ala Pro Ser Val Gln Pro Glu  
10 15 20

cgc cgt gct gat tca acg ggg gct cct gcg gca gct tcc aag gaa gct 211  
Arg Arg Ala Asp Ser Thr Gly Ala Pro Ala Ala Ala Ser Lys Glu Ala  
25 30 35

tcc caa caa atg gac gct gcc gga gtt ctt gag tgg gcc agg acc gct 259  
Ser Gln Gln Met Asp Ala Ala Gly Val Leu Glu Trp Ala Arg Thr Ala  
40 45 50

gtc gag cag ctt tct gaa cgt cgt gca gag atc aat gca ctg aat gtc 307  
Val Glu Gln Leu Ser Glu Arg Arg Ala Glu Ile Asn Ala Leu Asn Val  
55 60 65

ttt cct gtt cca gat gca gac act gga tca aac atg acc tac acc atg 355  
Phe Pro Val Pro Asp Ala Asp Thr Gly Ser Asn Met Thr Tyr Thr Met  
70 75 80 85

aca gct gcg ttg gat gaa gcg ctg aaa ctg ggg gag ttg ggt gat gtc 403  
Thr Ala Ala Leu Asp Glu Ala Leu Lys Leu Gly Glu Leu Gly Asp Val  
90 95 100

gca agg att act gag gct ttg gct gtt ggt tct gtg cgt gga gcc cga 451  
Ala Arg Ile Thr Glu Ala Leu Ala Val Gly Ser Val Arg Gly Ala Arg  
105 110 115

gga aat tct gga gta gtc ctt agt cag gtc ctt cgc gct att gct cag 499  
Gly Asn Ser Gly Val Val Leu Ser Gln Val Leu Arg Ala Ile Ala Gln  
120 125 130

gca gct gct gac ggg gtt att gat ggc cac aca atc caa gaa gcg cta 547  
Ala Ala Ala Asp Gly Val Ile Asp Gly His Thr Ile Gln Glu Ala Leu  
135 140 145

tcc att gct cgc tcc cta gtt gat cgc gca att aca gat cct gtg gag 595  
Ser Ile Ala Arg Ser Leu Val Asp Arg Ala Ile Thr Asp Pro Val Glu  
150 155 160 165

ggc act gtt gtc act gtg ttg cgt tct 622  
Gly Thr Val Val Thr Val Leu Arg Ser  
170

<210> 518  
<211> 174  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 518  
Met Ser Ser Ser Glu Ser Ser Arg Ser Glu Gly Ser Gln Pro Ala Pro  
1 5 10 15  
Ser Val Gln Pro Glu Arg Arg Ala Asp Ser Thr Gly Ala Pro Ala Ala

002290"0420960



<400> 519																
tttagaagcc acatgacata tgtcatgaaa attatgtgca aagtgcagta atactcctga																60
catatggctc taccagcgcc aatgcgaagt aggaagaatt																
Met Pro Met Thr Thr																115
1 5																
aca cca gca atc gac gta aca gac ctc gtg aga acc tac ggc gac tac																163
Thr Pro Ala Ile Asp Val Thr Asp Leu Val Arg Thr Tyr Gly Asp Tyr																
10 15 20																
acc gca gtc aag ggc ctg aat ttc cat gta cag cgc ggt gaa gta ttt																211
Thr Ala Val Lys Gly Leu Asn Phe His Val Gln Arg Gly Glu Val Phe																
25 30 35																
ggg ctg ctc ggc acc aac ggg gcc ggc aaa acc tcc acc ttg gaa gtc																259
Gly Leu Leu Gly Thr Asn Gly Ala Gly Lys Thr Ser Thr Leu Glu Val																
40 45 50																
atc gaa gga ctt tcc gca ccc agc tcc ggc acc gtg cgc atc tcc ggg																307
Ile Glu Gly Leu Ser Ala Pro Ser Ser Gly Thr Val Arg Ile Ser Gly																



Figure 1 shows a sequence of 11 diagrams illustrating the evolution of a 2D lattice over time steps  $t=0$  to  $t=10$ . The lattice is composed of black and white squares. At  $t=0$ , there is a single black square in the center. As time progresses, black squares spread outwards, forming a diamond-like shape. By  $t=10$ , the black squares form a large, complex, fractal-like pattern. The diagrams are arranged in a single row, with time steps labeled below each diagram.



1047

<400> 520															
Met 1	Pro	Met	Thr	Thr 5	Thr	Pro	Ala	Ile	Asp 10	Val	Thr	Asp	Leu	Val 15	Arg
Thr	Tyr	Gly	Asp 20	Tyr	Thr	Ala	Val	Lys 25	Gly	Leu	Asn	Phe	His 30	Val	Gln
Arg	Gly	Glu 35	Val	Phe	Gly	Leu	Leu 40	Gly	Thr	Asn	Gly	Ala 45	Gly	Lys	Thr
Ser	Thr 50	Leu	Glu	Val	Ile	Glu 55	Gly	Leu	Ser	Ala	Pro 60	Ser	Ser	Gly	Thr
Val 65	Arg	Ile	Ser	Gly	Leu 70	Asp	Pro	Val	Ala	Asp 75	Arg	Ala	Ile	Leu	Arg 80
Pro	Glu	Leu	Gly	Ile 85	Met	Leu	Gln	Ser	Gly 90	Gly	Leu	Pro	Ser	Gln 95	Leu
Thr	Val	Ala	Glu 100	Thr	Met	Asp	Met	Trp 105	His	Gly	Thr	Cys	Thr 110	Tyr	Pro
Arg	Ala	Ile 115	Lys	Asp	Val	Leu	Ala 120	Asp	Val	Asp	Leu	Leu 125	His	Arg	Glu
Asn	Val 130	Lys	Val	Gly	Ala	Leu 135	Ser	Gly	Gly	Glu	Gln 140	Arg	Arg	Leu	Asp
Leu 145	Ala	Cys	Ala	Leu	Leu 150	Gly	Asp	Pro	Ser	Ile 155	Leu	Phe	Leu	Asp	Glu 160
Pro	Thr	Thr	Gly	Leu 165	Asp	Pro	Glu	Ser	Arg 170	Arg	His	Thr	Trp	Gln 175	Leu
Leu	Leu	Asp	Leu 180	Lys	Gln	Arg	Gly	Val 185	Thr	Met	Met	Leu	Thr 190	Thr	His
Tyr	Leu	Glu 195	Glu	Ala	Glu	Phe	Leu 200	Cys	Asp	Arg	Ile	Ala 205	Ile	Met	Asn
Ala	Gly 210	Glu	Ile	Ala	Val	Glu 215	Gly	Thr	Leu	Asp	Glu 220	Leu	Val	Ala	Arg
Glu 225	Lys	Ser	Ile	Ile	Ser 230	Phe	Val	Leu	Arg	Gly 235	Gly	Gln	Val	Glu	Leu 240
Pro	Val	Leu	Ser	Gly 245	Ala	Glu	Ile	Ile	Arg 250	Asp	Asn	Asn	His	Val 255	Arg
Ile	Ala	Thr	Thr 260	Thr	Leu	Gln	Gln	His 265	Thr	Leu	Glu	Ile	Leu 270	Thr	Trp



<400> 521																
tgttttagag gtagagcgaa acgtgcctgt aaaactggcg ctcgctgtgc tcgaagacca																60
cccagacaat caccocgctc cgaaggagaa tcgctaagcc atg act gaa tgg tat																115
Met Thr Glu Trp Tyr																5
1																
gtc gtt tta ccc gcc act att cta ctc atc gcg ctg tct gcg ttt ttc																163
Val Val Leu Pro Ala Thr Ile Leu Leu Ile Ala Leu Ser Ala Phe Phe																20
10 15																
gtc atc att gag ttc gct ttg ctt gca gct agg cgg aac cgg tta gag																211
Val Ile Ile Glu Phe Ala Leu Leu Ala Ala Arg Arg Asn Arg Leu Glu																35
25 30																
gag act gtg gaa acc tcg cgg tct tcc cgc gct gcg ttg cga agc ctc																259
Glu Thr Val Glu Thr Ser Arg Ser Ser Arg Ala Ala Leu Arg Ser Leu																40 45 50
aat gaa ctt act ctc atg ctc gcg ggc gcg cag ttg gga atc acc atg																307
Asn Glu Leu Thr Leu Met Leu Ala Gly Ala Gln Leu Gly Ile Thr Met																55 60 65
gtg act ttc gcg ttg ggt gct atc acg aag ccg tgg gtt cat tat gct																355
Val Thr Phe Ala Leu Gly Ala Ile Thr Lys Pro Trp Val His Tyr Ala																70 75 80 85
ttg atg ccg ctc ttc gaa tgg gcg cgt ata ccg ctg gtt atg gca gat																403
Leu Met Pro Leu Phe Glu Trp Ala Arg Ile Pro Leu Val Met Ala Asp																90 95 100
gtc att gcg ttt att ttg tcg ctg ttt atc gta acg ttt ctg cac ttg																451
Val Ile Ala Phe Ile Leu Ser Leu Phe Ile Val Thr Phe Leu His Leu																105 110 115
gtc atc ggc gaa atg gct ccg aaa tcc tgg gca atc gcg cat ccg gag																499
Val Ile Gly Glu Met Ala Pro Lys Ser Trp Ala Ile Ala His Pro Glu																120 125 130
acg gca ctt cga act atc gcg att ccc gca ccg ggc ttc att aac ctg																547
Thr Ala Leu Arg Thr Ile Ala Ile Pro Ala Arg Gly Phe Ile Asn Leu																



```
<400> 522
Met Thr Glu Trp Tyr Val Val Leu Pro Ala Thr Ile Leu Leu Ile Ala
  1             5             10             15
```

**THE UNIVERSITY OF CHICAGO**



Leu Ser Ala Phe Phe Val Ile Ile Glu Phe Ala Leu Leu Ala Ala Arg  
 20 25 30  
 Arg Asn Arg Leu Glu Glu Thr Val Glu Thr Ser Arg Ser Ser Arg Ala  
 35 40 45  
 Ala Leu Arg Ser Leu Asn Glu Leu Thr Leu Met Leu Ala Gly Ala Gln  
 50 55 60  
 Leu Gly Ile Thr Met Val Thr Phe Ala Leu Gly Ala Ile Thr Lys Pro  
 65 70 75 80  
 Trp Val His Tyr Ala Leu Met Pro Leu Phe Glu Trp Ala Arg Ile Pro  
 85 90 95  
 Leu Val Met Ala Asp Val Ile Ala Phe Ile Leu Ser Leu Phe Ile Val  
 100 105 110  
 Thr Phe Leu His Leu Val Ile Gly Glu Met Ala Pro Lys Ser Trp Ala  
 115 120 125  
 Ile Ala His Pro Glu Thr Ala Leu Arg Thr Ile Ala Ile Pro Ala Arg  
 130 135 140  
 Gly Phe Ile Asn Leu Phe Arg Pro Leu Leu Gln Trp Ile Asn Lys Met  
 145 150 155 160  
 Ala Asn Asp Leu Val Arg Lys Val Gly Glu Thr Pro Val Asp Arg Ala  
 165 170 175  
 Ala Ala Gly Gly Tyr Asp Thr Asp Thr Leu His Ala Leu Ile Glu His  
 180 185 190  
 Ser Arg Glu Thr Gly Ala Leu Asp Gln Gln Ser Ala Ala Gln Ile Ser  
 195 200 205  
 Gly Ile Ile Lys Leu Asp Lys Ile Thr Val Gly Gln Thr Leu Thr Ala  
 210 215 220  
 Ser Pro Phe Thr His Ser Ala Ser Ala Thr Val Ala Glu Val Gln Ala  
 225 230 235 240  
 Ala Ala Gln Arg Ser Gly Ser Leu Arg Val Leu Ile Asp Ala Pro Ser  
 245 250 255  
 His Leu Phe Pro His Val Ile His Val Arg Asp Thr Leu Gly Ala Ser  
 260 265 270  
 Pro Asp Glu Lys Ala Ser Lys Trp Ser Arg Pro Ile Leu Thr Val Ala  
 275 280 285  
 Glu Thr Asp Thr Leu His Gln Ala Leu Glu Tyr Met Arg Glu His Asn  
 290 295 300  
 Glu Gln Ile Ser Ala Val Leu Ser Ala Asp Gly Lys Thr Val Leu Gly  
 305 310 315 320  
 Val Ile Thr Trp Asp His Ile Leu Lys Tyr Leu Trp Pro Ala Ser Val  
 325 330 335

006290" 0420960



09602740 = 062300

09602740 = 062300

09602740 = 062300

09602740 = 062300



cat acc ggc cga act gat gtg gga ctc gcg att gcc aac gtt atc gcc 288



Glu Leu Met Glu Ser Leu Pro Glu Leu Arg Gly Pro Glu Pro Ile Thr  
115 120 125



Asp Asp Ile Phe His Asp Pro Phe Ile Asp Asp Glu Pro Gly Val Val  
 130 135 140  
 Pro Phe Arg Ala Val Val Trp Ala Glu Glu Glu Pro Gly Ile Pro Asp  
 145 150 155 160  
 Ala Met Ala Gln Ser Cys Asp Gly Pro Ser Lys Gly Ala Leu Thr Gln  
 165 170 175  
 Ala Leu Arg Leu Leu Val Arg Gly Gln Ser Ala Thr Thr Tyr Ser Ile  
 180 185 190  
 Glu Glu Lys Asp Leu  
 195

<210> 527  
 <211> 669  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(646)  
 <223> RXC01659

<400> 527  
 ttgatgcgcg ccgcggtgag cagcctgccg atccagagcg tgaagaatct gatgatttag 60  
 tcgagattga taccgtctct ggattccgcc tgctcagtac gtg gcg ggg gtt gcg 115  
 Val Ala Gly Val Ala  
 1 5  
 cag cgt ttt gtc gac gag cgc att cac gtc ggt ttg gat tcc atg cca 163  
 Gln Arg Phe Val Asp Glu Arg Ile His Val Gly Leu Asp Ser Met Pro  
 10 15 20  
 gaa gct gtg act gct gtg tgg atg gaa tct gat tgg gtg ttg gcg gaa 211  
 Glu Ala Val Thr Ala Val Trp Met Glu Ser Asp Trp Val Leu Ala Glu  
 25 30 35  
 acc atc aag ggt tcc acg cct tcc gat tgg gaa gag att ttg cgg ccg 259  
 Thr Ile Lys Gly Ser Thr Pro Ser Asp Trp Glu Glu Ile Leu Arg Pro  
 40 45 50  
 ttg gcg ctg ctc acg gac gcg tct ttc acg ttg cca cct cgt tcc acg 307  
 Leu Ala Leu Leu Thr Asp Ala Ser Phe Thr Leu Pro Pro Arg Ser Thr  
 55 60 65  
 cgt gcg caa acc ttg gat ttg aag cat ttg gaa cca agc cgt ctg aag 355  
 Arg Ala Gln Thr Leu Asp Leu Lys His Leu Glu Pro Ser Arg Leu Lys  
 70 75 80 85  
 ccg gag cag cca gaa aag cca gcg ttt act ccc aat gct tcg gaa gaa 403  
 Pro Glu Gln Pro Glu Lys Pro Ala Phe Thr Pro Asn Ala Ser Glu Glu  
 90 95 100  
 gat ttg tct cag ccg ttg gtg atc cgc ccc gag gag ccg ttg cag atg 451  
 Asp Leu Ser Gln Pro Leu Val Ile Arg Pro Glu Glu Pro Leu Gln Met  
 105 110 115

09602740.062300



```
<210> 528
<211> 182
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 528															
Val 1	Ala	Gly	Val	Ala 5	Gln	Arg	Phe	Val	Asp 10	Glu	Arg	Ile	His	Val 15	Gly
Leu	Asp	Ser	Met 20	Pro	Glu	Ala	Val	Thr 25	Ala	Val	Trp	Met	Glu 30	Ser	Asp
Trp	Val	Leu 35	Ala	Glu	Thr	Ile	Lys 40	Gly	Ser	Thr	Pro	Ser 45	Asp	Trp	Glu
Glu	Ile 50	Leu	Arg	Pro	Leu	Ala 55	Leu	Leu	Thr	Asp	Ala 60	Ser	Phe	Thr	Leu
Pro 65	Pro	Arg	Ser	Thr	Arg 70	Ala	Gln	Thr	Leu	Asp 75	Leu	Lys	His	Leu	Glu 80
Pro	Ser	Arg	Leu	Lys 85	Pro	Glu	Gln	Pro	Glu 90	Lys	Pro	Ala	Phe	Thr 95	Pro
Asn	Ala	Ser	Glu 100	Glu	Asp	Leu	Ser	Gln 105	Pro	Leu	Val	Ile	Arg 110	Pro	Glu
Glu	Pro	Leu 115	Gln	Met	Pro	Val	Arg 120	Gly	Val	Gln	Glu 125	Ser	Arg	Gly	Val
Val 130	Glu	Pro	Arg	Ser	Leu	Gly 135	Ala	Asp	Asp	Val	Glu 140	Ser	Ile	Ala	Glu
Gly 145	Asp	Pro	Glu	Arg	Pro 150	Ser	Asp	Leu	Tyr	Gly 155	Thr	Arg	Val	Leu	Arg 160
Asp	Leu	Asn	Gly	Gln 165	Ser	Ser	Ile	Phe	Gln 170	Asp	Ser	Thr	Asp	Ala 175	Asp



Glu Pro Pro Lys Lys Trp  
180

<210> 529

<211> 981

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(958)

<223> RXC01663

<400> 529

```
tatttttgctg gttggtcaca gtggagcgct aaccccgaga atcctatcga ggcctaaaat 60

cgtggcttga gtacgcactg ccagtaaggt gtgtgatgtg atg gaa ata agt gtc 115
                                         Met Glu Ile Ser Val
                                         1                               5

ttg atc atc gcc gca ctg atc ttg gtg gca ggc atc gta ctg tgg cgc 163
Leu Ile Ile Ala Ala Leu Ile Leu Val Ala Gly Ile Val Leu Trp Arg
                               10                               15                               20

gcg gac tcg tct aaa cag gca gct aaa aag gct gaa tca cct gtg ggc 211
Ala Asp Ser Ser Lys Gln Ala Ala Lys Lys Ala Glu Ser Pro Val Gly
                               25                               30                               35

tca gtc gca cct gcg ccc gtg ctg gtt gaa gaa gag ccg gac cct gag 259
Ser Val Ala Pro Ala Pro Val Leu Val Glu Glu Glu Pro Asp Pro Glu
                               40                               45                               50

ttt gag cca gaa ctg gac cct gaa cca gaa gcg caa cca gaa cca gag 307
Phe Glu Pro Glu Leu Asp Pro Glu Pro Glu Ala Gln Pro Glu Pro Glu
                               55                               60                               65

ctg gaa gtt gcg cct aga ttt gcg cca gaa cca gtt caa gat ctt gag 355
Leu Glu Val Ala Pro Arg Phe Ala Pro Glu Pro Val Gln Asp Leu Glu
                               70                               75                               80                               85

ccg gat cag gct gag gac att tat ttt gat gat tcc cct gaa ctc gat 403
Pro Asp Gln Ala Glu Asp Ile Tyr Phe Asp Asp Ser Pro Glu Leu Asp
                               90                               95                               100

gct gat gtt gaa aat gcc ttg gct gag ctt act gag gta gaa gac tac 451
Ala Asp Val Glu Asn Ala Leu Ala Glu Leu Thr Glu Val Glu Asp Tyr
                               105                               110                               115

ccg gaa gag cca gtg cag tct gag caa cct caa gcc cct gcc acg gcg 499
Pro Glu Glu Pro Val Gln Ser Glu Gln Pro Gln Ala Pro Ala Thr Ala
                               120                               125                               130

gag gta gct gcg gac gag gag caa cgg ggc gtc gat aag cat tcg ttt 547
Glu Val Ala Ala Asp Glu Glu Gln Arg Gly Val Asp Lys His Ser Phe
                               135                               140                               145

ttg agc tct ttg cct ggt tcg cag cgc cgg gag cgc cga aac tgg gcg 595
Leu Ser Ser Leu Pro Gly Ser Gln Arg Arg Glu Arg Arg Asn Trp Ala
150                               155                               160                               165
```

09602740-062300



gcg aag cac cac ttc gat ttc atc aag gaa gat gcc ttt ttg acc gat 643  
 Ala Lys His His Phe Asp Phe Ile Lys Glu Asp Ala Phe Leu Thr Asp  
 170 175 180

gaa tgg tca agg ggt gcg gca tcg act ggt gcc gtt gca cgt gat gtg 691  
 Glu Trp Ser Arg Gly Ala Ala Ser Thr Gly Ala Val Ala Arg Asp Val  
 185 190 195

gtc agt ggc atg gct gaa gga tat gaa acg cat ctg gtg gat ttg gcg 739  
 Val Ser Gly Met Ala Glu Gly Tyr Glu Thr His Leu Val Asp Leu Ala  
 200 205 210

ggc gtg ccc gtg atg gcg atg cgc cgt gga att acc tct gac gtg gtc 787  
 Gly Val Pro Val Met Ala Met Arg Arg Gly Ile Thr Ser Asp Val Val  
 215 220 225

att gat gcg cgc cgc ggt gag cag cct gcc gat cca gag cgt gaa gaa 835  
 Ile Asp Ala Arg Arg Gly Glu Gln Pro Ala Asp Pro Glu Arg Glu Glu  
 230 235 240 245

tct gat gat tta gtc gag att gat acc gtc tct gga ttc cgc ctg ctc 883  
 Ser Asp Asp Leu Val Glu Ile Asp Thr Val Ser Gly Phe Arg Leu Leu  
 250 255 260

agt acg tgg cgg ggg ttg cgc agc gtt ttg tcg acg agc gca ttc acg 931  
 Ser Thr Trp Arg Gly Leu Arg Ser Val Leu Ser Thr Ser Ala Phe Thr  
 265 270 275

tcg gtt tgg att cca tgc cag aag ctg tgactgctgt gtggatggaa 978  
 Ser Val Trp Ile Pro Cys Gln Lys Leu  
 280 285

tct 981

<210> 530  
 <211> 286  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 530  
 Met Glu Ile Ser Val Leu Ile Ile Ala Ala Leu Ile Leu Val Ala Gly  
 1 5 10 15  
 Ile Val Leu Trp Arg Ala Asp Ser Ser Lys Gln Ala Ala Lys Lys Ala  
 20 25 30  
 Glu Ser Pro Val Gly Ser Val Ala Pro Ala Pro Val Leu Val Glu Glu  
 35 40 45  
 Glu Pro Asp Pro Glu Phe Glu Pro Glu Leu Asp Pro Glu Pro Glu Ala  
 50 55 60  
 Gln Pro Glu Pro Glu Leu Glu Val Ala Pro Arg Phe Ala Pro Glu Pro  
 65 70 75 80  
 Val Gln Asp Leu Glu Pro Asp Gln Ala Glu Asp Ile Tyr Phe Asp Asp  
 85 90 95  
 Ser Pro Glu Leu Asp Ala Asp Val Glu Asn Ala Leu Ala Glu Leu Thr  
 100 105 110

002290" 04/20/96



[illegible]

000074-0698

[illegible][illegible][illegible]

096740-0630

00000740-0639-0000

096740-03E



0960270-06060000



<400> 532  
Met Asn Thr Ala Pro Phe Lys Leu Glu Ala Asp Phe Ala Ser Ala Leu  
1 5 10 15  
Pro Thr Met Ala Ala Pro Trp Gln Gly Glu Glu Ala Pro Asn Pro Glu

[illegible]



20					25					30					
Leu	Val	Ile	Leu	Asn	Asp	Asp	Leu	Ala	Tyr	Ser	Leu	Gly	Leu	Asp	Pro
		35					40					45			
Thr	Trp	Leu	Arg	Thr	Pro	Glu	Gly	Val	Gln	Phe	Leu	Leu	Gly	Leu	Asn
	50					55					60				
Pro	Glu	Pro	Leu	Thr	Lys	Ala	Val	Ala	Gln	Ala	Tyr	Ser	Gly	His	Gln
	65					70					75				80
Phe	Gly	Gln	Phe	Val	Ala	Ser	Leu	Gly	Asp	Gly	Arg	Ala	Leu	Leu	Leu
				85					90					95	
Gly	Glu	Ala	Arg	Ser	Ala	Asp	Gly	Val	Leu	His	Asp	Ile	His	Leu	Lys
			100					105					110		
Gly	Ser	Gly	Arg	Thr	Gln	Phe	Ser	Arg	Gly	Ala	Asp	Gly	Arg	Ala	Val
		115					120					125			
Leu	Gly	Pro	Val	Leu	Arg	Glu	Tyr	Ile	Ile	Ser	Glu	Ala	Met	His	Ala
	130					135					140				
Leu	Gly	Val	Pro	Thr	Thr	Arg	Ser	Leu	Ala	Val	Ile	Ser	Thr	Gly	Arg
	145					150					155				160
Lys	Ile	Gln	Arg	Gly	Ser	Val	Ala	Pro	Gly	Ala	Val	Leu	Val	Arg	Val
				165					170					175	
Ala	Thr	Ser	Leu	Ile	Arg	Val	Gly	Ser	Phe	Gln	Tyr	Ser	Asn	Ile	Ser
			180					185					190		
Gly	Gly	Ile	Glu	Leu	Ser	Gln	His	Leu	Ala	Asn	Tyr	Thr	Ile	Thr	Arg
		195					200					205			
His	Phe	Pro	Ser	Leu	Val	Ala	Glu	Leu	Ser	Ala	Pro	Thr	Pro	Ala	Thr
	210					215					220				
Tyr	Val	Ser	Leu	Phe	Lys	Ala	Ile	Leu	Gln	Arg	Gln	Ala	Asp	Thr	Val
	225					230					235				240
Gly	Lys	Trp	Thr	Arg	Leu	Gly	Phe	Val	His	Gly	Ala	Leu	Asn	Thr	Asp
				245					250					255	
Asn	Thr	Leu	Ile	Ser	Gly	Glu	Thr	Val	Asp	Tyr	Gly	Pro	Cys	Ala	Phe
			260					265					270		
Met	Glu	Arg	Tyr	Arg	Gly	Asp	Ala	Lys	Phe	Ser	Ser	Ile	Asp	Thr	Tyr
		275					280					285			
Gly	Arg	Tyr	Lys	Phe	Glu	Asn	Gln	Pro	Met	Ile	Leu	Gly	Trp	Asn	Met
	290					295					300				
Ala	Arg	Leu	Val	Glu	Thr	Leu	Leu	Pro	Leu	Leu	Gly	Ala	Thr	Pro	Asp
	305					310					315				320
Glu	Gly	Met	Thr	Ala	Ala	Gln	Glu	Ala	Leu	Val	Glu	Phe	Asp	Asp	Leu
				325					330					335	
Cys	Glu	Gln	Ala	Ile	Arg	Lys	Glu	Phe	Ala	Thr	Ala	Leu	Gly	Leu	Asp
			340					345					350		

006602740"062300



Glu Ser Asp Thr Gly Thr Val Glu Gln Phe Arg Glu Leu Leu Tyr Leu  
355 360 365

His Asn Pro Asp Ile Thr Thr Leu Leu Arg Ala Leu Thr Asp Asn Thr  
370 375 380

Ala Pro Pro Ser Gly Phe Glu Ala Phe Val His Asp Trp Lys Thr Gln  
385 390 395 400

Asp Pro Asp Ile Glu Ala Met Arg Ala Val Asn Pro Leu Phe Ile Pro  
405 410 415

Arg Asn His Leu Val Glu Ala Ala Leu Ala Asp Ala Val Glu Gly Asn  
420 425 430

Leu Glu Lys Phe His Glu Leu Leu Ala Ala Val Thr Asn Pro Phe Asp  
435 440 445

Pro Thr Ala Gly Pro Asp Glu Leu Arg Leu Pro Ser Glu Glu Gly Phe  
450 455 460

Glu Glu Asp Tyr Met Thr Phe Cys Gly Thr  
465 470

<210> 533

<211> 1236

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1213)

<223> RXC01703

<400> 533

gttagacaaa tgggtaaaca gagctgacct agcggaatcc gccatcaacg aaaggcattc 60

cgcgagggtt tggggctctgc ctcgaacaaa tcttggggtt gtg gca tgg cca tcc 115  
Val Ala Trp Pro Ser  
1 5

aac gcc aaa gaa aaa ctg ttt atc cac tgg cac tac tgg tgg caa gcg 163  
Asn Ala Lys Glu Lys Leu Phe Ile His Trp His Tyr Trp Trp Gln Ala  
10 15 20

cat tat cta gac tgc ctg gtg gat gct gct cgt cga cgc acc aca aag 211  
His Tyr Leu Asp Cys Leu Val Asp Ala Ala Arg Arg Arg Thr Thr Lys  
25 30 35

gcc cgt cgc gac cgc atc agg gac acc atc cgc ggc att tcg gtg cgc 259  
Ala Arg Arg Asp Arg Ile Arg Asp Thr Ile Arg Gly Ile Ser Val Arg  
40 45 50

aat gtg ggc aag ctg acc tcg aat cgt tat tac gac gac aaa gct tgg 307  
Asn Val Gly Lys Leu Thr Ser Asn Arg Tyr Tyr Asp Asp Lys Ala Trp  
55 60 65

ctg gcc ctt gct ctt ggg cgt gcc gga aaa gtg cga aag gtg cgc aca 355  
Leu Ala Leu Ala Leu Gly Arg Ala Gly Lys Val Arg Lys Val Arg Thr

0002290" 04220960



70	75	80	85	
cca aaa tca ttg ccc tcg ttg gaa caa aac atc gtc gat ggc att gat	403			
Pro Lys Ser Leu Pro Ser Leu Glu Gln Asn Ile Val Asp Gly Ile Asp				
90 95 100				
tcc ctt act ggt gtg ctg ccg tgg cgt tcc ggc gaa acc ttc tac aac	451			
Ser Leu Thr Gly Val Leu Pro Trp Arg Ser Gly Glu Thr Phe Tyr Asn				
105 110 115				
gtt ccc tcc aac ggt cct gct gcg atc atg atg gcc cgc acc gac cgt	499			
Val Pro Ser Asn Gly Pro Ala Ala Ile Met Met Ala Arg Thr Asp Arg				
120 125 130				
ttg gac gag gct atg aaa atc acc gat tgg att ttt gac aac ctg atc	547			
Leu Asp Glu Ala Met Lys Ile Thr Asp Trp Ile Phe Asp Asn Leu Ile				
135 140 145				
gat ggc gac ggc ctt gtg atg gac gga ttg cgc atg cgc atg cac gga	595			
Asp Gly Asp Gly Leu Val Met Asp Gly Leu Arg Met Arg Met His Gly				
150 155 160 165				
cct gag ctt gtc cgt tcc atc cac ccg tat tgc caa ggt gtc gcc att	643			
Pro Glu Leu Val Arg Ser Ile His Pro Tyr Cys Gln Gly Val Ala Ile				
170 175 180				
ggg gcg tgt ttg gaa att gct ctc aaa ctg cgt gag cgc gca ggc ttg	691			
Gly Ala Cys Leu Glu Ile Ala Leu Lys Leu Arg Glu Arg Ala Gly Leu				
185 190 195				
acc act act gtg gtg gat cac tgg tcg gat gcc gat aag gca gaa gac	739			
Thr Thr Thr Val Val Asp His Trp Ser Asp Ala Asp Lys Ala Glu Asp				
200 205 210				
tcc ctc aaa tac ttt gca cac atc cac gct gtg gtt cag gct gtg tcg	787			
Ser Leu Lys Tyr Phe Ala His Ile His Ala Val Val Gln Ala Val Ser				
215 220 225				
cgg aag atg acc aac ttc cac ggc gtt att gat tgg gac acc ggt gac	835			
Arg Lys Met Thr Asn Phe His Gly Val Ile Asp Trp Asp Thr Gly Asp				
230 235 240 245				
ggc gac ggc ggt ttg ttc aag ggc att ttg gtc cgc tat tta gct gat	883			
Gly Asp Gly Gly Leu Phe Lys Gly Ile Leu Val Arg Tyr Leu Ala Asp				
250 255 260				
gtg gcc atc cgc ctg cct gac gat tca cca acc aac cgg gaa acc aaa	931			
Val Ala Ile Arg Leu Pro Asp Asp Ser Pro Thr Asn Arg Glu Thr Lys				
265 270 275				
aag att gca gca cgc ctg gta ctg gaa tcg gcg gaa agc gta tgg aac	979			
Lys Ile Ala Ala Arg Leu Val Leu Glu Ser Ala Glu Ser Val Trp Asn				
280 285 290				
cac cga ttg gaa gtt gat ggc ctt ccg gta ttc gcc aca gac tgg aca	1027			
His Arg Leu Glu Val Asp Gly Leu Pro Val Phe Ala Thr Asp Trp Thr				
295 300 305				
acg gat gca cgc ctg cca caa aac ttt ggt ttg agt tcc tct agt ttg	1075			
Thr Asp Ala Arg Leu Pro Gln Asn Phe Gly Leu Ser Ser Ser Ser Leu				
310 315 320 325				

002290 0420960



agc gat ctg gtg agt gtt gtg cgc gtg gat gaa cgt gat ctg tcc gtg 1123  
 Ser Asp Leu Val Ser Val Val Arg Val Asp Glu Arg Asp Leu Ser Val  
 330 335 340

caa ttg tcc ggt tgg atg ctc atg gaa gca gca gcg aaa gtg gcc gaa 1171  
Gln Leu Ser Gly Trp Met Leu Met Glu Ala Ala Ala Lys Val Ala Glu  
345 350 355

gaa ctg gaa aac aac ggc aat agt tac acc ggt cgc tcc cga 1213  
Glu Leu Glu Asn Asn Gly Asn Ser Tyr Thr Gly Arg Ser Arg  
360 365 370

tagccccgat agtgtatgtg ctg 1236

<210> 534

<211> 371

<212> PRT

<213> Corynebacterium glutamicum

<400> 534

Val Ala Trp Pro Ser Asn Ala Lys Glu Lys Leu Phe Ile His Trp His  
1 5 10 15

Tyr Trp Trp Gln Ala His Tyr Leu Asp Cys Leu Val Asp Ala Ala Arg  
20 25 30

Arg Arg Thr Thr Lys Ala Arg Arg Asp Arg Ile Arg Asp Thr Ile Arg  
35 40 45

Gly Ile Ser Val Arg Asn Val Gly Lys Leu Thr Ser Asn Arg Tyr Tyr  
50 55 60

Asp Asp Lys Ala Trp Leu Ala Leu Ala Leu Gly Arg Ala Gly Lys Val  
65 70 75 80

Arg Lys Val Arg Thr Pro Lys Ser Leu Pro Ser Leu Glu Gln Asn Ile  
85 90 95

Val Asp Gly Ile Asp Ser Leu Thr Gly Val Leu Pro Trp Arg Ser Gly  
100 105 110

Glu Thr Phe Tyr Asn Val Pro Ser Asn Gly Pro Ala Ala Ile Met Met  
115 120 125

Ala Arg Thr Asp Arg Leu Asp Glu Ala Met Lys Ile Thr Asp Trp Ile  
130 135 140

Phe Asp Asn Leu Ile Asp Gly Asp Gly Leu Val Met Asp Gly Leu Arg  
145 150 155 160

Met Arg Met His Gly Pro Glu Leu Val Arg Ser Ile His Pro Tyr Cys  
165 170 175

Gln Gly Val Ala Ile Gly Ala Cys Leu Glu Ile Ala Leu Lys Leu Arg  
180 185 190

Glu Arg Ala Gly Leu Thr Thr Thr Val Val Asp His Trp Ser Asp Ala  
195 200 205

[illegible]



<400> 535																
atc	gcc	gtt	gcc	gaa	gaa	ggc	gga	ttg	tgg	gaa	aac	ctc	ctg	cag	cac	48
Ile	Ala	Val	Ala	Glu	Glu	Gly	Gly	Leu	Trp	Glu	Asn	Leu	Leu	Gln	His	
1				5				10						15		
cgc	ttc	ggt	gga	cat	ggt	gcg	cta	gct	ggg	cac	gcc	ttg	gga	aac	ctc	96
Arg	Phe	Gly	Gly	His	Gly	Ala	Leu	Ala	Gly	His	Ala	Leu	Gly	Asn	Leu	
			20					25					30			
gtg	atc	gcg	gcg	ttg	acc	gac	att	ttg	ggc	acc	tcc	cag	cat	gcg	ctt	144
Val	Ile	Ala	Ala	Leu	Thr	Asp	Ile	Leu	Gly	Thr	Ser	Gln	His	Ala	Leu	
		35					40					45				
gat	caa	atc	gct	caa	ctc	gct	gga	gcc	aaa	gga	cgc	atc	atc	ccg	gta	192
Asp	Gln	Ile	Ala	Gln	Leu	Ala	Gly	Ala	Lys	Gly	Arg	Ile	Ile	Pro	Val	
	50					55					60					



tgt gct gaa cct ttg gat ctt gaa gcg gaa gta tca ggt cta gac tct 240  
 Cys Ala Glu Pro Leu Asp Leu Glu Ala Glu Val Ser Gly Leu Asp Ser  
 65 70 75 80  
 gat gct cga gtc atg cgt caa gtt cgt ggt caa gtg gcg gta gct gca 288  
 Asp Ala Arg Val Met Arg Gln Val Arg Gly Gln Val Ala Val Ala Ala  
 85 90 95  
 acc ccc ggg cag gtg cga cgc gtt cga atc att ccg gac aat cca gaa 336  
 Thr Pro Gly Gln Val Arg Arg Val Arg Ile Ile Pro Asp Asn Pro Glu  
 100 105 110  
 ccg aac ccc gct gcc atc gag gcc att ctc gat gca gat ttg gtc acc 384  
 Pro Asn Pro Ala Ala Ile Glu Ala Ile Leu Asp Ala Asp Leu Val Thr  
 115 120 125  
 ctt ggc cca ggt tcc tgg ttc tcc tct gtg att cca cac att ttg gtc 432  
 Leu Gly Pro Gly Ser Trp Phe Ser Ser Val Ile Pro His Ile Leu Val  
 130 135 140  
 cca ggg atc gtt gat gcc ttg gcg cag aca aaa gca acc aaa acc gtg 480  
 Pro Gly Ile Val Asp Ala Leu Ala Gln Thr Lys Ala Thr Lys Thr Val  
 145 150 155 160  
 gtg tta aac ctg acg tcc gag cca ggg gag acc gcg gga ttc tct gca 528  
 Val Leu Asn Leu Thr Ser Glu Pro Gly Glu Thr Ala Gly Phe Ser Ala  
 165 170 175  
 gaa cga cac atc cat gtg ctc cgc cag cat gct cga aac ctt cag gtt 576  
 Glu Arg His Ile His Val Leu Arg Gln His Ala Arg Asn Leu Gln Val  
 180 185 190  
 gac caa gtc att gtc gat gcc aag aca ctg tcc tca caa acc gaa cgc 624  
 Asp Gln Val Ile Val Asp Ala Lys Thr Leu Ser Ser Gln Thr Glu Arg  
 195 200 205  
 aat cat gta gaa cga gct gct cgc acc ctt ggt gca gaa gtc tcc ttc 672  
 Asn His Val Glu Arg Ala Ala Arg Thr Leu Gly Ala Glu Val Ser Phe  
 210 215 220  
 cat gat gtc cag gct gaa gat ggc cgt ggt cga ttc acc agt att cac 720  
 His Asp Val Gln Ala Glu Asp Gly Arg Gly Arg Phe Thr Ser Ile His  
 225 230 235 240  
 gat cca gca aag ctg tgt gca gcg ttg ctg gca agt ttt gct gga gca 768  
 Asp Pro Ala Lys Leu Cys Ala Ala Leu Leu Ala Ser Phe Ala Gly Ala  
 245 250 255  
 cga aag cgt taaggagtag gcgtgtcact gac 800  
 Arg Lys Arg

&lt;210&gt; 536

&lt;211&gt; 259

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 536

Ile Ala Val Ala Glu Glu Gly Gly Leu Trp Glu Asn Leu Leu Gln His  
 1 5 10 15

00602740-062300



[illegible]

```
<210> 537
<211> 1059
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1036)
<223> RXC02255

<400> 537
```



[illegible]



Leu Ala Leu Val Gly Cys Ala Arg Arg Ile Gly Ile Ala Ala Lys Thr  
145 150 155 160

[illegible]



Lys Asp Ser Arg Gly Phe Asp Arg Val Asn Val Arg Asp Ala Glu Ala  
 165 170 175  
 Ile Gly Ala Leu Leu Thr Arg Met Gly Ala Gln Lys Thr Arg Met Leu  
 180 185 190  
 Trp Glu Glu Lys Arg Ile Lys Arg Glu Ser Arg Thr Pro Gln Thr Gly  
 195 200 205  
 Leu Ala Asn Phe Asp Asp Ala Asn Leu Arg Arg Ser Ala Arg Ala Ala  
 210 215 220  
 Val Ala Ala Ala Ala Arg Val Glu Arg Ala Met Lys Ile Leu Gly Asp  
 225 230 235 240  
 Asp Val Pro Glu His Leu Ala Glu Ala Gly Gln Leu Arg Val Gln His  
 245 250 255  
 Arg Gln Ala Ser Leu Glu Glu Leu Gly Arg Leu Ala Asp Pro Gln Met  
 260 265 270  
 Thr Lys Asp Ala Val Ala Gly Arg Ile Arg Arg Leu Leu Thr Met Ala  
 275 280 285  
 Asp Lys Arg Ala Glu Asp Leu Lys Ile Pro Asp Thr Asn Ser Val Val  
 290 295 300  
 Thr Glu Asp Leu Leu Glu Glu Ile  
 305 310

<210> 539  
 <211> 681  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(658)  
 <223> RXC02435

<400> 539  
 tcatgaatgt agaacggatt tatcgacaag cgccagcaag tacgttgatc tcttttagcca 60  
 tcatcgctgt gtacgcagtg cggccattca atcgagatca gtg aca gac aac ctg 115  
 Val Thr Asp Asn Leu 5  
 ggt tca acc agt atc ggt gac gcg tgg att ctg tac gca ccg ctg atg 163  
 Gly Ser Thr Ser Ile Gly Asp Ala Trp Ile Leu Tyr Ala Pro Leu Met 20  
 10 15  
 gat gat ggt ggc ttt ggt cca ctg cgt gcc atc gga gga atg ttc ctg 211  
 Asp Asp Gly Gly Phe Gly Pro Leu Arg Ala Ile Gly Gly Met Phe Leu 35  
 25 30  
 cac att ggc ccc ggg cac atg ctg ttg aac ctt gtg ttg ttg tgg ttg 259  
 His Ile Gly Pro Gly His Met Leu Leu Asn Leu Val Leu Leu Trp Leu 50  
 40 45 50

00602740 062300



[illegible]

```
<210> 540
<211> 186
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 540															
Val	Thr	Asp	Asn	Leu	Gly	Ser	Thr	Ser	Ile	Gly	Asp	Ala	Trp	Ile	Leu
1				5					10					15	
Tyr	Ala	Pro	Leu	Met	Asp	Asp	Gly	Gly	Phe	Gly	Pro	Leu	Arg	Ala	Ile
			20					25					30		
Gly	Gly	Met	Phe	Leu	His	Ile	Gly	Pro	Gly	His	Met	Leu	Leu	Asn	Leu
		35					40					45			
Val	Leu	Leu	Trp	Leu	Leu	Gly	Arg	Glu	Ile	Glu	Arg	Asp	Phe	Gly	Ser
	50					55					60				
Ala	Leu	Phe	Thr	Ala	Met	Tyr	Phe	Val	Gly	Gly	Ile	Gly	Ala	Ser	Ala
65					70					75					80
Ala	Val	Ile	Trp	Met	Asp	Pro	Tyr	Ser	Pro	Thr	Ala	Gly	Ala	Ser	Gly
				85					90					95	

[illegible]



Ala Ile Tyr Ala Met Met Ala Ile Leu Val Gly Leu Phe Val Leu Arg  
 100 105 110

Ser Ala Asp Ile Arg Ala Pro Leu Ile Leu Ile Ala Ile Asn Ile Ala  
 115 120 125

Tyr Thr Leu Met Ser Thr Asn Val Ser Leu Trp Gly His Leu Gly Gly  
 130 135 140

Leu Ile Thr Gly Ala Leu Ile Thr Trp Pro Met Val Lys Ala Lys Thr  
 145 150 155 160

Gln Arg Thr Arg Trp Ile Ile Val Leu Ile Gly Phe Ala Val Val Val  
 165 170 175

Ala Ala Val Ile Leu Gly Ile Asp Arg Val  
 180 185

<210> 541  
 <211> 681  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(658)  
 <223> FRXA02435

<400> 541  
 tcatgaatgt agaacggatt tatcgacaag cgccagcaag tacgttgatc tcttttagcca 60

tcatcgctgt gtacgcagtg cggccattca atcgagatca gtg aca gac aac ctg 115  
 Val Thr Asp Asn Leu  
 1 5

ggt tca acc agt atc ggt gac gcg tgg att ctg tac gca ccg ctg atg 163  
 Gly Ser Thr Ser Ile Gly Asp Ala Trp Ile Leu Tyr Ala Pro Leu Met  
 10 15 20

gat gat ggt ggc ttt ggt cca ctg cgt gcc atc gga gga atg ttc ctg 211  
 Asp Asp Gly Gly Phe Gly Pro Leu Arg Ala Ile Gly Gly Met Phe Leu  
 25 30 35

cac att ggc ccc ggg cac atg ctg ttg aac ctt gtg ttg ttg tgg ttg 259  
 His Ile Gly Pro Gly His Met Leu Leu Asn Leu Val Leu Leu Trp Leu  
 40 45 50

ctg gga aga gaa att gaa cga gac ttc ggt tct gcg ctt ttc act gcg 307  
 Leu Gly Arg Glu Ile Glu Arg Asp Phe Gly Ser Ala Leu Phe Thr Ala  
 55 60 65

atg tac ttt gtg ggc ggt att ggt gcg tct gca gct gtc atc tgg atg 355  
 Met Tyr Phe Val Gly Gly Ile Gly Ala Ser Ala Ala Val Ile Trp Met  
 70 75 80 85

gat ccc tat tca ccg aca gca ggt gct tcc ggc gcc att tac gcc atg 403  
 Asp Pro Tyr Ser Pro Thr Ala Gly Ala Ser Gly Ala Ile Tyr Ala Met  
 90 95 100

atg gct att ttg gtg ggg ctt ttt gtg tta aga agc gcg gat atc cga 451

00E290"0420960



```
<210> 542
<211> 186
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 542

Val Thr Asp Asn Leu Gly Ser Thr Ser Ile Gly Asp Ala Trp Ile Leu  
1 5 10 15

Tyr Ala Pro Leu Met Asp Asp Gly Gly Phe Gly Pro Leu Arg Ala Ile  
20 25 30

Gly Gly Met Phe Leu His Ile Gly Pro Gly His Met Leu Leu Asn Leu  
35 40 45

Val Leu Leu Trp Leu Leu Gly Arg Glu Ile Glu Arg Asp Phe Gly Ser  
50 55 60

Ala Leu Phe Thr Ala Met Tyr Phe Val Gly Gly Ile Gly Ala Ser Ala  
65 70 75 80

Ala Val Ile Trp Met Asp Pro Tyr Ser Pro Thr Ala Gly Ala Ser Gly  
85 90 95

Ala Ile Tyr Ala Met Met Ala Ile Leu Val Gly Leu Phe Val Leu Arg  
100 105 110

Ser Ala Asp Ile Arg Ala Pro Leu Ile Leu Ile Ala Ile Asn Ile Ala  
115 120 125

Tyr Thr Leu Met Ser Thr Asn Val Ser Leu Trp Gly His Leu Gly Gly  
130 135 140

Leu Ile Thr Gly Ala Leu Ile Thr Trp Pro Met Val Lys Ala Lys Thr  
145 150 155 160

Gln Arg Thr Arg Trp Ile Ile Val Leu Ile Gly Phe Ala Val Val Val

**09602405**



[illegible]



```

<400> 544
Met Lys Leu Gly Leu Tyr Asn Ala Ile Phe His Asp Arg Thr Leu Pro
  1             5             10             15

Glu Ala Leu Ala Ala Ile Lys Ala Ala Gly Leu Thr Gly Ile Glu Leu
      20             25             30

```

Figure 1: Schematic representation of the experimental design. The figure shows a vertical sequence of 10 frames. Frame 1: A rectangular box with '100%' and '100%' at the top and bottom. Frame 2: A rectangular box with '100%' and '100%' at the top and bottom. Frame 3: A rectangular box with '100%' and '100%' at the top and bottom. Frame 4: A rectangular box with '100%' and '100%' at the top and bottom. Frame 5: A rectangular box with '100%' and '100%' at the top and bottom. Frame 6: A rectangular box with '100%' and '100%' at the top and bottom. Frame 7: A rectangular box with '100%' and '100%' at the top and bottom. Frame 8: A rectangular box with '100%' and '100%' at the top and bottom. Frame 9: A rectangular box with '100%' and '100%' at the top and bottom. Frame 10: A rectangular box with '100%' and '100%' at the top and bottom.







```
<220>
<221> CDS
<222> (101) .. (1393)
<223> BXA02175
```

0960740-062300



cgc aag ggt gct cct tac atg tac cca gac aac tcc ctc aat gcg cgt	691
Arg Lys Gly Ala Pro Tyr Met Tyr Pro Asp Asn Ser Leu Asn Ala Arg	
185 190 195	
gag aac ttc ctg cgc atg atg ttc ggt tac cca acc gag cca tac gag	739
Glu Asn Phe Leu Arg Met Met Phe Gly Tyr Pro Thr Glu Pro Tyr Glu	
200 205 210	
atc gac cca atc atg gtc aag gct ctg gac aag ctg ctc atc ctg cac	787
Ile Asp Pro Ile Met Val Lys Ala Leu Asp Lys Leu Leu Ile Leu His	
215 220 225	
gct gac cac gag cag aac tgc tcc acc tcc acc gtt cgt atg atc ggt	835
Ala Asp His Glu Gln Asn Cys Ser Thr Ser Thr Val Arg Met Ile Gly	
230 235 240 245	
tcc gca cag gcc aac atg ttt gtc tcc atc gct ggt ggc atc aac gct	883
Ser Ala Gln Ala Asn Met Phe Val Ser Ile Ala Gly Gly Ile Asn Ala	
250 255 260	
ctg tcc ggc cca ctg cac ggt ggc gca aac cag gct gtt ctg gag atg	931
Leu Ser Gly Pro Leu His Gly Gly Ala Asn Gln Ala Val Leu Glu Met	
265 270 275	
ctc gaa gac atc aag agc aac cac ggt ggc gac gca acc gag ttc atg	979
Leu Glu Asp Ile Lys Ser Asn His Gly Gly Asp Ala Thr Glu Phe Met	
280 285 290	
aac aag gtc aag aac aag gaa gac ggc gtc cgc ctc atg ggc ttc gga	1027
Asn Lys Val Lys Asn Lys Glu Asp Gly Val Arg Leu Met Gly Phe Gly	
295 300 305	
cac cgc gtt tac aag aac tac gat cca cgt gca gca atc gtc aag gag	1075
His Arg Val Tyr Lys Asn Tyr Asp Pro Arg Ala Ala Ile Val Lys Glu	
310 315 320 325	
acc gca cac gag atc ctc gag cac ctc ggt ggc gac gat ctt ctg gat	1123
Thr Ala His Glu Ile Leu Glu His Leu Gly Gly Asp Asp Leu Leu Asp	
330 335 340	
ctg gca atc aag ctg gaa gaa att gca ctg gct gat gat tac ttc atc	1171
Leu Ala Ile Lys Leu Glu Glu Ile Ala Leu Ala Asp Asp Tyr Phe Ile	
345 350 355	
tcc cgc aag ctc tac ccg aac gta gac ttc tac acc ggc ctg atc tac	1219
Ser Arg Lys Leu Tyr Pro Asn Val Asp Phe Tyr Thr Gly Leu Ile Tyr	
360 365 370	
cgc gca atg ggc ttc cca act gac ttc ttc acc gta ttg ttc gca atc	1267
Arg Ala Met Gly Phe Pro Thr Asp Phe Phe Thr Val Leu Phe Ala Ile	
375 380 385	
ggt cgt ctg cca gga tgg atc gct cac tac cgc gag cag ctc ggt gca	1315
Gly Arg Leu Pro Gly Trp Ile Ala His Tyr Arg Glu Gln Leu Gly Ala	
390 395 400 405	
gca ggc aac aag atc aac cgc cca cgc cag gtc tac acc ggc aac gaa	1363
Ala Gly Asn Lys Ile Asn Arg Pro Arg Gln Val Tyr Thr Gly Asn Glu	
410 415 420	
tcc cgc aag ttg gtt cct cgc gag gag cgc taaatttagc ggatgattct	1413

09602740-062300



1416

<400> 546															
Val 1	Ala	Thr	Asp	Asn 5	Asn	Lys	Ala	Val	Leu 10	His	Tyr	Pro	Gly	Gly 15	Glut
Phe	Glu	Met	Asp 20	Ile	Ile	Glu	Ala	Ser 25	Glu	Gly	Asn	Asn	Gly 30	Val	Val
Leu	Gly	Lys 35	Met	Leu	Ser	Glu	Thr 40	Gly	Leu	Ile	Thr	Phe 45	Asp	Pro	Gly
Tyr	Val 50	Ser	Thr	Gly	Ser	Thr 55	Glu	Ser	Lys	Ile	Thr 60	Tyr	Ile	Asp	Gly
Asp 65	Ala	Gly	Ile	Leu	Arg 70	Tyr	Arg	Gly	Tyr	Asp 75	Ile	Ala	Asp	Leu	Ala 80
Glu	Asn	Ala	Thr	Phe 85	Asn	Glu	Val	Ser	Tyr 90	Leu	Leu	Ile	Asn	Gly 95	Glut
Leu	Pro	Thr	Pro 100	Asp	Glu	Leu	His	Lys 105	Phe	Asn	Asp	Glu	Ile 110	Arg	His
His	Thr	Leu 115	Leu	Asp	Glu	Asp	Phe 120	Lys	Ser	Gln	Phe 125	Asn	Val	Phe	Pro
Arg	Asp 130	Ala	His	Pro	Met	Ala 135	Thr	Leu	Ala	Ser	Ser 140	Val	Asn	Ile	Leu
Ser 145	Thr	Tyr	Tyr	Gln	Asp 150	Gln	Leu	Asn	Pro	Leu 155	Asp	Glu	Ala	Gln	Leu 160
Asp	Lys	Ala	Thr	Val 165	Arg	Leu	Met	Ala	Lys 170	Val	Pro	Met	Leu	Ala 175	Ala
Tyr	Ala	His	Arg 180	Ala	Arg	Lys	Gly	Ala 185	Pro	Tyr	Met	Tyr	Pro 190	Asp	Asn
Ser	Leu	Asn 195	Ala	Arg	Glu	Asn	Phe 200	Leu	Arg	Met	Met	Phe 205	Gly	Tyr	Pro
Thr	Glu 210	Pro	Tyr	Glu	Ile	Asp 215	Pro	Ile	Met	Val	Lys 220	Ala	Leu	Asp	Lys
Leu 225	Leu	Ile	Leu	His	Ala 230	Asp	His	Glu	Gln	Asn 235	Cys	Ser	Thr	Ser	Thr 240
Val	Arg	Met	Ile	Gly 245	Ser	Ala	Gln	Ala	Asn 250	Met	Phe	Val	Ser	Ile 255	Ala
Gly	Gly	Ile	Asn	Ala	Leu	Ser	Gly	Pro	Leu	His	Gly	Gly	Ala	Asn	Gln



260					265					270					
Ala	Val	Leu	Glu	Met	Leu	Glu	Asp	Ile	Lys	Ser	Asn	His	Gly	Gly	Asp
		275					280					285			
Ala	Thr	Glu	Phe	Met	Asn	Lys	Val	Lys	Asn	Lys	Glu	Asp	Gly	Val	Arg
	290					295					300				
Leu	Met	Gly	Phe	Gly	His	Arg	Val	Tyr	Lys	Asn	Tyr	Asp	Pro	Arg	Ala
305					310					315					320
Ala	Ile	Val	Lys	Glu	Thr	Ala	His	Glu	Ile	Leu	Glu	His	Leu	Gly	Gly
				325					330					335	
Asp	Asp	Leu	Leu	Asp	Leu	Ala	Ile	Lys	Leu	Glu	Glu	Ile	Ala	Leu	Ala
			340					345					350		
Asp	Asp	Tyr	Phe	Ile	Ser	Arg	Lys	Leu	Tyr	Pro	Asn	Val	Asp	Phe	Tyr
		355					360					365			
Thr	Gly	Leu	Ile	Tyr	Arg	Ala	Met	Gly	Phe	Pro	Thr	Asp	Phe	Phe	Thr
	370					375					380				
Val	Leu	Phe	Ala	Ile	Gly	Arg	Leu	Pro	Gly	Trp	Ile	Ala	His	Tyr	Arg
385					390					395					400
Glu	Gln	Leu	Gly	Ala	Ala	Gly	Asn	Lys	Ile	Asn	Arg	Pro	Arg	Gln	Val
				405					410					415	
Tyr	Thr	Gly	Asn	Glu	Ser	Arg	Lys	Leu	Val	Pro	Arg	Glu	Glu	Arg	
			420					425					430		
<210> 547															
<211> 942															
<212> DNA															
<213> Corynebacterium glutamicum															
<220>															
<221> CDS															
<222> (101)..(919)															
<223> RXA02621															
<400> 547															
atgtacctga ctggtgcgcg acacttcgct cactaaagtt tttaaagatt tcgcttgaag 60															
gcagaccata aggtctgcct ttctgcgtat taatgagtac atg tct gaa ctt att 115															
Met Ser Glu Leu Ile 5															
tgt gga cca gct att ctc ttc gca cca gct gga cgt gct gag atc att 163															
Cys Gly Pro Ala Ile Leu Phe Ala Pro Ala Gly Arg Ala Glu Ile Ile 20															
cca aaa gca gca tcg aag gcc gat atg gtc atc att gat ttg gaa gat 211															
Pro Lys Ala Ala Ser Lys Ala Asp Met Val Ile Ile Asp Leu Glu Asp 35															
ggg gca ggg gag gta gac cgt gag gtc gcc tac agg aac att aga gaa 259															
Gly Ala Gly Glu Val Asp Arg Glu Val Ala Tyr Arg Asn Ile Arg Glu 50															



<210> 548



<400> 548

<210> 549

[illegible]



```
<220>  
<221> CDS  
<222> (101)..(2314)  
<223> RXN00519
```

<400> 549																
tttccatgcg gggctgaaac tgccaccata ggcgccagca attagtagaa cactgtattc																60
taggtagctg aacaaaagag cccatcaacc aaggagactc																115
Met Ala Lys Ile Ile 1 5																
tgg acc cgc acc gac gaa gca ccg ctg ctc gcg acc tac tcg ctg aag																163
Trp Thr Arg Thr Asp Glu Ala Pro Leu Leu Ala Thr Tyr Ser Leu Lys 10 15 20																
ccg gtc gtc gag gca ttt gct gct acc gcg ggc att gag gtc gag acc																211
Pro Val Val Glu Ala Phe Ala Ala Thr Ala Gly Ile Glu Val Glu Thr 25 30 35																
cgg gac att tca ctc gct gga cgc atc ctc gcc cag ttc cca gag cgc																259
Arg Asp Ile Ser Leu Ala Gly Arg Ile Leu Ala Gln Phe Pro Glu Arg 40 45 50																
ctc acc gaa gat cag aag gta ggc aac gca ctc gca gaa ctc ggc gag																307
Leu Thr Glu Asp Gln Lys Val Gly Asn Ala Leu Ala Glu Leu Gly Glu 55 60 65																
ctt gct aag act cct gaa gca aac atc att aag ctt cca aac atc tcc																355
Leu Ala Lys Thr Pro Glu Ala Asn Ile Ile Lys Leu Pro Asn Ile Ser 70 75 80 85																
gct tct gtt cca cag ctc aag gct gct att aag gaa ctg cag gac cag																403
Ala Ser Val Pro Gln Leu Lys Ala Ala Ile Lys Glu Leu Gln Asp Gln 90 95 100																
ggc tac gac atc cca gaa ctg cct gat aac gcc acc acc gac gag gaa																451
Gly Tyr Asp Ile Pro Glu Leu Pro Asn Ala Thr Thr Asp Glu Glu 105 110 115																
aaa gac atc ctc gca cgc tac aac gct gtt aag ggt tcc gct gtg aac																499
Lys Asp Ile Leu Ala Arg Tyr Asn Ala Val Lys Gly Ser Ala Val Asn 120 125 130																
cca gtg ctg cgt gaa ggc aac tct gac cgc cgc gca cca atc gct gtc																547
Pro Val Leu Arg Glu Gly Asn Ser Asp Arg Arg Ala Pro Ile Ala Val 135 140 145																
aag aac ttt gtt aag aag ttc cca cac cgc atg ggc gag tgg tct gca																595
Lys Asn Phe Val Lys Lys Phe Pro His Arg Met Gly Glu Trp Ser Ala 150 155 160 165																
gat tcc aag acc aac gtt gca acc atg gat gca aac gac ttc cgc cac																643
Asp Ser Lys Thr Asn Val Ala Thr Met Asp Ala Asn Asp Phe Arg His 170 175 180																
aac gag aag tcc atc atc ctc gac gct gct gat gaa gtt cag atc aag																691







				425				430				435							
ggc	gac	gtt	ctc	atc	gag	cac	gac	gtt	gag	gca	aat	gac	atc	tgg	cgt	1459			
Gly	Asp	Val	Leu	Ile	Glu	His	Asp	Val	Glu	Ala	Asn	Asp	Ile	Trp	Arg				
				440				445				450							
gca	tgc	cag	gtc	aag	gat	gcc	cca	atc	cag	gat	tgg	gta	aag	ctt	gct	1507			
Ala	Cys	Gln	Val	Lys	Asp	Ala	Pro	Ile	Gln	Asp	Trp	Val	Lys	Leu	Ala				
				455				460				465							
gtc	acc	cgc	tcc	cgt	ctc	tcc	gga	atg	cct	gca	gtg	ttc	tgg	ttg	gat	1555			
Val	Thr	Arg	Ser	Arg	Leu	Ser	Gly	Met	Pro	Ala	Val	Phe	Trp	Leu	Asp				
				470				475				480				485			
cca	gag	cgc	gca	cac	gac	cgc	aac	ctg	gct	tcc	ctc	gtt	gag	aag	tac	1603			
Pro	Glu	Arg	Ala	His	Asp	Arg	Asn	Leu	Ala	Ser	Leu	Val	Glu	Lys	Tyr				
				490				495				500							
ctg	gct	gac	cac	gac	acc	gag	ggc	ctg	gac	atc	cag	atc	ctc	tcc	cct	1651			
Leu	Ala	Asp	His	Asp	Thr	Glu	Gly	Leu	Asp	Ile	Gln	Ile	Leu	Ser	Pro				
				505				510				515							
gtt	gag	gca	acc	cag	ctc	tcc	atc	gac	cgc	atc	cgc	cgt	ggc	gag	gac	1699			
Val	Glu	Ala	Thr	Gln	Leu	Ser	Ile	Asp	Arg	Ile	Arg	Arg	Gly	Glu	Asp				
				520				525				530							
acc	atc	tct	gtc	acc	ggt	aac	gtt	ctg	cgt	gac	tac	aac	acc	gac	ctc	1747			
Thr	Ile	Ser	Val	Thr	Gly	Asn	Val	Leu	Arg	Asp	Tyr	Asn	Thr	Asp	Leu				
				535				540				545							
ttc	cca	atc	ctg	gag	ctg	ggc	acc	tct	gca	aag	atg	ctg	tct	gtc	gtt	1795			
Phe	Pro	Ile	Leu	Glu	Leu	Gly	Thr	Ser	Ala	Lys	Met	Leu	Ser	Val	Val				
				550				555				560				565			
cct	ttg	atg	gct	ggc	ggc	gga	ctg	ttc	gag	acc	ggt	gct	ggt	gga	tct	1843			
Pro	Leu	Met	Ala	Gly	Gly	Gly	Leu	Phe	Glu	Thr	Gly	Ala	Gly	Gly	Ser				
				570				575				580							
gct	cct	aag	cac	gtc	cag	cag	gtt	cag	gaa	gaa	aac	cac	ctg	cgt	tgg	1891			
Ala	Pro	Lys	His	Val	Gln	Gln	Val	Gln	Glu	Glu	Asn	His	Leu	Arg	Trp				
				585				590				595							
gat	tcc	ctc	ggt	gag	ttc	ctc	gca	ctg	gct	gag	tcc	ttc	cgc	cac	gag	1939			
Asp	Ser	Leu	Gly	Glu	Phe	Leu	Ala	Leu	Ala	Glu	Ser	Phe	Arg	His	Glu				
				600				605				610							
ctc	aac	aac	aac	ggc	aac	acc	aag	gcc	ggc	gtt	ctg	gct	gac	gct	ctg	1987			
Leu	Asn	Asn	Asn	Gly	Asn	Thr	Lys	Ala	Gly	Val	Leu	Ala	Asp	Ala	Leu				
				615				620				625							
gac	aag	gca	act	gag	aag	ctg	ctg	aac	gaa	gag	aag	tcc	cca	tcc	cgc	2035			
Asp	Lys	Ala	Thr	Glu	Lys	Leu	Leu	Asn	Glu	Glu	Lys	Ser	Pro	Ser	Arg				
				630				635				640				645			
aag	gtt	ggc	gag	atc	gac	aac	cgt	ggc	tcc	cac	ttc	tgg	ctg	acc	aag	2083			
Lys	Val	Gly	Glu	Ile	Asp	Asn	Arg	Gly	Ser	His	Phe	Trp	Leu	Thr	Lys				
				650				655				660							
ttc	tgg	gct	gac	gag	ctc	gct	gct	cag	acc	gag	gac	gca	gat	ctg	gct	2131			
Phe</																			

**Q** What are the most common types of errors made by students?

**A** The most common error is the omission of units. Students often forget to include units in their answers, which can lead to incorrect results. Another common error is the misuse of mathematical symbols, such as using  $\times$  instead of  $\cdot$  for multiplication or  $/$  instead of  $\div$  for division.

**Q** How can I help my student understand the importance of units?

**A** One way to help your student understand the importance of units is to emphasize the concept of dimensional analysis. This involves checking the units of each term in an equation to ensure they are consistent. For example, if you are calculating speed, the units should be distance divided by time, resulting in units like meters per second ( $m/s$ ) or kilometers per hour ( $km/h$ ).

**Q** What are some strategies for teaching unit conversion?

**A** There are several strategies for teaching unit conversion. One effective method is to use the "factor-label" method, also known as the "dimensional analysis" method. This involves multiplying the given quantity by a series of conversion factors (fractions) that cancel out the unwanted units and leave the desired units. For example, to convert 100 feet to meters, you would multiply 100 feet by the conversion factor  $\frac{1 \text{ meter}}{3.28 \text{ feet}}$ , resulting in approximately 30.48 meters.

**Q** How can I help my student avoid rounding errors?

**A** To help your student avoid rounding errors, it's important to teach them when to round and how many significant figures to keep. A general rule is to round at the end of a calculation, after all other operations have been completed. Additionally, encourage your student to use scientific notation to represent very large or very small numbers, which can help prevent confusion and errors.

**Q** What are some resources available for additional practice problems?

**A** There are many online resources available for additional practice problems. Websites like Khan Academy, Coursera, and Blackboard offer interactive exercises and quizzes on various topics related to physics and mathematics. You can also find textbooks and workbooks that provide a wealth of practice problems for your student to work on.



```

<210> 550
<211> 738
<212> PRT
<213> Corynebacterium glutamicum

<400> 550
Met Ala Lys Ile Ile Trp Thr Arg Thr Asp Glu Ala Pro Leu Leu Ala
  1      5      10
Thr Tyr Ser Leu Lys Pro Val Val Glu Ala Phe Ala Ala Thr Ala Gly
      20      25      30
Ile Glu Val Glu Thr Arg Asp Ile Ser Leu Ala Gly Arg Ile Leu Ala
      35      40      45
Gln Phe Pro Glu Arg Leu Thr Glu Asp Gln Lys Val Gly Asn Ala Leu
      50      55      60
Ala Glu Leu Gly Glu Leu Ala Lys Thr Pro Glu Ala Asn Ile Ile Lys
      65      70      75      80
Leu Pro Asn Ile Ser Ala Ser Val Pro Gln Leu Lys Ala Ala Ile Lys
      85      90      95
Glu Leu Gln Asp Gln Gly Tyr Asp Ile Pro Glu Leu Pro Asp Asn Ala
      100      105      110
Thr Thr Asp Glu Glu Lys Asp Ile Leu Ala Arg Tyr Asn Ala Val Lys
      115      120      125
Gly Ser Ala Val Asn Pro Val Leu Arg Glu Gly Asn Ser Asp Arg Arg
      130      135      140
Ala Pro Ile Ala Val Lys Asn Phe Val Lys Lys Phe Pro His Arg Met
      145      150      155      160
Gly Glu Trp Ser Ala Asp Ser Lys Thr Asn Val Ala Thr Met Asp Ala
      165      170      175
Asn Asp Phe Arg His Asn Glu Lys Ser Ile Ile Leu Asp Ala Ala Asp
      180      185      190

```

```
<210> 550
<211> 738
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 550															
Met	Ala	Lys	Ile	Ile	Trp	Thr	Arg	Thr	Asp	Glu	Ala	Pro	Leu	Leu	Ala
1				5					10					15	
Thr	Tyr	Ser	Leu	Lys	Pro	Val	Val	Glu	Ala	Phe	Ala	Ala	Thr	Ala	Gly
			20					25					30		
Ile	Glu	Val	Glu	Thr	Arg	Asp	Ile	Ser	Leu	Ala	Gly	Arg	Ile	Leu	Ala
		35					40					45			
Gln	Phe	Pro	Glu	Arg	Leu	Thr	Glu	Asp	Gln	Lys	Val	Gly	Asn	Ala	Leu
	50					55					60				
Ala	Glu	Leu	Gly	Glu	Leu	Ala	Lys	Thr	Pro	Glu	Ala	Asn	Ile	Ile	Lys
65					70					75					80
Leu	Pro	Asn	Ile	Ser	Ala	Ser	Val	Pro	Gln	Leu	Lys	Ala	Ala	Ile	Lys
				85					90					95	
Glu	Leu	Gln	Asp	Gln	Gly	Tyr	Asp	Ile	Pro	Glu	Leu	Pro	Asp	Asn	Ala
			100					105					110		
Thr	Thr	Asp	Glu	Glu	Lys	Asp	Ile	Leu	Ala	Arg	Tyr	Asn	Ala	Val	Lys
		115					120					125			
Gly	Ser	Ala	Val	Asn	Pro	Val	Leu	Arg	Glu	Gly	Asn	Ser	Asp	Arg	Arg
	130					135					140				
Ala	Pro	Ile	Ala	Val	Lys	Asn	Phe	Val	Lys	Lys	Phe	Pro	His	Arg	Met
145					150					155					160
Gly	Glu	Trp	Ser	Ala	Asp	Ser	Lys	Thr	Asn	Val	Ala	Thr	Met	Asp	Ala
				165					170					175	
Asn	Asp	Phe	Arg	His	Asn	Glu	Lys	Ser	Ile	Ile	Leu	Asp	Ala	Ala	Asp
			180					185					190		



Glu	Val	Gln	Ile	Lys	His	Ile	Ala	Ala	Asp	Gly	Thr	Glu	Thr	Ile	Leu
		195					200					205			
Lys	Asp	Ser	Leu	Lys	Leu	Leu	Glu	Gly	Glu	Val	Leu	Asp	Gly	Thr	Val
	210					215					220				
Leu	Ser	Ala	Lys	Ala	Leu	Asp	Ala	Phe	Leu	Leu	Glu	Gln	Val	Ala	Arg
225					230					235					240
Ala	Lys	Ala	Glu	Gly	Ile	Leu	Phe	Ser	Ala	His	Leu	Lys	Ala	Thr	Met
				245					250					255	
Met	Lys	Val	Ser	Asp	Pro	Ile	Ile	Phe	Gly	His	Val	Val	Arg	Ala	Tyr
			260					265					270		
Phe	Ala	Asp	Val	Phe	Ala	Gln	Tyr	Gly	Glu	Gln	Leu	Leu	Ala	Ala	Gly
	275						280					285			
Leu	Asn	Gly	Glu	Asn	Gly	Leu	Ala	Ala	Ile	Leu	Ser	Gly	Leu	Glu	Ser
	290					295					300				
Leu	Asp	Asn	Gly	Glu	Glu	Ile	Lys	Ala	Ala	Phe	Glu	Lys	Gly	Leu	Glu
305					310					315					320
Asp	Gly	Pro	Asp	Leu	Ala	Met	Val	Asn	Ser	Ala	Arg	Gly	Ile	Thr	Asn
				325					330					335	
Leu	His	Val	Pro	Ser	Asp	Val	Ile	Val	Asp	Ala	Ser	Met	Pro	Ala	Met
			340					345					350		
Ile	Arg	Thr	Ser	Gly	His	Met	Trp	Asn	Lys	Asp	Asp	Gln	Glu	Gln	Asp
		355					360					365			
Thr	Leu	Ala	Ile	Ile	Pro	Asp	Ser	Ser	Tyr	Ala	Gly	Val	Tyr	Gln	Thr
	370					375					380				
Val	Ile	Glu	Asp	Cys	Arg	Lys	Asn	Gly	Ala	Phe	Asp	Pro	Thr	Thr	Met
385					390					395					400
Gly	Thr	Val	Pro	Asn	Val	Gly	Leu	Met	Ala	Gln	Lys	Ala	Glu	Glu	Tyr
				405					410					415	
Gly	Ser	His	Asp	Lys	Thr	Phe	Arg	Ile	Glu	Ala	Asp	Gly	Val	Val	Gln
			420					425					430		
Val	Val	Ser	Ser	Asn	Gly	Asp	Val	Leu	Ile	Glu	His	Asp	Val	Glu	Ala
		435					440					445			
Asn	Asp	Ile	Trp	Arg	Ala	Cys	Gln	Val	Lys	Asp	Ala	Pro	Ile	Gln	Asp
	450					455					460				
Trp	Val	Lys	Leu	Ala	Val	Thr	Arg	Ser	Arg	Leu	Ser	Gly	Met	Pro	Ala
465					470					475					480
Val	Phe	Trp	Leu	Asp	Pro	Glu	Arg	Ala	His	Asp	Arg	Asn	Leu	Ala	Ser
				485					490					495	
Leu	Val	Glu	Lys	Tyr	Leu	Ala	Asp	His	Asp	Thr	Glu	Gly	Leu	Asp	Ile
			500					505					510		



Gln	Ile	Leu	Ser	Pro	Val	Glu	Ala	Thr	Gln	Leu	Ser	Ile	Asp	Arg	Ile
		515				520					525				
Arg	Arg	Gly	Glu	Asp	Thr	Ile	Ser	Val	Thr	Gly	Asn	Val	Leu	Arg	Asp
530						535				540					
Tyr	Asn	Thr	Asp	Leu	Phe	Pro	Ile	Leu	Glu	Leu	Gly	Thr	Ser	Ala	Lys
545					550				555						560
Met	Leu	Ser	Val	Val	Pro	Leu	Met	Ala	Gly	Gly	Gly	Leu	Phe	Glu	Thr
				565					570					575	
Gly	Ala	Gly	Gly	Ser	Ala	Pro	Lys	His	Val	Gln	Gln	Val	Gln	Glu	Glu
			580					585					590		
Asn	His	Leu	Arg	Trp	Asp	Ser	Leu	Gly	Glu	Phe	Leu	Ala	Leu	Ala	Glu
		595					600				605				
Ser	Phe	Arg	His	Glu	Leu	Asn	Asn	Asn	Gly	Asn	Thr	Lys	Ala	Gly	Val
610						615				620					
Leu	Ala	Asp	Ala	Leu	Asp	Lys	Ala	Thr	Glu	Lys	Leu	Leu	Asn	Glu	Glu
625					630				635						640
Lys	Ser	Pro	Ser	Arg	Lys	Val	Gly	Glu	Ile	Asp	Asn	Arg	Gly	Ser	His
				645					650					655	
Phe	Trp	Leu	Thr	Lys	Phe	Trp	Ala	Asp	Glu	Leu	Ala	Ala	Gln	Thr	Glu
			660					665					670		
Asp	Ala	Asp	Leu	Ala	Ala	Thr	Phe	Ala	Pro	Val	Ala	Glu	Ala	Leu	Asn
		675					680				685				
Thr	Gly	Ala	Ala	Asp	Ile	Asp	Ala	Ala	Leu	Leu	Ala	Val	Gln	Gly	Gly
690						695				700					
Ala	Thr	Asp	Leu	Gly	Gly	Tyr	Tyr	Ser	Pro	Asn	Glu	Glu	Lys	Leu	Thr
705					710					715					720
Asn	Ile	Met	Arg	Pro	Val	Ala	Gln	Phe	Asn	Glu	Ile	Val	Asp	Ala	Leu
				725					730					735	
Lys	Lys														

```
<210> 551
<211> 1059
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (1)..(1059)
<223> FRXA00521
```

<400> 551  
ctc gac gct gct gat gaa gtt cag atc aag cac atc gca gct gac ggc 48  
Leu Asp Ala Ala Asp Glu Val Gln Ile Lys His Ile Ala Ala Asp Gly  
1 5 10 15







[illegible]



Arg Gly Ile Thr Asn Leu His Val Pro Ser Asp Val Ile Val Asp Ala  
 145 150 155 160  
 Ser Met Pro Ala Met Ile Arg Thr Ser Gly His Met Trp Asn Lys Asp  
 165 170 175  
 Asp Gln Glu Gln Asp Thr Leu Ala Ile Ile Pro Asp Ser Ser Tyr Ala  
 180 185 190  
 Gly Val Tyr Gln Thr Val Ile Glu Asp Cys Arg Lys Asn Gly Ala Phe  
 195 200 205  
 Asp Pro Thr Thr Met Gly Thr Val Pro Asn Val Gly Leu Met Ala Gln  
 210 215 220  
 Lys Ala Glu Glu Tyr Gly Ser His Asp Lys Thr Phe Arg Ile Glu Ala  
 225 230 235 240  
 Asp Gly Val Val Gln Val Val Ser Ser Asn Gly Asp Val Leu Ile Glu  
 245 250 255  
 His Asp Val Glu Ala Asn Asp Ile Trp Arg Ala Cys Gln Val Lys Asp  
 260 265 270  
 Ala Pro Ile Gln Asp Trp Val Lys Leu Ala Val Thr Arg Ser Arg Leu  
 275 280 285  
 Ser Gly Met Pro Ala Val Phe Trp Leu Asp Pro Glu Arg Ala His Asp  
 290 295 300  
 Arg Asn Leu Ala Ser Leu Val Glu Lys Tyr Leu Ala Asp His Asp Thr  
 305 310 315 320  
 Glu Gly Leu Asp Ile Gln Ile Leu Tyr Pro Val Glu Ala Thr Gln Leu  
 325 330 335  
 Ser Ile Asp Arg Ile Arg Arg Gly Glu Asp Thr Ile Ser Val Thr Gly  
 340 345 350

Asn

<210> 553  
 <211> 1694  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(1671)  
 <223> RXN02209

<400> 553  
 acc gag tcc acc gtt gtt cct tcc atc gct ggc cct aag cgc cca cag 48  
 Thr Glu Ser Thr Val Val Pro Ser Ile Ala Gly Pro Lys Arg Pro Gln  
 1 5 10 15  
 gac cgc atc ctt ctc tcc gag gca aag gag cag ttc cgt aag gat ctg 96  
 Asp Arg Ile Leu Leu Ser Glu Ala Lys Glu Gln Phe Arg Lys Asp Leu  
 20 25 30

0062290" 04720960



[illegible]



[illegible]



```
<210> 554
<211> 557
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 554															
Thr 1	Glu	Ser	Thr	Val 5	Val	Pro	Ser	Ile	Ala 10	Gly	Pro	Lys	Arg	Pro 15	Gln
Asp	Arg	Ile	Leu 20	Leu	Ser	Glu	Ala	Lys 25	Glu	Gln	Phe	Arg	Lys 30	Asp	Leu
Pro	Thr	Tyr 35	Thr	Asp	Asp	Ala	Val 40	Ser	Val	Asp	Thr	Ser 45	Ile	Pro	Ala
Thr	Arg 50	Met	Val	Asn	Glu	Gly 55	Gly	Gly	Gln	Pro	Glu 60	Gly	Gly	Val	Glu
Ala 65	Asp	Asn	Tyr	Asn	Ala 70	Ser	Trp	Ala	Gly	Ser 75	Gly	Glu	Ser	Leu	Ala 80
Thr	Gly	Ala	Glu	Gly 85	Arg	Pro	Ser	Lys	Pro 90	Val	Thr	Val	Ala	Ser 95	Pro
Gln	Gly	Gly	Glu 100	Tyr	Thr	Ile	Asp	His 105	Gly	Met	Val	Ala	Ile 110	Ala	Ser
Ile	Thr	Ser 115	Cys	Thr	Asn	Thr	Ser 120	Asn	Pro	Ser	Val	Met 125	Ile	Gly	Ala
Gly 130	Leu	Ile	Ala	Arg	Lys	Ala 135	Ala	Glu	Lys	Gly	Leu 140	Lys	Ser	Lys	Pro
Trp 145	Val	Lys	Thr	Ile	Cys 150	Ala	Pro	Gly	Ser	Gln 155	Val	Val	Asp	Gly	Tyr 160
Tyr	Gln	Arg	Ala 165	Asp	Leu	Trp	Lys	Asp	Leu 170	Glu	Ala	Met	Gly	Phe 175	Tyr
Leu	Ser	Gly	Phe 180	Gly	Cys	Thr	Thr	Cys 185	Ile	Gly	Asn	Ser	Gly 190	Pro	Leu
Pro	Glu	Glu 195	Ile	Ser	Ala	Ala	Ile 200	Asn	Glu	His	Asp	Leu 205	Thr	Ala	Thr
Ala 210	Val	Leu	Ser	Gly	Asn	Arg 215	Asn	Phe	Glu	Gly	Arg 220	Ile	Ser	Pro	Asp

[illegible]



Val Lys Met Asn Tyr Leu Ala Ser Pro Ile Met Val Ile Ala Tyr Ala  
 225 230 235 240  
 Ile Ala Gly Thr Met Asp Phe Asp Phe Glu Asn Glu Ala Leu Gly Gln  
 245 250 255  
 Asp Gln Asp Gly Asn Asp Val Phe Leu Lys Asp Ile Trp Pro Ser Thr  
 260 265 270  
 Glu Glu Ile Glu Asp Thr Ile Gln Gln Ala Ile Ser Arg Glu Leu Tyr  
 275 280 285  
 Glu Ala Asp Tyr Ala Asp Val Phe Lys Gly Asp Lys Gln Trp Gln Glu  
 290 295 300  
 Leu Asp Val Pro Thr Gly Asp Thr Phe Glu Trp Asp Glu Asn Ser Thr  
 305 310 315 320  
 Tyr Ile Arg Lys Ala Pro Tyr Phe Asp Gly Met Pro Val Glu Pro Val  
 325 330 335  
 Ala Val Thr Asp Ile Gln Gly Ala Arg Val Leu Ala Lys Leu Gly Asp  
 340 345 350  
 Ser Val Thr Thr Asp His Ile Ser Pro Ala Ser Ser Ile Lys Pro Gly  
 355 360 365  
 Thr Pro Ala Ala Gln Tyr Leu Asp Glu His Gly Val Glu Arg His Asp  
 370 375 380  
 Tyr Asn Ser Leu Gly Ser Arg Arg Gly Asn His Glu Val Met Met Arg  
 385 390 395 400  
 Gly Thr Phe Ala Asn Ile Arg Leu Gln Asn Gln Leu Val Asp Ile Ala  
 405 410 415  
 Gly Gly Tyr Thr Arg Asp Phe Thr Gln Glu Gly Ala Pro Gln Ala Phe  
 420 425 430  
 Ile Tyr Asp Ala Ser Val Asn Tyr Lys Ala Ala Gly Ile Pro Leu Val  
 435 440 445  
 Val Leu Gly Gly Lys Glu Tyr Gly Thr Gly Ser Ser Arg Asp Trp Ala  
 450 455 460  
 Ala Lys Gly Thr Asn Leu Leu Gly Ile Arg Ala Val Ile Thr Glu Ser  
 465 470 475 480  
 Phe Glu Arg Ile His Arg Ser Asn Leu Ile Gly Met Gly Val Val Pro  
 485 490 495  
 Leu Gln Phe Pro Ala Gly Glu Ser His Glu Ser Leu Gly Leu Asp Gly  
 500 505 510  
 Thr Glu Thr Phe Asp Ile Thr Gly Leu Thr Ala Leu Asn Glu Gly Glu  
 515 520 525  
 Thr Pro Lys Thr Val Lys Val Thr Ala Thr Lys Glu Asn Gly Asp Val  
 530 535 540

003290" 0420960



Val Glu Phe Asp Ala Ile Cys Pro His Arg His Pro Arg  
545 550 555

<210> 555

<211> 1682

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1659)

<223> FRXA02209

<400> 555

gtt gtt cct tcc atc gct ggc cct aag cgc cca cag gac cgc atc ctt	48
Val Val Pro Ser Ile Ala Gly Pro Lys Arg Pro Gln Asp Arg Ile Leu	
1 5 10 15	
ctc tcc gag gca aag gag cag ttc cgt aag gat ctg cca acc tac acc	96
Leu Ser Glu Ala Lys Glu Gln Phe Arg Lys Asp Leu Pro Thr Tyr Thr	
20 25 30	
gac gac gct gtt tcc gta gac acc tcc atc cct gca acc cgc atg gtt	144
Asp Asp Ala Val Ser Val Asp Thr Ser Ile Pro Ala Thr Arg Met Val	
35 40 45	
aac gaa ggt ggc gga cag cct gaa ggc ggc gtc gaa gct gac aac tac	192
Asn Glu Gly Gly Gly Gln Pro Glu Gly Gly Val Glu Ala Asp Asn Tyr	
50 55 60	
aac gct tcc tgg gct ggc tcc ggc gag tcc ttg gct act ggc gca gaa	240
Asn Ala Ser Trp Ala Gly Ser Gly Glu Ser Leu Ala Thr Gly Ala Glu	
65 70 75 80	
gga cgt cct tcc aag cca gtc acc gtt gca tcc cca cag ggt ggc gag	288
Gly Arg Pro Ser Lys Pro Val Thr Val Ala Ser Pro Gln Gly Gly Glu	
85 90 95	
tac acc atc gac cac ggc atg gtt gca att gca tcc atc acc tct tgc	336
Tyr Thr Ile Asp His Gly Met Val Ala Ile Ala Ser Ile Thr Ser Cys	
100 105 110	
acc aac acc tct aac cca tcc gtg atg atc ggc gct ggc ctg atc gca	384
Thr Asn Thr Ser Asn Pro Ser Val Met Ile Gly Ala Gly Leu Ile Ala	
115 120 125	
cgt aag gca gca gaa aag ggc ctc aag tcc aag cct tgg gtt aag acc	432
Arg Lys Ala Ala Glu Lys Gly Leu Lys Ser Lys Pro Trp Val Lys Thr	
130 135 140	
atc tgt gca cca ggt tcc cag gtt gtc gac ggc tac tac cag cgc gca	480
Ile Cys Ala Pro Gly Ser Gln Val Val Asp Gly Tyr Tyr Gln Arg Ala	
145 150 155 160	
gac ctc tgg aag gac ctt gag gcc atg ggc ttc tac ctc tcc ggc ttc	528
Asp Leu Trp Lys Asp Leu Glu Ala Met Gly Phe Tyr Leu Ser Gly Phe	
165 170 175	
ggc tgc acc acc tgt att ggt aac tcc ggc cca ctg cca gag gaa atc	576
Gly Cys Thr Thr Cys Ile Gly Asn Ser Gly Pro Leu Pro Glu Glu Ile	

002290"0420960







tcc gtc aac tac aag gct gct ggc att ccg ctg gtc gtc ttg ggc ggc .1344  
 Ser Val Asn Tyr Lys Ala Ala Gly Ile Pro Leu Val Val Leu Gly Gly  
           435                                  440                                  445

aag gag tac ggc acc ggt tct tcc cgt gac tgg gca gct aag ggc act 1392  
 Lys Glu Tyr Gly Thr Gly Ser Ser Arg Asp Trp Ala Ala Lys Gly Thr  
           450                                  455                                  460

aac ctg ctc gga att cgc gca gtt atc acc gag tcc ttc gag cgt att 1440  
 Asn Leu Leu Gly Ile Arg Ala Val Ile Thr Glu Ser Phe Glu Arg Ile  
           465                                  470                                  475                                  480

cac cgc tcc aac ctc atc ggt atg ggc gtt gtc cca ctg cag ttc cct 1488  
 His Arg Ser Asn Leu Ile Gly Met Gly Val Val Pro Leu Gln Phe Pro  
                                   485                                  490                                  495

gca ggc gaa tcc cac gag tcc ctg ggc ctt gac ggc acc gag acc ttc 1536  
 Ala Gly Glu Ser His Glu Ser Leu Gly Leu Asp Gly Thr Glu Thr Phe  
                                   500                                  505                                  510

gac atc acc gga ctg acc gca ctt aac gag ggc gag act cct aag act 1584  
 Asp Ile Thr Gly Leu Thr Ala Leu Asn Glu Gly Glu Thr Pro Lys Thr  
                                   515                                  520                                  525

gtc aag gtc acc gca acc aag gag aac ggc gac gtc gtc gag ttc gac 1632  
 Val Lys Val Thr Ala Thr Lys Glu Asn Gly Asp Val Val Glu Phe Asp  
           530                                  535                                  540

gca att tgt ccg cat cga cac ccc agg tgaggctgac tactaccgcc 1679  
 Ala Ile Cys Pro His Arg His Pro Arg  
           545                                  550

acg 1682

<210> 556

<211> 553

<212> PRT

<213> Corynebacterium glutamicum

<400> 556

Val Val Pro Ser Ile Ala Gly Pro Lys Arg Pro Gln Asp Arg Ile Leu  
   1                                  5                                  10                                  15

Leu Ser Glu Ala Lys Glu Gln Phe Arg Lys Asp Leu Pro Thr Tyr Thr  
           20                                  25                                  30

Asp Asp Ala Val Ser Val Asp Thr Ser Ile Pro Ala Thr Arg Met Val  
           35                                  40                                  45

Asn Glu Gly Gly Gly Gln Pro Glu Gly Gly Val Glu Ala Asp Asn Tyr  
           50                                  55                                  60

Asn Ala Ser Trp Ala Gly Ser Gly Glu Ser Leu Ala Thr Gly Ala Glu  
           65                                  70                                  75                                  80

Gly Arg Pro Ser Lys Pro Val Thr Val Ala Ser Pro Gln Gly Gly Glu  
                                   85                                  90                                  95

Tyr Thr Ile Asp His Gly Met Val Ala Ile Ala Ser Ile Thr Ser Cys

006290"0720960



100					105					110					
Thr	Asn	Thr	Ser	Asn	Pro	Ser	Val	Met	Ile	Gly	Ala	Gly	Leu	Ile	Ala
	115						120					125			
Arg	Lys	Ala	Ala	Glu	Lys	Gly	Leu	Lys	Ser	Lys	Pro	Trp	Val	Lys	Thr
	130					135					140				
Ile	Cys	Ala	Pro	Gly	Ser	Gln	Val	Val	Asp	Gly	Tyr	Tyr	Gln	Arg	Ala
145					150					155					160
Asp	Leu	Trp	Lys	Asp	Leu	Glu	Ala	Met	Gly	Phe	Tyr	Leu	Ser	Gly	Phe
				165					170					175	
Gly	Cys	Thr	Thr	Cys	Ile	Gly	Asn	Ser	Gly	Pro	Leu	Pro	Glu	Glu	Ile
			180					185					190		
Ser	Ala	Ala	Ile	Asn	Glu	His	Asp	Leu	Thr	Ala	Thr	Ala	Val	Leu	Ser
		195					200					205			
Gly	Asn	Arg	Asn	Phe	Glu	Gly	Arg	Ile	Ser	Pro	Asp	Val	Lys	Met	Asn
	210					215					220				
Tyr	Leu	Ala	Ser	Pro	Ile	Met	Val	Ile	Ala	Tyr	Ala	Ile	Ala	Gly	Thr
225					230					235					240
Met	Asp	Phe	Asp	Phe	Glu	Asn	Glu	Ala	Leu	Gly	Gln	Asp	Gln	Asp	Gly
				245					250					255	
Asn	Asp	Val	Phe	Leu	Lys	Asp	Ile	Trp	Pro	Ser	Thr	Glu	Glu	Ile	Glu
			260					265					270		
Asp	Thr	Ile	Gln	Gln	Ala	Ile	Ser	Arg	Glu	Leu	Tyr	Glu	Ala	Asp	Tyr
		275					280					285			
Ala	Asp	Val	Phe	Lys	Gly	Asp	Lys	Gln	Trp	Gln	Glu	Leu	Asp	Val	Pro
	290					295					300				
Thr	Gly	Asp	Thr	Phe	Glu	Trp	Asp	Glu	Asn	Ser	Thr	Tyr	Ile	Arg	Lys
305					310					315					320
Ala	Pro	Tyr	Phe	Asp	Gly	Met	Pro	Val	Glu	Pro	Val	Ala	Val	Thr	Asp
				325					330					335	
Ile	Gln	Gly	Ala	Arg	Val	Leu	Ala	Lys	Leu	Gly	Asp	Ser	Val	Thr	Thr
			340					345					350		
Asp	His	Ile	Ser	Pro	Ala	Ser	Ser	Ile	Lys	Pro	Gly	Thr	Pro	Ala	Ala
		355					360					365			
Gln	Tyr	Leu	Asp	Glu	His	Gly	Val	Glu	Arg	His	Asp	Tyr	Asn	Ser	Leu
	370					375					380				
Gly	Ser	Arg	Arg	Gly	Asn	His	Glu	Val	Met	Met	Arg	Gly	Thr	Phe	Ala
385					390					395					400
Asn	Ile	Arg	Leu	Gln	Asn	Gln	Leu	Val	Asp	Ile	Ala	Gly	Gly	Tyr	Thr
				405					410					415	
Arg	Asp	Phe	Thr	Gln	Glu	Gly	Ala	Pro	Gln	Ala	Phe	Ile	Tyr	Asp	Ala
			420					425					430		

002290"0420960



tcc gat cca agc atc gaa atc cag ttc acc cca gcc cgt gtt ctc atg 355  
Ser Asp Pro Ser Ile Glu Ile Gln Phe Thr Pro Ala Arg Val Leu Met

[illegible]



<400> 558  
Val Thr Glu Ser Lys Asn Ser Phe Asn Ala Lys Ser Thr Leu Glu Val  
1 5 10 15  
Gly Asp Lys Ser Tyr Asp Tyr Phe Ala Leu Ser Ala Val Pro Gly Met  
20 25 30  
Glu Lys Leu Pro Tyr Ser Leu Lys Val Leu Gly Glu Asn Leu Leu Arg  
35 40 45



[illegible]

```
<210> 559
<211> 817
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(817)
<223> FRXA02213
```

<400> 559  
ttctgtggaa tgagaatccg atgtttttct cacgccggct cagccgaagc agacgccgtc 60

gcgaaatctc accctaaaaa agttagaatt ggagctcact gtg act gaa agc aag 115  
Val Thr Glu Ser Lys  
1 5



aac tcc ttc aat gct aag agc acc ctt gaa gtt ggc gac aag tcc tat	163
Asn Ser Phe Asn Ala Lys Ser Thr Leu Glu Val Gly Asp Lys Ser Tyr	
10 15 20	
gac tac ttc gcc ctc tct gca gtg cct ggc atg gag aag ctg ccg tac	211
Asp Tyr Phe Ala Leu Ser Ala Val Pro Gly Met Glu Lys Leu Pro Tyr	
25 30 35	
tcc ctc aag gtt ctc gga gag aac ctt ctt cgt acc gaa gac ggc gca	259
Ser Leu Lys Val Leu Gly Glu Asn Leu Leu Arg Thr Glu Asp Gly Ala	
40 45 50	
aac atc acc aac gag cac att gag gct atc gcc aac tgg gat gca tct	307
Asn Ile Thr Asn Glu His Ile Glu Ala Ile Ala Asn Trp Asp Ala Ser	
55 60 65	
tcc gat cca agc atc gaa atc cag ttc acc cca gcc cgt gtt ctc atg	355
Ser Asp Pro Ser Ile Glu Ile Gln Phe Thr Pro Ala Arg Val Leu Met	
70 75 80 85	
cag gac ttc acc ggt gtc cct tgt gta gtt gac ctc gca acc atg cgt	403
Gln Asp Phe Thr Gly Val Pro Cys Val Val Asp Leu Ala Thr Met Arg	
90 95 100	
gag gca gtt gct gca ctc ggt ggc gac cct aac gac gtc aac cca ctg	451
Glu Ala Val Ala Ala Leu Gly Gly Asp Pro Asn Asp Val Asn Pro Leu	
105 110 115	
aac cca gcc gag atg gtc att gag cac tcc gtc atc gtg gag gct ttc	499
Asn Pro Ala Glu Met Val Ile Asp His Ser Val Ile Val Glu Ala Phe	
120 125 130	
ggc cgc cca gat gca ctg gct aag aac gtt gag atc gag tac gag cgc	547
Gly Arg Pro Asp Ala Leu Ala Lys Asn Val Glu Ile Glu Tyr Glu Arg	
135 140 145	
aac gag gag cgt tac cag ttc ctg cgt tgg ggt tcc gag tcc ttc tcc	595
Asn Glu Glu Arg Tyr Gln Phe Leu Arg Trp Gly Ser Glu Ser Phe Ser	
150 155 160 165	
aac ttc cgc gtt gtt cct cca gga acc ggt atc gtc cac cag gtc aac	643
Asn Phe Arg Val Val Pro Pro Gly Thr Gly Ile Val His Gln Val Asn	
170 175 180	
att gag tac ttg gct cgc gtc gtc ttc gac aac gag ggc ctt gca tac	691
Ile Glu Tyr Leu Ala Arg Val Val Phe Asp Asn Glu Gly Leu Ala Tyr	
185 190 195	
cca gat acc tgc atc ggt acc gac tcc cac acc acc atg gaa aac ggc	739
Pro Asp Thr Cys Ile Gly Thr Asp Ser His Thr Thr Met Glu Asn Gly	
200 205 210	
ctg ggc atc ctg ggc tgg ggc gtt ggt ggc att gag gct gaa gca gca	787
Leu Gly Ile Leu Gly Trp Gly Val Gly Gly Ile Glu Ala Glu Ala Ala	
215 220 225	
atg ctc ggc cag cca gtg tcc atg ctg atc	817
Met Leu Gly Gln Pro Val Ser Met Leu Ile	
230 235	

00602740.062300



<400>	560														
Val	Thr	Glu	Ser	Lys	Asn	Ser	Phe	Asn	Ala	Lys	Ser	Thr	Leu	Glu	Val
1				5					10					15	
Gly	Asp	Lys	Ser	Tyr	Asp	Tyr	Phe	Ala	Leu	Ser	Ala	Val	Pro	Gly	Met
			20					25					30		
Glu	Lys	Leu	Pro	Tyr	Ser	Leu	Lys	Val	Leu	Gly	Glu	Asn	Leu	Leu	Arg
		35					40					45			
Thr	Glu	Asp	Gly	Ala	Asn	Ile	Thr	Asn	Glu	His	Ile	Glu	Ala	Ile	Ala
	50					55					60				
Asn	Trp	Asp	Ala	Ser	Ser	Asp	Pro	Ser	Ile	Glu	Ile	Gln	Phe	Thr	Pro
65					70					75					80
Ala	Arg	Val	Leu	Met	Gln	Asp	Phe	Thr	Gly	Val	Pro	Cys	Val	Val	Asp
				85					90					95	
Leu	Ala	Thr	Met	Arg	Glu	Ala	Val	Ala	Ala	Leu	Gly	Gly	Asp	Pro	Asn
			100					105					110		
Asp	Val	Asn	Pro	Leu	Asn	Pro	Ala	Glu	Met	Val	Ile	Asp	His	Ser	Val
		115					120					125			
Ile	Val	Glu	Ala	Phe	Gly	Arg	Pro	Asp	Ala	Leu	Ala	Lys	Asn	Val	Glu
	130					135					140				
Ile	Glu	Tyr	Glu	Arg	Asn	Glu	Glu	Arg	Tyr	Gln	Phe	Leu	Arg	Trp	Gly
145					150					155					160
Ser	Glu	Ser	Phe	Ser	Asn	Phe	Arg	Val	Val	Pro	Pro	Gly	Thr	Gly	Ile
				165					170					175	
Val	His	Gln	Val	Asn	Ile	Glu	Tyr	Leu	Ala	Arg	Val	Val	Phe	Asp	Asn
			180					185					190		
Glu	Gly	Leu	Ala	Tyr	Pro	Asp	Thr	Cys	Ile	Gly	Thr	Asp	Ser	His	Thr
		195					200					205			
Thr	Met	Glu	Asn	Gly	Leu	Gly	Ile	Leu	Gly	Trp	Gly	Val	Gly	Gly	Ile
	210					215					220				
Glu	Ala	Glu	Ala	Ala	Met	Leu	Gly	Gln	Pro	Val	Ser	Met	Leu	Ile	
225					230					235					

```
<210> 561
<211> 2891
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(2868)
<223> RXA02056
```



cgc Arg 1	cac His	tct Ser	gtt Val	cca Pro 5	cgt Arg	cta Leu	acc Thr	aag Lys	ggc Gly 10	cag Gln	ggc Gly	acc Thr	atc Ile	atc Ile 15	ggt Gly	48
gtc Val	ggt Gly	tcc Ser	atg Met 20	gat Asp	tac Tyr	cca Pro	gca Ala	gag Glu 25	ttc Phe	cag Gln	ggc Gly	gct Ala	tca Ser 30	gaa Glu	gac Asp	96
cgc Arg	ctt Leu	gca Ala 35	gag Glu	ctc Leu	ggc Gly	gtt Val	ggc Gly 40	aaa Lys	ctt Leu	gtc Val	acc Thr 45	atc Ile	acc Thr	tcc Ser	acc Thr	144
tac Tyr	gat Asp 50	cac His	cgc Arg	gtg Val	atc Ile	cag Gln 55	ggt Gly	gct Ala	gtg Val	tcc Ser	ggg Gly 60	gaa Glu	ttc Phe	ctg Leu	cgc Arg	192
acc Thr 65	atg Met	tct Ser	cgc Arg	ctg Leu	ctc Leu 70	acc Thr	gat Asp	gat Asp	tcc Ser	ttc Phe 75	tgg Trp	gat Asp	gag Glu	atc Ile	ttc Phe 80	240
gac Asp	gca Ala	atg Met	aac Asn	gtt Val 85	cct Pro	tac Tyr	acc Thr	cca Pro	atg Met 90	cgt Arg	tgg Trp	gca Ala	cag Gln	gac Asp 95	gtt Val	288
cca Pro	aac Asn	acc Thr	ggg Gly 100	gtt Val	gat Asp	aag Lys	aac Asn 105	acc Thr	cgc Arg	gtc Val	atg Met	cag Gln	ctc Leu 110	att Ile	gag Glu	336
gca Ala	tac Tyr	cgc Arg 115	tcc Ser	cgt Arg	gga Gly	cac His	ctc Leu 120	atc Ile	gct Ala	gac Asp	acc Thr 125	aac Asn	cca Pro	ctt Leu	tca Ser	384
tgg Trp	gtt Val 130	cag Gln	cct Pro	ggc Gly	atg Met	cca Pro 135	gtt Val	cca Pro	gac Asp	cac His	cgc Arg 140	gac Asp	ctc Leu	gac Asp	atc Ile	432
gag Glu 145	acc Thr	cac His	aac Asn	ctg Leu	acc Thr 150	atc Ile	tgg Trp	gat Asp	ctg Leu	gac Asp 155	cgt Arg	acc Thr	ttc Phe	aac Asn	gtc Val 160	480
ggg Gly	ggc Gly	ttc Phe	ggc Gly	ggc Gly 165	aag Lys	gag Glu	acc Thr	atg Met	acc Thr 170	ctg Leu	cgc Arg	gag Glu	gta Val	ctg Leu 175	tcc Ser	528
cgc Arg	ctc Leu	cgc Arg	gct Ala 180	gcg Ala	tac Tyr	acc Thr	ctc Leu	aag Lys 185	gtc Val	ggc Gly	tcc Ser	gaa Glu	tac Tyr 190	acc Thr	cac His	576
atc Ile	ctg Leu	gac Asp 195	cgc Arg	gac Asp	gag Glu	cgc Arg	acc Thr 200	tgg Trp	ctg Leu	cag Gln	gac Asp 205	cgc Arg	ctc Leu	gag Glu	gcc Ala	624
gga Gly	atg Met 210	cca Pro	aag Lys	cca Pro	acc Thr	cag Gln 215	gca Ala	gag Glu	cag Gln	aag Lys 220	tac Tyr	atc Ile	ctg Leu	cag Gln	aag Lys	672
ctg Leu 225	aac Asn	gcc Ala	gcg Ala	gag Glu	gct Ala 230	ttc Phe	gag Glu	aac Asn	ttc Phe 235	ctg Leu	cag Gln	acc Thr	aag Lys	tac Tyr	gtc Val 240	720



[illegible]



ggc cac aac gaa gct gat gat cct tcc atg acc cag cca aag atg tat	1488
Gly His Asn Glu Ala Asp Asp Pro Ser Met Thr Gln Pro Lys Met Tyr	
485 490 495	
gag ctc atc acc ggc cgc gag acc gtt cgt gct cag tac acc gaa gac	1536
Glu Leu Ile Thr Gly Arg Glu Thr Val Arg Ala Gln Tyr Thr Glu Asp	
500 505 510	
ctg ctc gga cgt gga gac ctc tcc aac gaa gat gca gaa gca gtc gtc	1584
Leu Leu Gly Arg Gly Asp Leu Ser Asn Glu Asp Ala Glu Ala Val Val	
515 520 525	
cgc gac ttc cac gac cag atg gaa tct gtg ttc aac gaa gtc aag gaa	1632
Arg Asp Phe His Asp Gln Met Glu Ser Val Phe Asn Glu Val Lys Glu	
530 535 540	
ggc ggc aag aag cag gct gag gca cag acc ggc atc acc ggc tcc cag	1680
Gly Gly Lys Lys Gln Ala Glu Ala Gln Thr Gly Ile Thr Gly Ser Gln	
545 550 555 560	
aag ctt cca cac ggc ctt gag acc aac atc tcc cgt gaa gag ctc ctg	1728
Lys Leu Pro His Gly Leu Glu Thr Asn Ile Ser Arg Glu Glu Leu Leu	
565 570 575	
gaa ctg gga cag gct ttc gcc aac acc cca gaa ggc ttc aac tac cac	1776
Glu Leu Gly Gln Ala Phe Ala Asn Thr Pro Glu Gly Phe Asn Tyr His	
580 585 590	
cca cgt gtg gct ccc gtt gct aag aag cgc gtc tcc tct gtc acc gaa	1824
Pro Arg Val Ala Pro Val Ala Lys Lys Arg Val Ser Ser Val Thr Glu	
595 600 605	
ggt ggc atc gac tgg gca tgg ggc gag ctc ctc gcc ttc ggt tcc ctg	1872
Gly Gly Ile Asp Trp Ala Trp Gly Glu Leu Leu Ala Phe Gly Ser Leu	
610 615 620	
gct aac tcc ggc cgc ttg gtt cgc ctt gca ggt gaa gat tcc cgc cgc	1920
Ala Asn Ser Gly Arg Leu Val Arg Leu Ala Gly Glu Asp Ser Arg Arg	
625 630 635 640	
ggt acc ttc acc cag cgc cac gca gtt gcc atc gac cca gcg acc gct	1968
Gly Thr Phe Thr Gln Arg His Ala Val Ala Ile Asp Pro Ala Thr Ala	
645 650 655	
gaa gag ttc aac cca ctc cac gag ctt gca cag tcc aag ggc aac aac	2016
Glu Glu Phe Asn Pro Leu His Glu Leu Ala Gln Ser Lys Gly Asn Asn	
660 665 670	
ggt aag ttc ctg gtc tac aac tcc gca ctg acc gag tac gca ggc atg	2064
Gly Lys Phe Leu Val Tyr Asn Ser Ala Leu Thr Glu Tyr Ala Gly Met	
675 680 685	
ggc ttc gag tac ggc tac tcc gta gga aac gaa gac tcc atc gtt gca	2112
Gly Phe Glu Tyr Gly Tyr Ser Val Gly Asn Glu Asp Ser Ile Val Ala	
690 695 700	
tgg gaa gca cag ttc ggc gac ttc gcc aac ggc gct cag acc atc atc	2160
Trp Glu Ala Gln Phe Gly Asp Phe Ala Asn Gly Ala Gln Thr Ile Ile	
705 710 715 720	
gat gag tac gtc tcc tca ggc gaa gct aag tgg ggc cag acc tcc aag	2208

09602740-062300



[illegible]



<400> 562

Val Ile Gly Met Pro His Arg Gly Arg Leu Asn Val Leu Phe Asn Ile  
275 280 285

**Figure 1**

Number of Subjects per Group ( $n$ )	Number of Groups ( $g$ )
100	1
90	2
80	3
70	4
60	5
50	6
40	7
30	8
20	9
10	10
...	...
1	100



Val Gly Lys Pro Leu Ala Ser Ile Phe Asn Glu Phe Glu Gly Gln Met  
 290 295 300  
 Glu Gln Gly Gln Ile Gly Gly Ser Gly Asp Val Lys Tyr His Leu Gly  
 305 310 315 320  
 Ser Glu Gly Gln His Leu Gln Met Phe Gly Asp Gly Glu Ile Lys Val  
 325 330 335  
 Ser Leu Thr Ala Asn Pro Ser His Leu Glu Ala Val Asn Pro Ala Met  
 340 345 350  
 Glu Gly Ile Val Arg Ala Lys Gln Asp Tyr Leu Asp Lys Gly Val Asp  
 355 360 365  
 Gly Lys Thr Val Val Pro Leu Leu Leu His Gly Asp Ala Ala Phe Ala  
 370 375 380  
 Gly Leu Gly Ile Val Pro Glu Thr Ile Asn Leu Ala Lys Leu Arg Gly  
 385 390 395 400  
 Tyr Asp Val Gly Gly Thr Ile His Ile Val Val Asn Asn Gln Ile Gly  
 405 410 415  
 Phe Thr Thr Thr Pro Asp Ser Ser Arg Ser Met His Tyr Ala Thr Asp  
 420 425 430  
 Tyr Ala Lys Ala Phe Gly Cys Pro Val Phe His Val Asn Gly Asp Asp  
 435 440 445  
 Pro Glu Ala Val Val Trp Val Gly Gln Leu Ala Thr Glu Tyr Arg Arg  
 450 455 460  
 Arg Phe Gly Lys Asp Val Phe Ile Asp Leu Val Cys Tyr Arg Leu Arg  
 465 470 475 480  
 Gly His Asn Glu Ala Asp Asp Pro Ser Met Thr Gln Pro Lys Met Tyr  
 485 490 495  
 Glu Leu Ile Thr Gly Arg Glu Thr Val Arg Ala Gln Tyr Thr Glu Asp  
 500 505 510  
 Leu Leu Gly Arg Gly Asp Leu Ser Asn Glu Asp Ala Glu Ala Val Val  
 515 520 525  
 Arg Asp Phe His Asp Gln Met Glu Ser Val Phe Asn Glu Val Lys Glu  
 530 535 540  
 Gly Gly Lys Lys Gln Ala Glu Ala Gln Thr Gly Ile Thr Gly Ser Gln  
 545 550 555 560  
 Lys Leu Pro His Gly Leu Glu Thr Asn Ile Ser Arg Glu Glu Leu Leu  
 565 570 575  
 Glu Leu Gly Gln Ala Phe Ala Asn Thr Pro Glu Gly Phe Asn Tyr His  
 580 585 590  
 Pro Arg Val Ala Pro Val Ala Lys Lys Arg Val Ser Ser Val Thr Glu  
 595 600 605  
 Gly Gly Ile Asp Trp Ala Trp Gly Glu Leu Leu Ala Phe Gly Ser Leu

00E2290-0620960



Figure 1 consists of six histograms arranged horizontally, each representing a different value of the parameter  $\alpha$ . The x-axis for all histograms is 'Number of nodes' ranging from 0 to 100. The y-axis is 'Frequency' ranging from 0 to 100. The histograms are labeled with their respective  $\alpha$  values: 0.0, 0.1, 0.2, 0.3, 0.4, and 0.5. As  $\alpha$  increases, the distribution of node counts shifts towards higher values, indicating a more centralized network structure.



<400>	563															
atc	ctt	gca	gac	gaa	gac	gac	acc	gtc	gac	gtc	ggc	gca	gtc	atc	gcc	48
Ile	Leu	Ala	Asp	Glu	Asp	Asp	Thr	Val	Asp	Val	Gly	Ala	Val	Ile	Ala	
1				5					10					15		
cgc	atc	ggt	gac	gca	aac	gca	gct	gca	gca	cct	gcc	gaa	gag	gaa	gca	96
Arg	Ile	Gly	Asp	Ala	Asn	Ala	Ala	Ala	Ala	Pro	Ala	Glu	Glu	Glu	Ala	
			20					25					30			
gct	cct	gcc	gaa	gag	gaa	gaa	cca	gtt	aag	gaa	gag	cca	aag	aag	gag	144
Ala	Pro	Ala	Glu	Glu	Glu	Glu	Pro	Val	Lys	Glu	Glu	Pro	Lys	Lys	Glu	
		35					40					45				
gca	gct	cct	gaa	gct	cca	gca	gca	act	ggc	gcc	gca	acc	gat	gtg	gaa	192
Ala	Ala	Pro	Glu	Ala	Pro	Ala	Ala	Thr	Gly	Ala	Ala	Thr	Asp	Val	Glu	
	50					55					60					
atg	cca	gaa	ctc	ggc	gaa	tcc	gtc	acc	gaa	ggc	acc	att	acc	cag	tgg	240
Met	Pro	Glu	Leu	Gly	Glu	Ser	Val	Thr	Glu	Gly	Thr	Ile	Thr	Gln	Trp	
65					70					75					80	
ctc	aag	gct	gtc	ggc	gac	acc	gtc	gaa	gta	gac	gaa	cca	ctt	ctt	gag	288
Leu	Lys	Ala	Val	Gly	Asp	Thr	Val	Glu	Val	Asp	Glu	Pro	Leu	Leu	Glu	
				85					90					95		
gtc	tcc	acc	gac	aag	gtc	gac	acc	gaa	atc	cca	tcc	cca	gta	gca	ggc	336
Val	Ser	Thr	Asp	Lys	Val	Asp	Thr	Glu	Ile	Pro	Ser	Pro	Val	Ala	Gly	
			100					105					110			
acc	atc	gtg	gag	atc	ctt	gca	gac	gaa	gac	gac	acc	gtc	gac	gtc	ggc	384
Thr	Ile	Val	Glu	Ile	Leu	Ala	Asp	Glu	Asp	Asp	Thr	Val	Asp	Val	Gly	
		115					120					125				
gca	gtc	atc	gcc	cgc	atc	ggt	gac	gca	aac	gca	gct	gca	gca	cct	gcc	432
Ala	Val	Ile	Ala	Arg	Ile	Gly	Asp	Ala	Asn	Ala	Ala	Ala	Ala	Pro	Ala	
	130					135					140					
gaa	gag	gaa	gca	gct	cct	gcc	gaa	gag	gag	gaa	cca	gtt	aag	gaa	gag	480
Glu	Glu	Glu	Ala	Ala	Pro	Ala	Glu	Glu	Glu	Glu	Pro	Val	Lys	Glu	Glu	
145					150					155					160	
cca	aag	aag	gaa	gag	ccc	aag	aag	gaa	gag	ccc	aag	aag	gaa	gca	gct	528
Pro	Lys	Lys	Glu	Glu	Pro	Lys	Lys	Glu	Glu	Pro	Lys	Lys	Glu	Ala	Ala	
				165					170					175		
act	aca	cct	gct	gcg	gca	tcc	gca	act	gtg	tcc	gct	tct	ggc	gac	aac	576



**060607**



```

<210> 564
<211> 498
<212> PRT
<213> Corynebacterium glutamicum

<400> 564
Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly Ala Val Ile Ala
  1          5          10          15
Arg Ile Gly Asp Ala Asn Ala Ala Ala Ala Pro Ala Glu Glu Glu Ala
          20          25          30
Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu Pro Lys Lys Glu
          35          40          45
Ala Ala Pro Glu Ala Pro Ala Ala Thr Gly Ala Ala Thr Asp Val Glu
  50          55          60
Met Pro Glu Leu Gly Glu Ser Val Thr Glu Gly Thr Ile Thr Gln Trp
  65          70          75          80
Leu Lys Ala Val Gly Asp Thr Val Glu Val Asp Glu Pro Leu Leu Glu
          85          90          95
Val Ser Thr Asp Lys Val Asp Thr Glu Ile Pro Ser Pro Val Ala Gly
          100          105          110
Thr Ile Val Glu Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly
          115          120          125
Ala Val Ile Ala Arg Ile Gly Asp Ala Asn Ala Ala Ala Ala Pro Ala
          130          135          140
Glu Glu Glu Ala Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu
  145          150          155          160
Pro Lys Lys Glu Glu Pro Lys Lys Glu Glu Pro Lys Lys Glu Ala Ala
          165          170          175

```

<400> 564															
Ile	Leu	Ala	Asp	Glu	Asp	Asp	Thr	Val	Asp	Val	Gly	Ala	Val	Ile	Ala
1				5					10					15	
Arg	Ile	Gly	Asp	Ala	Asn	Ala	Ala	Ala	Ala	Pro	Ala	Glu	Glu	Glu	Ala
			20					25					30		
Ala	Pro	Ala	Glu	Glu	Glu	Glu	Pro	Val	Lys	Glu	Glu	Pro	Lys	Lys	Glu
		35					40					45			
Ala	Ala	Pro	Glu	Ala	Pro	Ala	Ala	Thr	Gly	Ala	Ala	Thr	Asp	Val	Glu
	50					55					60				
Met	Pro	Glu	Leu	Gly	Glu	Ser	Val	Thr	Glu	Gly	Thr	Ile	Thr	Gln	Trp
65					70					75					80
Leu	Lys	Ala	Val	Gly	Asp	Thr	Val	Glu	Val	Asp	Glu	Pro	Leu	Leu	Glu
				85					90					95	
Val	Ser	Thr	Asp	Lys	Val	Asp	Thr	Glu	Ile	Pro	Ser	Pro	Val	Ala	Gly
			100					105					110		
Thr	Ile	Val	Glu	Ile	Leu	Ala	Asp	Glu	Asp	Asp	Thr	Val	Asp	Val	Gly
		115					120					125			
Ala	Val	Ile	Ala	Arg	Ile	Gly	Asp	Ala	Asn	Ala	Ala	Ala	Ala	Pro	Ala
	130					135				140					
Glu	Glu	Glu	Ala	Ala	Pro	Ala	Glu	Glu	Glu	Glu	Pro	Val	Lys	Glu	Glu
145					150				155						160
Pro	Lys	Lys	Glu	Glu	Pro	Lys	Lys	Glu	Glu	Pro	Lys	Lys	Glu	Ala	Ala
				165					170					175	







Gln Leu

&lt;210&gt; 565

&lt;211&gt; 1005

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(982)

&lt;223&gt; RXA00782

&lt;400&gt; 565

gggtatggat gcagcggctg atcacgctgc ccatttggcc aatcttgccc agcacggcca 60

gttcgcaacc gctaattagt taaggagcac ctgtttaatc atg tct att ttt ctc 115  
 Met Ser Ile Phe Leu  
 1 5

aat tca gat tcc cgc atc atc att cag ggc att acc ggt tcg gaa ggt 163  
 Asn Ser Asp Ser Arg Ile Ile Ile Gln Gly Ile Thr Gly Ser Glu Gly  
 10 15 20

tca gag cat gcg cgt cga att tta gcc tct ggt gcg aag ctc gtg ggt 211  
 Ser Glu His Ala Arg Arg Ile Leu Ala Ser Gly Ala Lys Leu Val Gly  
 25 30 35

ggc acc aac ccc cgc aaa gct ggg caa acc att ttg atc aat gac act 259  
 Gly Thr Asn Pro Arg Lys Ala Gly Gln Thr Ile Leu Ile Asn Asp Thr  
 40 45 50

gag ttg cct gta ttt ggc act gtt aag gaa gca atg gag gaa acg ggt 307  
 Glu Leu Pro Val Phe Gly Thr Val Lys Glu Ala Met Glu Glu Thr Gly  
 55 60 65

gcg gat gtc acc gta att ttc gtt cct cca gcc ttt gcc aaa gct gcg 355  
 Ala Asp Val Thr Val Ile Phe Val Pro Pro Ala Phe Ala Lys Ala Ala  
 70 75 80 85

atc att gaa gct atc gac gct cac atc cca ctg tgc gtg att att act 403  
 Ile Ile Glu Ala Ile Asp Ala His Ile Pro Leu Cys Val Ile Ile Thr  
 90 95 100

gag ggc atc cca gtg cgt gac gct tct gag gcg tgg gct tat gcc aag 451  
 Glu Gly Ile Pro Val Arg Asp Ala Ser Glu Ala Trp Ala Tyr Ala Lys  
 105 110 115

aag gtg gga cac acc cgc atc att ggc cct aac tgc cca ggc att att 499  
 Lys Val Gly His Thr Arg Ile Ile Gly Pro Asn Cys Pro Gly Ile Ile  
 120 125 130

act ccc ggc gaa tct ctt gcg gga att acg ccg gca aac att gca ggt 547  
 Thr Pro Gly Glu Ser Leu Ala Gly Ile Thr Pro Ala Asn Ile Ala Gly  
 135 140 145

tcc ggc ccg atc ggg ttg atc tca aag tcg gga aca ctg act tat cag 595  
 Ser Gly Pro Ile Gly Leu Ile Ser Lys Ser Gly Thr Leu Thr Tyr Gln  
 150 155 160 165

09602740-062300



atg atg tac gaa ctt tca gat att ggc att tct acg gcg att ggt att 643  
 Met Met Tyr Glu Leu Ser Asp Ile Gly Ile Ser Thr Ala Ile Gly Ile  
 170 175 180  
  
 ggc ggt gac cca atc atc ggt aca acc cat atc gac gct ctg gag gcc 691  
 Gly Gly Asp Pro Ile Ile Gly Thr Thr His Ile Asp Ala Leu Glu Ala  
 185 190 195  
  
 ttt gaa gct gat cct gag acc aag gca atc gtc atg atc ggt gag atc 739  
 Phe Glu Ala Asp Pro Glu Thr Lys Ala Ile Val Met Ile Gly Glu Ile  
 200 205 210  
  
 ggt gga gat gca gag gaa cgc gct gct gac ttc att tct aag cac gtg 787  
 Gly Gly Asp Ala Glu Glu Arg Ala Ala Asp Phe Ile Ser Lys His Val  
 215 220 225  
  
 aca aaa cca gtt gtg ggt tac gtg gca ggc ttt acc gcc cct gaa gga 835  
 Thr Lys Pro Val Val Gly Tyr Val Ala Gly Phe Thr Ala Pro Glu Gly  
 230 235 240 245  
  
 aag acc atg ggg cat gct ggc gcc atc gtg aca ggt tca gaa ggc act 883  
 Lys Thr Met Gly His Ala Gly Ala Ile Val Thr Gly Ser Glu Gly Thr  
 250 255 260  
  
 gcg cga gca aag aag cat gca ttg gag gcc gtg ggt gtt cgc gtg gga 931  
 Ala Arg Ala Lys Lys His Ala Leu Glu Ala Val Gly Val Arg Val Gly  
 265 270 275  
  
 aca act ccg agt gaa acc gcg aag ctt atg cgt gag gta gtt gca gct 979  
 Thr Thr Pro Ser Glu Thr Ala Lys Leu Met Arg Glu Val Val Ala Ala  
 280 285 290  
  
 ttg taactaacag gccacagatc tta 1005  
 Leu

&lt;210&gt; 566

&lt;211&gt; 294

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 566

Met Ser Ile Phe Leu Asn Ser Asp Ser Arg Ile Ile Ile Gln Gly Ile  
 1 5 10 15  
  
 Thr Gly Ser Glu Gly Ser Glu His Ala Arg Arg Ile Leu Ala Ser Gly  
 20 25 30  
  
 Ala Lys Leu Val Gly Gly Thr Asn Pro Arg Lys Ala Gly Gln Thr Ile  
 35 40 45  
  
 Leu Ile Asn Asp Thr Glu Leu Pro Val Phe Gly Thr Val Lys Glu Ala  
 50 55 60  
  
 Met Glu Glu Thr Gly Ala Asp Val Thr Val Ile Phe Val Pro Pro Ala  
 65 70 75 80  
  
 Phe Ala Lys Ala Ala Ile Ile Glu Ala Ile Asp Ala His Ile Pro Leu  
 85 90 95

09602740-062360



```
<400> 567
aaagttccca aggggtgagg gctgagcacc acggatccaa ttttgttgca atttgcaaag 60

tttacagtgt tagacttcac aatacgatca tattggtgag ttg aaa cac tta ctt      115
                                         Leu Lys His Leu Leu
                                           1                               5

tta cgg gaa gac ttt gtt aaa gac gca gaa ggc tct aag cat ggg ccg      163
Leu Arg Glu Asp Phe Val Lys Asp Ala Glu Gly Ser Lys His Gly Pro
                10                        15                      20
```



[illegible]



Leu Lys Ala Lys Lys Asn Asp Leu Asn Tyr Val Lys Leu Asp Gly Ser  
                   265                                  270                                  275  
 gtg ggc atc att ggc aat ggt gca ggt ttg gtg atg tcc acg ttg gat 979  
 Val Gly Ile Ile Gly Asn Gly Ala Gly Leu Val Met Ser Thr Leu Asp  
                   280                                  285                                  290  
 atc gtg gct gca gct ggt gaa cgc cat ggt ggg cag cgc ccc gcg aac 1027  
 Ile Val Ala Ala Ala Gly Glu Arg His Gly Gly Gln Arg Pro Ala Asn  
                   295                                  300                                  305  
 ttc cta gac att ggt ggc gga gca tca gct gaa tcg atg gct gct ggt 1075  
 Phe Leu Asp Ile Gly Gly Gly Ala Ser Ala Glu Ser Met Ala Ala Gly  
                   310                                  315                                  320                                  325  
 ctc gat gtg atc ctt ggg gat agc cag gta cgc agt gtg ttt gtg aat 1123  
 Leu Asp Val Ile Leu Gly Asp Ser Gln Val Arg Ser Val Phe Val Asn  
                   330                                  335                                  340  
 gtg ttt ggt ggc atc acc gcg tgt gat gtg gtg gca aag gga atc gtt 1171  
 Val Phe Gly Gly Ile Thr Ala Cys Asp Val Val Ala Lys Gly Ile Val  
                   345                                  350                                  355  
 gga gct ttg gat gtg ctc ggc gat caa gca acg aag cct ctt gtg gtg 1219  
 Gly Ala Leu Asp Val Leu Gly Asp Gln Ala Thr Lys Pro Leu Val Val  
                   360                                  365                                  370  
 cgc ctt gat ggc aac aac gtg gtg gaa ggc aga cga atc ctc gcg gaa 1267  
 Arg Leu Asp Gly Asn Asn Val Val Glu Gly Arg Arg Ile Leu Ala Glu  
                   375                                  380                                  385  
 tat aac cac cct ttg gtc acc gtt gtg gag ggt atg gat gca gcg gct 1315  
 Tyr Asn His Pro Leu Val Thr Val Val Glu Gly Met Asp Ala Ala Ala  
                   390                                  395                                  400                                  405  
 gat cac gct gcc cat ttg gcc aat ctt gcc cag cac ggc cag ttc gca 1363  
 Asp His Ala Ala His Leu Ala Asn Leu Ala Gln His Gly Gln Phe Ala  
                   410                                  415                                  420  
 acc gct aat tagttaagga gcacctgttt aat 1395  
 Thr Ala Asn

&lt;210&gt; 568

&lt;211&gt; 424

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 568

Leu Lys His Leu Leu Leu Arg Glu Asp Phe Val Lys Asp Ala Glu Gly  
   1                  5                                  10                                  15  
 Ser Lys His Gly Pro Glu Met Glu Leu Ala Val Asp Leu Phe Glu Tyr  
                   20                                  25                                  30  
 Gln Ala Arg Asp Leu Phe Glu Thr His Gly Val Pro Val Leu Lys Gly  
                   35                                  40                                  45  
 Ile Val Ala Ser Thr Pro Glu Ala Ala Arg Lys Ala Ala Glu Glu Ile  
                   50                                  55                                  60

002290"04220960



Gly Gly Leu Thr Val Val Lys Ala Gln Val Lys Val Gly Gly Arg Gly  
 65 70 75 80  
 Lys Ala Gly Gly Val Arg Val Ala Pro Thr Ser Ala Gln Ala Phe Asp  
 85 90 95  
 Ala Ala Asp Ala Ile Leu Gly Met Asp Ile Lys Gly His Thr Val Asn  
 100 105 110  
 Gln Val Met Val Ala Gln Gly Ala Asp Ile Ala Glu Glu Tyr Tyr Phe  
 115 120 125  
 Ser Ile Leu Leu Asp Arg Ala Asn Arg Ser Tyr Leu Ala Met Cys Ser  
 130 135 140  
 Val Glu Gly Gly Met Glu Ile Glu Ile Leu Ala Lys Glu Lys Pro Glu  
 145 150 155 160  
 Ala Leu Ala Lys Val Glu Val Asp Pro Leu Thr Gly Ile Asp Glu Asp  
 165 170 175  
 Lys Ala Arg Glu Ile Val Thr Ala Ala Gly Phe Glu Thr Glu Val Ala  
 180 185 190  
 Glu Lys Val Ile Pro Val Leu Ile Lys Ile Trp Gln Val Tyr Tyr Glu  
 195 200 205  
 Glu Glu Ala Thr Leu Val Glu Val Asn Pro Leu Val Leu Thr Asp Asp  
 210 215 220  
 Gly Asp Val Ile Ala Leu Asp Gly Lys Ile Thr Leu Asp Asp Asn Ala  
 225 230 235 240  
 Asp Phe Arg His Asp Asn Arg Gly Ala Leu Ala Glu Ser Ala Gly Gly  
 245 250 255  
 Leu Asp Ile Leu Glu Leu Lys Ala Lys Lys Asn Asp Leu Asn Tyr Val  
 260 265 270  
 Lys Leu Asp Gly Ser Val Gly Ile Ile Gly Asn Gly Ala Gly Leu Val  
 275 280 285  
 Met Ser Thr Leu Asp Ile Val Ala Ala Ala Gly Glu Arg His Gly Gly  
 290 295 300  
 Gln Arg Pro Ala Asn Phe Leu Asp Ile Gly Gly Gly Ala Ser Ala Glu  
 305 310 315 320  
 Ser Met Ala Ala Gly Leu Asp Val Ile Leu Gly Asp Ser Gln Val Arg  
 325 330 335  
 Ser Val Phe Val Asn Val Phe Gly Gly Ile Thr Ala Cys Asp Val Val  
 340 345 350  
 Ala Lys Gly Ile Val Gly Ala Leu Asp Val Leu Gly Asp Gln Ala Thr  
 355 360 365  
 Lys Pro Leu Val Val Arg Leu Asp Gly Asn Asn Val Val Glu Gly Arg  
 370 375 380

002290" 0420960



His Gly Gln Phe Ala Thr Ala Asn  
420

<213> *Corynebacterium glutamicum*

<223> RXN01695

tatggccaac acttgcatte gggtgctggc gatcatttat gagatgacgc cttgtgttgg 60

aag aac gca ccg agg att acc gat gag gca gat gta gtt ctc att ggt 163  
Lys Asn Ala Pro Arg Ile Thr Asp Glu Ala Asp Val Val Leu Ile Gly  
10 15 20

gcc ggt atc atg agc tcc acg ctg ggt gca atg ctg cgt cag ctg gag 211  
Ala Gly Ile Met Ser Ser Thr Leu Gly Ala Met Leu Arg Gln Leu Glu  
25 30 35

cca agc tgg act cag atc gtc ttc gag cgt ttg gat gga ccg gca caa 259  
Pro Ser Trp Thr Gln Ile Val Phe Glu Arg Leu Asp Gly Pro Ala Gln  
40 45 50

gag tcg tcc tcc ccg tgg aac aat gca gga acc ggc cac tct gct cta 307  
Glu Ser Ser Ser Pro Trp Asn Asn Ala Gly Thr Gly His Ser Ala Leu  
55 60 65

tgc	gag	ctg	aac	tac	acc	cca	gag	gtt	aag	ggc	aag	gtt	gaa	att	gcc	355
Cys	Glu	Leu	Asn	Tyr	Thr	Pro	Glu	Val	Lys	Gly	Lys	Val	Glu	Ile	Ala	
70					75					80					85	

aag gct gta gga atc aac gag aag ttc cag gtt tcc cgt cag ttc tgg 403  
Lys Ala Val Gly Ile Asn Glu Lys Phe Gln Val Ser Arg Gln Phe Trp  
90 95 100

tct cac ctc gtt gaa gag gga gtg ctg tct gat cct aag gaa ttc atc 451  
Ser His Leu Val Glu Glu Gly Val Leu Ser Asp Pro Lys Glu Phe Ile  
105 110 115

aac cct gtt cct cac gta tct ttc ggc cag ggc gca gat cag gtt gca 499  
Asn Pro Val Pro His Val Ser Phe Gly Gln Gly Ala Asp Gln Val Ala  
120 125 130

tac atc aag gct cgc tac gaa gct ttg aag gat cac cca ctc ttc cag 547  
Tyr Ile Lys Ala Arg Tyr Glu Ala Leu Lys Asp His Pro Leu Phe Gln

Figure 1 consists of seven histograms, labeled (a) through (g), each representing the distribution of the number of non-zero elements in the rows of the matrix  $A_k$  for  $k = 1, 2, \dots, 7$ . The x-axis for all histograms is 'Number of non-zero elements' ranging from 0 to 10. The y-axis is 'Frequency' ranging from 0 to 10. The distributions are as follows:

- (a)  $k=1$ : All frequencies are 1 for values 0 through 10.
- (b)  $k=2$ : All frequencies are 1 for values 0 through 10.
- (c)  $k=3$ : All frequencies are 1 for values 0 through 10.
- (d)  $k=4$ : All frequencies are 1 for values 0 through 10.
- (e)  $k=5$ : All frequencies are 1 for values 0 through 10.
- (f)  $k=6$ : All frequencies are 1 for values 0 through 10.
- (g)  $k=7$ : All frequencies are 1 for values 0 through 10.



[illegible]



aag cct gca gga ttc cct aag ttc ggt tcc ctg gaa ttc ggc acc acc 1363  
Lys Pro Ala Gly Phe Pro Lys Phe Gly Ser Leu Glu Phe Gly Thr Thr  
410 415 420

ttg	atc	aac	aac	tcc	gaa	ggc	acc	atc	gcc	gga	ttg	ctc	ggt	gct	tcc	1411
Leu	Ile	Asn	Asn	Ser	Glu	Gly	Thr	Ile	Ala	Gly	Leu	Leu	Gly	Ala	Ser	
			425					430					435			

cct gga gca tcc atc gca cct tcc gca atg atc gag ctg ctt gag cgt 1459  
Pro Gly Ala Ser Ile Ala Pro Ser Ala Met Ile Glu Leu Leu Glu Arg  
440 445 450

tgc	ttc	ggg	gac	cgc	atg	atc	gag	tgg	ggc	gac	aag	ctg	aag	gac	atg	1507
Cys	Phe	Gly	Asp	Arg	Met	Ile	Glu	Trp	Gly	Asp	Lys	Leu	Lys	Asp	Met	
	455					460					465					

atc cct tcc tac ggc aag aag ctt gct tcc gag cca gca ctg ttt gag 1555  
Ile Pro Ser Tyr Gly Lys Lys Leu Ala Ser Glu Pro Ala Leu Phe Glu  
470 475 480 485

cag cag tgg gca cgc acc cag aag acc ctg aag ctt gag gaa gcc 1600  
Gln Gln Trp Ala Arg Thr Gln Lys Thr Leu Lys Leu Glu Glu Ala  
490 495 500

taaatcttct aactgctttc ttt 1623

<210> 570

<211> 500

&lt;212&gt; PRT

<213> Corynebacterium glutamicum

<400> 570

Met Ser Asp Ser Pro Lys Asn Ala Pro Arg Ile Thr Asp Glu Ala Asp  
1 5 10 15

Val Val Leu Ile Gly Ala Gly Ile Met Ser Ser Thr Leu Gly Ala Met  
20 25 30

Leu Arg Gln Leu Glu Pro Ser Trp Thr Gln Ile Val Phe Glu Arg Leu  
35 40 45

Asp Gly Pro Ala Gln Glu Ser Ser Ser Pro Trp Asn Asn Ala Gly Thr  
50 55 60

Gly His Ser Ala Leu Cys Glu Leu Asn Tyr Thr Pro Glu Val Lys Gly  
65 70 75 80

Lys Val Glu Ile Ala Lys Ala Val Gly Ile Asn Glu Lys Phe Gln Val  
85 90 95

Ser Arg Gln Phe Trp Ser His Leu Val Glu Glu Gly Val Leu Ser Asp  
100 105 110

Pro Lys Glu Phe Ile Asn Pro Val Pro His Val Ser Phe Gly Gln Gly  
115 120 125

[illegible]



Ala Asp Gln Val Ala Tyr Ile Lys Ala Arg Tyr Glu Ala Leu Lys Asp  
 130 135 140  
 His Pro Leu Phe Gln Gly Met Thr Tyr Ala Asp Asp Glu Ala Thr Phe  
 145 150 155 160  
 Thr Glu Lys Leu Pro Leu Met Ala Lys Gly Arg Asp Phe Ser Asp Pro  
 165 170 175  
 Val Ala Ile Ser Trp Ile Asp Glu Gly Thr Asp Ile Asn Tyr Gly Ala  
 180 185 190  
 Gln Thr Lys Gln Tyr Leu Asp Ala Ala Glu Val Glu Gly Thr Glu Ile  
 195 200 205  
 Arg Tyr Gly His Glu Val Lys Ser Ile Lys Ala Asp Gly Ala Lys Trp  
 210 215 220  
 Ile Val Thr Val Lys Asn Val His Thr Gly Asp Thr Lys Thr Ile Lys  
 225 230 235 240  
 Ala Asn Phe Val Phe Val Gly Ala Gly Gly Tyr Ala Leu Asp Leu Leu  
 245 250 255  
 Arg Ser Ala Gly Ile Pro Gln Val Lys Gly Phe Ala Gly Phe Pro Val  
 260 265 270  
 Ser Gly Leu Trp Leu Arg Cys Thr Asn Glu Glu Leu Ile Glu Gln His  
 275 280 285  
 Ala Ala Lys Val Tyr Gly Lys Ala Ser Val Gly Ala Pro Pro Met Ser  
 290 295 300  
 Val Pro His Leu Asp Thr Arg Val Ile Glu Gly Glu Lys Gly Leu Leu  
 305 310 315 320  
 Phe Gly Pro Tyr Gly Gly Trp Thr Pro Lys Phe Leu Lys Glu Gly Ser  
 325 330 335  
 Tyr Leu Asp Leu Phe Lys Ser Ile Arg Pro Asp Asn Ile Pro Ser Tyr  
 340 345 350  
 Leu Gly Val Ala Ala Gln Glu Phe Asp Leu Thr Lys Tyr Leu Val Thr  
 355 360 365  
 Glu Val Leu Lys Asp Gln Asp Lys Arg Met Asp Ala Leu Arg Glu Tyr  
 370 375 380  
 Met Pro Glu Ala Gln Asn Gly Asp Trp Glu Thr Ile Val Ala Gly Gln  
 385 390 395 400  
 Arg Val Gln Val Ile Lys Pro Ala Gly Phe Pro Lys Phe Gly Ser Leu  
 405 410 415  
 Glu Phe Gly Thr Thr Leu Ile Asn Asn Ser Glu Gly Thr Ile Ala Gly  
 420 425 430  
 Leu Leu Gly Ala Ser Pro Gly Ala Ser Ile Ala Pro Ser Ala Met Ile  
 435 440 445

002290" 0420960



<400> 571																
tatggccaac acttgcatc gggtgctggc gatcatttat gagatgacgc cttgtgttgg																60
tgttcggcag agaactcgcg gagataaaag gaagttgaac																115
Met Ser Asp Ser Pro																15
aag aac gca ccg agg att acc gat gag gca gat gta gtt ctc att ggt																163
Lys Asn Ala Pro Arg Ile Thr Asp Glu Ala Asp Val Val Leu Ile Gly																20
gcc ggt atc atg agc tcc acg ctg ggt gca atg ctg cgt cag ctg gag																211
Ala Gly Ile Met Ser Ser Thr Leu Gly Ala Met Leu Arg Gln Leu Glu																25
cca agc tgg act cag atc gtc ttc gag cgt ttg gat gga ccg gca caa																259
Pro Ser Trp Thr Gln Ile Val Phe Glu Arg Leu Asp Gly Pro Ala Gln																40
gag tcg tcc tcc ccg tgg aac aat gca gga acc ggc cac tct gct cta																307
Glu Ser Ser Ser Pro Trp Asn Asn Ala Gly Thr Gly His Ser Ala Leu																55
tgc gag ctg aac tac acc cca gag gtt aag ggc aag gtt gaa att gcc																355
Cys Glu Leu Asn Tyr Thr Pro Glu Val Lys Gly Lys Val Glu Ile Ala																70
aag gct gta gga atc aac gag aag ttc cag gtt tcc cgt cag ttc tgg																403
Lys Ala Val Gly Ile Asn Glu Lys Phe Gln Val Ser Arg Gln Phe Trp																90
tct cac ctc gtt gaa gag gga gtg ctg tct gat cct aag gaa ttc atc																451
Ser His Leu Val Glu Glu Gly Val Leu Ser Asp Pro Lys Glu Phe Ile																105
aac cct gtt cct cac gta tct ttc ggc cag ggc gca gat cag gtt gca																499
Asn Pro Val Pro His Val Ser Phe Gly Gln Gly Ala Asp Gln Val Ala																120

**THE**  
**WORLD**  
**OF**  
**THE**  
**FUTURE**



Val Val Leu Ile Gly Ala Gly Ile Met Ser Ser Thr Leu Gly Ala Met  
20 25 30

[illegible]



Leu Arg Gln Leu Glu Pro Ser Trp Thr Gln Ile Val Phe Glu Arg Leu  
                   35                                  40                                  45  
 Asp Gly Pro Ala Gln Glu Ser Ser Ser Pro Trp Asn Asn Ala Gly Thr  
           50  55                                  60  
 Gly His Ser Ala Leu Cys Glu Leu Asn Tyr Thr Pro Glu Val Lys Gly  
   65  70                                  75                                  80  
 Lys Val Glu Ile Ala Lys Ala Val Gly Ile Asn Glu Lys Phe Gln Val  
                                   85                                  90                                  95  
 Ser Arg Gln Phe Trp Ser His Leu Val Glu Glu Gly Val Leu Ser Asp  
                   100                                  105                                  110  
 Pro Lys Glu Phe Ile Asn Pro Val Pro His Val Ser Phe Gly Gln Gly  
           115                                  120                                  125  
 Ala Asp Gln Val Ala Tyr Ile Lys Ala Arg Tyr Glu Ala Leu Lys Asp  
           130                                  135                                  140  
 His Pro Leu Phe Gln Gly Met Thr Tyr Ala Asp Asp Glu Ala Thr Phe  
   145                                  150                                  155                                  160  
 Thr Glu Lys Leu Pro Leu Met Ala Lys Gly Arg Asp Phe Ser Asp Pro  
                   165                                  170                                  175  
 Val Ala Ile Ser Trp Ile Asp Glu Gly Thr Asp Ile Asn Tyr Gly Ala  
                   180                                  185                                  190  
 Gln Thr Lys Gln Tyr Leu Asp Ala Ala Glu Val Glu Gly Thr Glu Ile  
           195                                  200                                  205  
 Arg Tyr Gly His Glu Val Lys Ser Ile Lys Ala Asp Gly Ala Lys Trp  
           210                                  215                                  220  
 Ile Val Thr Val Lys Asn Val His Thr Gly Asp Thr Lys Thr Ile Lys  
   225                                  230                                  235                                  240  
 Ala Asn Phe Val Phe Val Gly Ala Gly Gly Tyr Ala Leu Asp Leu Leu  
                   245                                  250                                  255  
 Arg Ser Ala Gly Ile Pro Gln Val Lys Gly Phe Ala Gly Phe Pro Val  
                   260                                  265                                  270  
 Ser Gly Leu Trp Leu Arg Cys Thr Asn Glu Glu Leu Ile Glu Gln His  
           275                                  280                                  285  
 Ala Ala Lys Val Tyr Gly Lys Ala Ser Val Gly Ala Pro Pro Met Ser  
           290                                  295                                  300  
 Val Pro His Leu Asp Thr Arg Val Ile  
   305                                  310

&lt;210&gt; 573

&lt;211&gt; 233

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

00E290" 0420960



&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(210)

&lt;223&gt; FRXA01695

&lt;400&gt; 573

gcc gga ttg ctc ggt gct tcc cct gga gca tcc atc gca cct tcc gca 48  
 Ala Gly Leu Leu Gly Ala Ser Pro Gly Ala Ser Ile Ala Pro Ser Ala  
 1 5 10 15

atg atc gag ctg ctt gag cgt tgc ttc ggt gac cgc atg atc gag tgg 96  
 Met Ile Glu Leu Leu Glu Arg Cys Phe Gly Asp Arg Met Ile Glu Trp  
 20 25 30

ggc gac aag ctg aag gac atg atc cct tcc tac ggc aag aag ctt gct 144  
 Gly Asp Lys Leu Lys Asp Met Ile Pro Ser Tyr Gly Lys Lys Leu Ala  
 35 40 45

tcc gag cca gca ctg ttt gag cag cag tgg gca cgc acc cag aag acc 192  
 Ser Glu Pro Ala Leu Phe Glu Gln Gln Trp Ala Arg Thr Gln Lys Thr  
 50 55 60

ctg aag ctt gag gaa gcc taaatcttct aactgctttc ttt 233  
 Leu Lys Leu Glu Glu Ala  
 65 70

&lt;210&gt; 574

&lt;211&gt; 70

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 574

Ala Gly Leu Leu Gly Ala Ser Pro Gly Ala Ser Ile Ala Pro Ser Ala  
 1 5 10 15

Met Ile Glu Leu Leu Glu Arg Cys Phe Gly Asp Arg Met Ile Glu Trp  
 20 25 30

Gly Asp Lys Leu Lys Asp Met Ile Pro Ser Tyr Gly Lys Lys Leu Ala  
 35 40 45

Ser Glu Pro Ala Leu Phe Glu Gln Gln Trp Ala Arg Thr Gln Lys Thr  
 50 55 60

Leu Lys Leu Glu Glu Ala  
 65 70

&lt;210&gt; 575

&lt;211&gt; 1063

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1063)

&lt;223&gt; RXA00290

&lt;400&gt; 575

agctacagat ttagctagtg tttttgttcc agaaccctaa atgaggttct acccttaaca 60

09602740.062300



00509070600



gac	agc	cgt	gag	gat	ctt	tcc	cca	ggt	aag	gct	gct	ctt	gca	gag	aag	835
Asp	Ser	Arg	Glu	Asp	Leu	Ser	Pro	Val	Lys	Ala	Ala	Leu	Ala	Glu	Lys	
230					235					240					245	
acc	aac	cct	cgt	ggc	atc	agc	ggt	ggc	atc	aat	gag	gct	ttc	acc	ggc	883
Thr	Asn	Pro	Arg	Gly	Ile	Ser	Gly	Gly	Ile	Asn	Glu	Ala	Phe	Thr	Gly	
				250					255					260		
gcg	gac	ctg	ttc	att	ggc	gtg	tcc	ggc	ggc	aac	atc	ggc	gag	gac	gct	931
Ala	Asp	Leu	Phe	Ile	Gly	Val	Ser	Gly	Gly	Asn	Ile	Gly	Glu	Asp	Ala	
			265					270					275			
ctc	aaa	ctc	atg	gcc	ccg	gag	cca	atc	ctg	ttc	acc	ctg	gcg	aac	cca	979
Leu	Lys	Leu	Met	Ala	Pro	Glu	Pro	Ile	Leu	Phe	Thr	Leu	Ala	Asn	Pro	
		280					285					290				
acc	cca	gag	atc	gat	cct	gag	ctg	tct	cag	aag	tac	ggc	gcc	atc	gtc	1027
Thr	Pro	Glu	Ile	Asp	Pro	Glu	Leu	Ser	Gln	Lys	Tyr	Gly	Ala	Ile	Val	
	295					300					305					
gcg	acc	ggg	ccg	gtc	ttg	acc	tgc	cta	acc	aga	tca					1063
Ala	Thr	Gly	Pro	Val	Leu	Thr	Cys	Leu	Thr	Arg	Ser					
310					315					320						
<210> 576																
<211> 321																
<212> PRT																
<213> Corynebacterium glutamicum																
<400> 576																
Met	Thr	Ile	Asp	Leu	Gln	Arg	Ser	Thr	Gln	Asn	Leu	Thr	His	Glu	Glu	
1				5					10					15		
Ile	Phe	Glu	Ala	His	Glu	Gly	Gly	Lys	Leu	Ser	Ile	Ser	Ser	Thr	Arg	
			20					25					30			
Pro	Leu	Arg	Asp	Met	Arg	Asp	Leu	Ser	Leu	Ala	Tyr	Thr	Pro	Gly	Val	
		35					40					45				
Ala	Gln	Val	Cys	Glu	Ala	Ile	Lys	Glu	Asp	Pro	Glu	Val	Ala	Arg	Thr	
	50					55					60					
His	Thr	Gly	Ile	Gly	Asn	Thr	Val	Ala	Val	Ile	Ser	Asp	Gly	Thr	Ala	
	65				70					75					80	
Val	Leu	Gly	Leu	Gly	Asp	Ile	Gly	Pro	Gln	Ala	Ser	Leu	Pro	Val	Met	
				85					90					95		
Glu	Gly	Lys	Ala	Gln	Leu	Phe	Ser	Ser	Phe	Ala	Gly	Leu	Lys	Ala	Ile	
			100					105					110			
Pro	Ile	Val	Leu	Asp	Val	His	Asp	Val	Asp	Ala	Leu	Val	Glu	Thr	Ile	
		115					120					125				
Ala	Ala	Ile	Ala	Pro	Ser	Phe	Gly	Ala	Ile	Asn	Leu	Glu	Asp	Ile	Ser	
	130					135					140					
Ala	Pro	Arg	Cys	Phe	Glu	Val	Glu	Arg	Arg	Leu	Ile	Glu	Arg	Leu	Asp	

[illegible]



Ile Pro Val Met His Asp Asp Gln His Gly Thr Ala Val Val Ile Leu  
 165 170 175  
 Ala Ala Leu Arg Asn Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp  
 180 185 190  
 Leu Lys Ile Val Ile Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val  
 195 200 205  
 Asp Met Leu Thr Asn Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser  
 210 215 220  
 Arg Gly Ile Ile His Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala  
 225 230 235 240  
 Ala Leu Ala Glu Lys Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn  
 245 250 255  
 Glu Ala Phe Thr Gly Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn  
 260 265 270  
 Ile Gly Glu Asp Ala Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe  
 275 280 285  
 Thr Leu Ala Asn Pro Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys  
 290 295 300  
 Tyr Gly Ala Ile Val Ala Thr Gly Pro Val Leu Thr Cys Leu Thr Arg  
 305 310 315 320  
 Ser

<210> 577  
 <211> 1347  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1324)  
 <223> RXN01048

<400> 577  
 agctacagat ttagctagtgt tttttgttcc agaaccctaa atgaggttct acccttaaca 60  
 gagcttcccg caaaaacacc gattaacaag gctaaatgat atg acc atc gac ctg 115  
 Met Thr Ile Asp Leu  
 1 5  
 cag cgt tcc acc caa aac ctc acc cat gag gaa atc ttc gag gca cac 163  
 Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu Ile Phe Glu Ala His  
 10 15 20  
 gag ggc gga aag ctc tcc att agt tcc act cgt ccg ctc cgc gac atg 211  
 Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg Pro Leu Arg Asp Met  
 25 30 35  
 cgc gat ctt tcc ctt gct tac acc cct ggt gtt gct cag gtt tgt gaa 259  
 Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val Ala Gln Val Cys Glu

0002290" 07220960



069874-063000



acc cca gag atc gat cct gag ctg tct cag aag tac ggc gcc atc gtc 1027  
 Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys Tyr Gly Ala Ile Val  
 295 300 305

gcg acc ggg cgc tct gac ctg cct aac cag atc aac aac gtg ctg gcg 1075  
 Ala Thr Gly Arg Ser Asp Leu Pro Asn Gln Ile Asn Asn Val Leu Ala  
 310 315 320 325

ttc cca gga att ttc gcc ggc gct ctc gca gcc aag gct aag aag atc 1123  
 Phe Pro Gly Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile  
 330 335 340

acc ccc gag atg aag ctc gcc gct cag agg caa tcg cag aca tcg cag 1171  
 Thr Pro Glu Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln  
 345 350 355

ctg agg acc tcg agg tcg gcc gca tcg tgc cta ccg ccc tgg atc ccc 1219  
 Leu Arg Thr Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro  
 360 365 370

gcg ttg ccc caa cag tca agg cag ctg tcc agg ccg tcg cca aag cgc 1267  
 Ala Leu Pro Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg  
 375 380 385

aaa acg ctt aaa aat ttg ctt atc gac gcc tcc ctc ccc gtc gag gcg 1315  
 Lys Thr Leu Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala  
 390 395 400 405

cca ata ttt taagagcaaa cttgaggccc aca 1347  
 Pro Ile Phe

&lt;210&gt; 578

&lt;211&gt; 408

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 578

Met Thr Ile Asp Leu Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu  
 1 5 10 15

Ile Phe Glu Ala His Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg  
 20 25 30

Pro Leu Arg Asp Met Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val  
 35 40 45

Ala Gln Val Cys Glu Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr  
 50 55 60

His Thr Gly Ile Gly Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala  
 65 70 75 80

Val Leu Gly Leu Gly Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met  
 85 90 95

Glu Gly Lys Ala Gln Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile  
 100 105 110

09602740.062300



Pro Ile Val Leu Asp Val His Asp Val Asp Ala Leu Val Glu Thr Ile  
 115 120 125  
 Ala Ala Ile Ala Pro Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser  
 130 135 140  
 Ala Pro Arg Cys Phe Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp  
 145 150 155 160  
 Ile Pro Val Met His Asp Asp Gln His Gly Thr Ala Val Val Ile Leu  
 165 170 175  
 Ala Ala Leu Arg Asn Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp  
 180 185 190  
 Leu Lys Ile Val Ile Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val  
 195 200 205  
 Asp Met Leu Thr Asn Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser  
 210 215 220  
 Arg Gly Ile Ile His Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala  
 225 230 235 240  
 Ala Leu Ala Glu Lys Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn  
 245 250 255  
 Glu Ala Phe Thr Gly Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn  
 260 265 270  
 Ile Gly Glu Asp Ala Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe  
 275 280 285  
 Thr Leu Ala Asn Pro Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys  
 290 295 300  
 Tyr Gly Ala Ile Val Ala Thr Gly Arg Ser Asp Leu Pro Asn Gln Ile  
 305 310 315 320  
 Asn Asn Val Leu Ala Phe Pro Gly Ile Phe Ala Gly Ala Leu Ala Ala  
 325 330 335  
 Lys Ala Lys Lys Ile Thr Pro Glu Met Lys Leu Ala Ala Gln Arg Gln  
 340 345 350  
 Ser Gln Thr Ser Gln Leu Arg Thr Ser Arg Ser Ala Ala Ser Cys Leu  
 355 360 365  
 Pro Pro Trp Ile Pro Ala Leu Pro Gln Gln Ser Arg Gln Leu Ser Arg  
 370 375 380  
 Pro Ser Pro Lys Arg Lys Thr Leu Lys Asn Leu Leu Ile Asp Ala Ser  
 385 390 395 400  
 Leu Pro Val Glu Ala Pro Ile Phe  
 405

<210> 579  
 <211> 311  
 <212> DNA

00602740.062300



<213> Corynebacterium glutamicum

$\langle 220 \rangle$

<221> CDS

<222> (1) . . (288)

<223> FRXA01048

<400> 579

cgc tct gac ttg cct aac cag atc aac aac gtg ctg gcg ttc cca gga 48  
 Arg Ser Asp Leu Pro Asn Gln Ile Asn Asn Val Leu Ala Phe Pro Gly  
 1 5 10 15

att ttc gcc ggc gct ctc gca gcc aag gct aag aag atc acc ccc gag 96  
Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile Thr Pro Glu  
20 25 30

atg aag ctc gcc gct cag agg caa tcg cag aca tcg cag ctg agg acc 144  
Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln Leu Arg Thr  
35 40 45

tcg agg tcg gcc gca tcg tgc cta ccg ccc tgg atc ccc gcg ttg ccc 192  
Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro Ala Leu Pro  
50 55 60

caa cag tca agg cag ctg tcc agg ccg tcg cca aag cgc aaa acg ctt 240  
Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg Lys Thr Leu  
65 70 75 80

aaa aat ttg ctt atc gac gcc tcc ctc ccc gtc gag gcg cca ata ttt 288  
Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala Pro Ile Phe  
85 90 95

taagaqcaaa cttgaggccc aca 311

<210> 580

<211> 96

&lt;212&gt; PRT

<213> Corynebacterium glutamicum

<400> 580

Arg Ser Asp Leu Pro Asn Gln Ile Asn Asn Val Leu Ala Phe Pro Gly  
1 5 10 15

Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile Thr Pro Glu  
20 25 30

Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln Leu Arg Thr  
35 40 45

Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro Ala Leu Pro  
50 55 60

Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg Lys Thr Leu  
65 70 75 80

Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala Pro Ile Phe  
85 90 95

060907Z JUL 80



```
<210> 581
<211> 1063
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(1063)
<223> FRXA00290
```

<400> 581																
agctacagat ttagctagtg tttttgttcc agaaccctaa atgaggttct acccttaaca 60																
gagcttcccg caaaaacacc gattaacaag gctaaatgat atg acc atc gac ctg 115																
Met Thr Ile Asp Leu 5																
cag cgt tcc acc caa aac ctc acc cat gag gaa atc ttc gag gca cac 163																
Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu Ile Phe Glu Ala His 20																
gag ggc gga aag ctc tcc att agt tcc act cgt ccg ctc cgc gac atg 211																
Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg Pro Leu Arg Asp Met 35																
cgc gat ctt tcc ctt gct tac acc cct ggt gtt gct cag gtt tgt gaa 259																
Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val Ala Gln Val Cys Glu 50																
gca atc aag gaa gat cca gag gtt gcg cgc acc cac acg ggc att gga 307																
Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr His Thr Gly Ile Gly 65																
aac acc gtc gcg gtt att tcc gac ggc acc gct gtt ctt ggc ctt ggc 355																
Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala Val Leu Gly Leu Gly 85																
gat atc gga cct cag gcc tcc ctt ccc gtc atg gag ggc aag gct cag 403																
Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met Glu Gly Lys Ala Gln 100																
ctg ttt agc tct ttc gct ggc ctg aag gct atc cct atc gtt ttg gac 451																
Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile Pro Ile Val Leu Asp 115																
gtt cac gat gtt gac gct ttg gtt gag acc atc gca gcc atc gcg cct 499																
Val His Asp Val Asp Ala Leu Val Glu Thr Ile Ala Ala Ile Ala Pro 130																
tct ttc ggt gct atc aac ttg gag gac atc tcc gct cct cgt tgc ttc 547																
Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser Ala Pro Arg Cys Phe 145																
gag gtg gag cgc cgc ctc atc gag cgt ctc gat att cca gtt atg cac 595																
Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp Ile Pro Val Met His 165																
gat gac cagcac ggc acc gct gtg gtt atc ctc gct gcg ctg cgc aac 643																
Asp Asp Gln His Gly Thr Ala Val Val Ile Leu Ala Ala Leu Arg Asn																

[illegible]



```

<400> 582
Met Thr Ile Asp Leu Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu
  1          5          10          15

Ile Phe Glu Ala His Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg
          20          25          30

Pro Leu Arg Asp Met Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val
          35          40          45

Ala Gln Val Cys Glu Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr
          50          55          60

His Thr Gly Ile Gly Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala
  65          70          75          80

Val Leu Gly Leu Gly Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met

```

**DECEMBER**



Ser

```
<220>  
<221> CDS  
<222> (1)..(582)  
<223> RXN03101
```

<400> 583  
atc ctt gca gac gaa gac gac acc gtc gac gtc ggc gca gtc atc gcc 48  
Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly Ala Val Ile Ala



<400> 584  
Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly Ala Val Ile Ala  
1 5 10 15  
Arg Ile Gly Asp Ala Asn Ala Ala Ala Ala Pro Ala Glu Glu Glu Ala



20				25				30							
Ala	Pro	Ala	Glu	Glu	Glu	Glu	Pro	Val	Lys	Glu	Glu	Pro	Lys	Lys	Glu
		35					40					45			
Ala	Ala	Pro	Glu	Ala	Pro	Ala	Ala	Thr	Gly	Ala	Ala	Thr	Asp	Val	Glu
	50					55					60				
Met	Pro	Glu	Leu	Gly	Glu	Ser	Val	Thr	Glu	Gly	Thr	Ile	Thr	Gln	Trp
65					70					75					80
Leu	Lys	Ala	Val	Gly	Asp	Thr	Val	Glu	Val	Asp	Glu	Pro	Leu	Leu	Glu
				85					90					95	
Val	Ser	Thr	Asp	Lys	Val	Asp	Thr	Glu	Ile	Pro	Ser	Pro	Val	Ala	Gly
			100					105					110		
Thr	Ile	Val	Glu	Ile	Leu	Ala	Asp	Glu	Asp	Asp	Thr	Val	Asp	Val	Gly
		115					120					125			
Ala	Val	Ile	Ala	Arg	Ile	Gly	Asp	Ala	Asn	Ala	Ala	Ala	Ala	Pro	Ala
	130					135					140				
Glu	Glu	Glu	Ala	Ala	Pro	Ala	Glu	Glu	Glu	Glu	Pro	Val	Lys	Glu	Glu
145					150					155					160
Pro	Lys	Lys	Glu	Glu	Pro	Lys	Lys	Glu	Glu	Pro	Lys	Lys	Glu	Ala	Ala
				165					170					175	
Thr	Thr	Pro	Ala	Ala	Ala	Ser	Ala	Thr	Val	Ser	Ala	Ser	Gly	Asp	Asn
			180					185					190		
Val	Pro														

```
<210> 585
<211> 540
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(517)  
<223> RXN02046
```

<400> 585																	
tccgtg	ccat	caccacc	ggc	gagat	cactg	gc	atc	gtg	ga	cg	aaaa	acaa	acag	caac	ag	60	
aaattatt	aa	catccg	acgc	aacgctt	cag	gagagt	cctc	atg	aaa	gag	aca	ctg				115	
								Met	Lys	Glu	Thr	Leu					
								1						5			
acc	acc	ggt	tta	acc	cac	caa	atg	acc	tac	ata	gtg	cca	gca	aac	cgc	163	
Thr	Thr	Gly	Leu	Thr	His	Gln	Met	Thr	Tyr	Ile	Val	Pro	Ala	Asn	Arg		
				10					15					20			
aca	gtt	ccg	cat	ctg	ctt	ccc	gaa	gca	gca	gaa	ttt	gaa	acc	atg	cca	211	
Thr	Val	Pro	His	Leu	Leu	Pro	Glu	Ala	Ala	Glu	Phe	Glu	Thr	Met	Pro		
			25				30				35						

Figure 1 shows a sequence of 12 diagrams illustrating the evolution of a 2D lattice system over time. The diagrams are labeled (a) through (l). Each diagram shows a grid of cells, with black and white squares representing different states. The system starts with a single black cell in the center (a) and evolves through various patterns of black and white cells as time progresses. The diagrams show the growth and spreading of the black cells, eventually forming a complex, fractal-like pattern (l).



atg gaa ctt ctg cgt ccc cat ttg gac gac ggt gaa atc tcg ctg ggc 307  
Met Glu Leu Leu Arg Pro His Leu Asp Asp Gly Glu Ile Ser Leu Gly  
55 60 65

act cat gtg aac ttc tcc cac gca gct cca acg gtt cct gga tcc acg 355  
Thr His Val Asn Phe Ser His Ala Ala Pro Thr Val Pro Gly Ser Thr  
70 75 80 85

gtc acc atc gat gtt gag gtg aca gag atc aac cgt cgt gca gtt acc 403  
Val Thr Ile Asp Val Glu Val Thr Glu Ile Asn Arg Arg Ala Val Thr  
90 95 100

ttc aac atc act gca gct gat gag ttc gcc acc atc agc acc ggc acc 451  
 Phe Asn Ile Thr Ala Ala Asp Glu Phe Ala Thr Ile Ser Thr Gly Thr  
 105 110 115

cac cag cgc ggt gtg gtt aac cgt gag aag ttt gtc tcc cgt ctg cct 499  
 His Gln Arg Gly Val Val Asn Arg Glu Lys Phe Val Ser Arg Leu Pro  
 120 125 130

gaa gca cct aag gaa aac taaatcatgg ccaagttggt tga 540  
Glu Ala Pro Lys Glu Asn  
135

<210> 586

<211> 139

<212> PRT

<213> Corynebacterium glutamicum

<400> 586

Met Lys Glu Thr Leu Thr Thr Gly Leu Thr His Gln Met Thr Tyr Ile  
1 5 10 15

Val Pro Ala Asn Arg Thr Val Pro His Leu Leu Pro Glu Ala Ala Glu  
20 25 30

Phe Glu Thr Met Pro Asp Val Leu Ala Thr Gly Tyr Met Val Gly Ile  
35 40 45

Ile Glu Trp Ala Cys Met Glu Leu Leu Arg Pro His Leu Asp Asp Gly  
50 55 60

Glu Ile Ser Leu Gly Thr His Val Asn Phe Ser His Ala Ala Pro Thr  
65 70 75 80

Val Pro Gly Ser Thr Val Thr Ile Asp Val Glu Val Thr Glu Ile Asn  
85 90 95

Arg Arg Ala Val Thr Phe Asn Ile Thr Ala Ala Asp Glu Phe Ala Thr  
100 105 110

Ile Ser Thr Gly Thr His Gln Arg Gly Val Val Asn Arg Glu Lys Phe  
115 120 125

Val Ser Arg Leu Pro Glu Ala Pro Lys Glu Asn  
130 135



```
<220>  
<221> CDS  
<222> (101)..(1660)  
<223> RXN00389
```



170								175								180								
gcg	cat	aat	gcg	cac	cct	gga	aca	gct	gag	ctc	gtc	ggg	caa	gcg	gtg	691								
Ala	His	Asn	Ala	His	Pro	Gly	Thr	Ala	Glu	Leu	Val	Gly	Gln	Ala	Val									
185								190								195								
cgg	gga	gcc	gtc	gaa	aag	cat	gag	ttt	gat	gct	ggt	gtg	ttt	aac	ctt	739								
Arg	Gly	Ala	Val	Glu	Lys	His	Glu	Phe	Asp	Ala	Gly	Val	Phe	Asn	Leu									
200								205								210								
gtc	tac	ggc	cgt	ggc	gtg	gaa	att	ggc	cag	gag	ctg	gct	gcg	gat	ccg	787								
Val	Tyr	Gly	Arg	Gly	Val	Glu	Ile	Gly	Gln	Glu	Leu	Ala	Ala	Asp	Pro									
215								220								225								
aat	atc	acg	gca	atc	ggt	ttt	acc	ggt	tca	cgc	cag	ggt	ggt	ttg	gca	835								
Asn	Ile	Thr	Ala	Ile	Gly	Phe	Thr	Gly	Ser	Arg	Gln	Gly	Gly	Leu	Ala									
230								235								240								
ctg	tca	cag	act	gcg	ttt	agc	cgc	cca	gtt	ccc	gtt	cca	gtc	ttt	gca	883								
Leu	Ser	Gln	Thr	Ala	Phe	Ser	Arg	Pro	Val	Pro	Val	Pro	Val	Phe	Ala									
250								255								260								
gaa	atg	agt	gcc	acc	aac	cct	gtg	ttc	gtc	ttc	ccc	ggc	gcg	ctg	gcg	931								
Glu	Met	Ser	Ala	Thr	Asn	Pro	Val	Phe	Val	Phe	Pro	Gly	Ala	Leu	Ala									
265								270								275								
gat	ttg	gat	gca	tcg	agt	tcc	ttg	gct	gag	gcg	ttt	acc	gct	tcc	gtc	979								
Asp	Leu	Asp	Ala	Ser	Ser	Ser	Leu	Ala	Glu	Ala	Phe	Thr	Ala	Ser	Val									
280								285								290								
acc	ggc	agt	tcc	ggg	caa	ttg	tgc	acc	aag	cct	ggc	ctc	gtt	ttc	atc	1027								
Thr	Gly	Ser	Ser	Gly	Gln	Leu	Cys	Thr	Lys	Pro	Gly	Leu	Val	Phe	Ile									
295								300								305								
ccg	cgc	ggt	gtt	gtt	ggt	gat	gct	ttt	gtg	gcg	ctc	gta	gca	gcc	aaa	1075								
Pro	Arg	Gly	Val	Val	Gly	Asp	Ala	Phe	Val	Ala	Leu	Val	Ala	Ala	Lys									
310								315								320								
ttt	aaa	gaa	acc	acg	ggt	caa	acg	atg	ctc	acg	caa	ggc	atc	gct	cag	1123								
Phe	Lys	Glu	Thr	Thr	Gly	Gln	Thr	Met	Leu	Thr	Gln	Gly	Ile	Ala	Gln									
330								335								340								
gca	tgg	cag	cgc	gga	gtc	gac	aac	ctt	gca	gca	cag	cca	agt	gta	aaa	1171								
Ala	Trp	Gln	Arg	Gly	Val	Asp	Asn	Leu	Ala	Ala	Gln	Pro	Ser	Val	Lys									
345								350								355								
atc	ctc	gcc	caa	ggc	acc	ccc	gga	gat	gga	gag	aac	gcg	ccg	ggc	ccg	1219								
Ile	Leu	Ala	Gln	Gly	Thr	Pro	Gly	Asp	Gly	Glu	Asn	Ala	Pro	Gly	Pro									
360								365								370								
gtg	gtg	ttt	gaa	agt	gat	gtg	cag	gcg	ttg	cta	aat	aat	gtg	gtg	ttg	1267								
Val	Val	Phe	Glu	Ser	Asp	Val	Gln	Ala	Leu	Leu	Asn	Asn	Val	Val	Leu									
375								380								385								
cag	gaa	gaa	atc	ttc	ggt	gcg	gca	tcg	ctg	gtg	gtg	cgt	tat	gat	tcc	1315								
Gln	Glu	Glu	Ile	Phe	Gly	Ala	Ala	Ser	Leu	Val	Val	Arg	Tyr	Asp	Ser									
390								395								400								
ccg	gat	caa	ctc	cac	caa	gta	gcc	aat	tca	ctc	gag	gga	caa	tta	aca	1363								
Pro	Asp	Gln	Leu	His	Gln	Val	Ala	Asn	Ser	Leu	Glu	Gly	Gln	Leu	Thr									
410								415								420								

002290"0420960



atc ccc ctc ttg gag gat ctc gcg ggc cgt gtt ctt tac ggc ggc tgg 1459  
Ile Pro Leu Leu Glu Asp Leu Ala Gly Arg Val Leu Tyr Gly Gly Trp  
440 445 450

ccg gcg acc tca aat gcg cag tcg aca agt gtt gga acc ctg gca atc 1555  
Pro Ala Thr Ser Asn Ala Gln Ser Thr Ser Val Gly Thr Leu Ala Ile  
470 475 480 485

ctt cca gat cca gtt tct gag gcg aat aaa tgg gct gta cct cgg gaa 1651  
Leu Pro Asp Pro Val Ser Glu Ala Asn Lys Trp Ala Val Pro Arg Glu  
505 510 515

```
<210> 588
<211> 520
<212> PRT
<213> Corynebacterium glutamicum
```

Trp Val Ala Gly Lys Asn Gly Glu Ile Thr Gly Phe Asp Pro Arg Thr  
20 25 30

Asn Ala Ser Leu Asn Pro Ser Tyr Ser Leu Ala Asn Ser Ala Gln Leu  
35 40 45

Arg Ala Ala Thr Thr Ser Ala Lys Arg Ala Phe Glu Ser Tyr Arg Leu  
50 55 60

Thr Thr Pro Glu Val Arg Ala Asp Phe Leu Asp Ser Ile Ala Asp Asn  
65 70 75 80

Ile Asp Ala Leu Ser Gly Glu Ile Val Gln Arg Ala Ser Leu Glu Thr  
85 90 95

Gly Leu Gly Thr Thr Arg Leu Thr Gly Glu Val Ala Arg Thr Ser Asn  
100 105 110

Gln Leu Arg Leu Phe Ala Glu Thr Val Arg Ser Gly Gln Phe His Arg  
115 120 125

Val Arg Ile Glu Arg Gly Pro Arg Ile Asp Leu Arg Gln Arg Gln Val

[illegible]



09602740-06E00



<400> 589																	
ttgacgcacc aatgcccgat ggagcaatgt gtgaaccacg ccaccacgcga aaccgatgca																60	
catcacgtcg aaacagtgac agtgcattag ctcatacttt										gtg	gtc	ggc	acc	gcc			
										Val	Val	Gly	Thr	Ala	115		
										1				5			
cat	tgc	gaa	tca	gca	ctt	aag	gaa	gtg	act	ttg	atg	tca	aac	gtt	gga	163	
His	Cys	Glu	Ser	Ala	Leu	Lys	Glu	Val	Thr	Leu	Met	Ser	Asn	Val	Gly		
				10					15					20			
aag	cca	cgt	acc	gca	cag	gaa	atc	cag	cag	gat	tgg	gac	acc	aac	cct	211	
Lys	Pro	Arg	Thr	Ala	Gln	Glu	Ile	Gln	Gln	Asp	Trp	Asp	Thr	Asn	Pro		
			25				30				35						
cgt	tgg	aac	ggc	atc	acc	cgc	gac	tac	acc	gca	gac	cag	gta	gct	gat	259	
Arg	Trp	Asn	Gly	Ile	Thr	Arg	Asp	Tyr	Thr	Ala	Asp	Gln	Val	Ala	Asp		
		40				45			50								
ctg	cag	ggg	tcc	gtc	atc	gag	gag	cac	act	ctt	gct	cgc	cgc	ggc	tca	307	
Leu	Gln	Gly	Ser	Val	Ile	Glu	Glu	His	Thr	Leu	Ala	Arg	Arg	Gly	Ser		
		55				60				65							
gag	atc	ctc	tgg	gac	gca	gtc	acc	cag	gaa	ggg	gac	gga	tac	atc	aac	355	
Glu	Ile	Leu	Trp	Asp	Ala	Val	Thr	Gln	Glu	Gly	Asp	Gly	Tyr	Ile	Asn		
		70				75				80				85			
gcg	ctt	ggc	gca	ctc	acc	ggg	aac	cag	gct	gtt	cag	cag	gtt	cgt	gca	403	
Ala	Leu	Gly	Ala	Leu	Thr	Gly	Asn	Gln	Ala	Val	Gln	Gln	Val	Arg	Ala		
				90					95					100			
ggc	ctg	aag	gct	gtc	tac	ctg	tcc	ggg	tgg	cag	gtc	gca	ggg	gac	gcc	451	
Gly	Leu	Lys	Ala	Val	Tyr	Leu	Ser	Gly	Trp	Gln	Val	Ala	Gly	Asp	Ala		
			105				110				115						
aac	ctc	tcc	ggc	cac	acc	tac	cct	gac	cag	tcc	ctc	tac	cca	gcg	aac	499	
Asn	Leu	Ser	Gly	His	Thr	Tyr	Pro	Asp	Gln	Ser	Leu	Tyr	Pro	Ala	Asn		

[illegible]



1992 1993 1994 1995 1996 1997 1998 1999 2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2192 2193 2194 2195 2196 2197 2198 2199 2200 2201 2202 2203 2204 2205 2206 2207 2208 2209 2210 2211 2212 2213 2214 2215 2216 2217 2218 2219 2220 2221 2222 2223 2224 2225 2226 2227 2228 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2320 2321 2322 2323 2324 2325 2326 2327 2328 2329 2330 2331 2332 2333 2334 2335 2336 2337 2338 2339 2340 2341 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361 2362 2363 2364 2365 2366 2367 2368 2369 2370 2371 2372 2373 2374 2375 2376 2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395 2396 2397 2398 2399 2400 2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 2443 2444 2445 2446 2447 2448 2449 2450 2451 2452 2453 2454 2455 2456 2457 2458 2459 2460 2461 2462 2463 2464 2465 2466 2467 2468 2469 2470 2471 2472 2473 2474 2475 2476 2477 2478 2479 2480 2481 2482 2483 2484 2485 2486 2487 2488 2489 2490 2491 2492 2493 2494 2495 2496 2497 2498 2499 2500 2501 2502 2503 2504 2505 2506 2507 2508 2509 2510 2511 2512 2513 2514 2515 2516 2517 2518 2519 2520 2521 2522 2523 2524 2525 2526 2527 2528 2529 2530 2531 2532 2533 2534 2535 2536 2537 2538 2539 2540 2541 2542 2543 2544 2545 2546 2547 2548 2549 2550 2551 2552 2553 2554 2555 2556 2557 2558 2559 2560 2561 2562 2563 2564 2565 2566 2567 2568 2569 2570 2571 2572 2573 2574 2575 2576 2577 2578 2579 2580 2581 2582 2583 2584 2585 2586 2587 2588 2589 2590 2591 2592 2593 2594 2595 2596 2597 2598 2599 2600 2601 2602 2603 2604 2605 2606 2607 2608 2609 2610 2611 2612 2613 2614 2615 2616 2617 2618 2619 2620 2621 2622 2623 2624 2625 2626 2627 2628 2629 2630 2631 2632 2633 2634 2635 2636 2637 2638 2639 2640 2641 2642 2643 2644 2645 2646 2647 2648 2649 2650 2651 2652 2653 2654 2655 2656 2657 2658 2659 2660 2661 2662 2663 2664 2665 2666 2667 2668 2669 2670 2671 2672 2673 2674 2675 2676 2677 2678 2679 2680 2681 2682 2683 2684 2685 2686 2687 2688 2689 2690 2691 2692 2693 2694 2695 2696 2697 2698 2699 2700 2701 2702 2703 2704 2705 2706 2707 2708 2709 2710 2711 2712 2713 2714 2715 2716 2717 2718 2719 2720 2721 2722 2723 2724 2725 2726 2727 2728 2729 2730 2731 2732 2733 2734 2735 2736 2737 2738 2739 2740 2741 2742 2743 2744 2745 2746 2747 2748 2749 2750 2751 2752 2753 2754 2755 2756 2757 2758 2759 2760 2761 2762 2763 2764 2765 2766 2767 2768 2769 2770 2771 2772 2773 2774 2775 2776 2777 2778 2779 2780 2781 2782 2783 2784 2785 2786 2787 2788 2789 2790 2791 2792 2793 2794 2795 2796 2797 2798 2799 2800 2801 2802 2803 2804 2805 2806 2807 2808 2809 2810



<400> 590															
Val 1	Val	Gly	Thr	Ala 5	His	Cys	Glu	Ser	Ala 10	Leu	Lys	Glu	Val	Thr 15	Leu
Met	Ser	Asn	Val 20	Gly	Lys	Pro	Arg	Thr 25	Ala	Gln	Glu	Ile	Gln 30	Gln	Asp
Trp	Asp	Thr 35	Asn	Pro	Arg	Trp	Asn 40	Gly	Ile	Thr	Arg	Asp 45	Tyr	Thr	Ala
Asp	Gln 50	Val	Ala	Asp	Leu	Gln 55	Gly	Ser	Val	Ile	Glu 60	Glu	His	Thr	Leu
Ala 65	Arg	Arg	Gly	Ser	Glu 70	Ile	Leu	Trp	Asp	Ala 75	Val	Thr	Gln	Glu	Gly 80
Asp	Gly	Tyr	Ile	Asn 85	Ala	Leu	Gly	Ala	Leu 90	Thr	Gly	Asn	Gln	Ala 95	Val
Gln	Gln	Val	Arg 100	Ala	Gly	Leu	Lys	Ala 105	Val	Tyr	Leu	Ser	Gly 110	Trp	Gln
Val	Ala	Gly 115	Asp	Ala	Asn	Leu	Ser 120	Gly	His	Thr	Tyr	Pro 125	Asp	Gln	Ser
Leu	Tyr 130	Pro	Ala	Asn	Ser	Val 135	Pro	Ser	Val	Val	Arg 140	Arg	Ile	Asn	Asn
Ala 145	Leu	Leu	Arg	Ser	Asp 150	Glu	Ile	Ala	Arg	Thr 155	Glu	Gly	Asp	Thr	Ser 160
Val	Asp	Asn	Trp	Val	Val	Pro	Ile	Val	Ala	Asp	Gly	Glu	Ala	Gly	Phe



```
<210> 591
<211> 1419
<212> DNA
<213> Corynebacterium glutamicum
```

<210>	591
<211>	1419
<212>	DNA



&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1396)

&lt;223&gt; FRXA02399

&lt;400&gt; 591

```

caaaccgatg cacatcacgt cgaaacagtg acagtgcatt agtcataact ttgtggtcgg 60

caccgccccat tgcgaatcag cacttaagga agtgactttg atg tca aac gtt gga 115
                                         Met Ser Asn Val Gly
                                         1 5

aag cca cgt acc gca cag gaa atc cag cag gat tgg gac acc aac cct 163
Lys Pro Arg Thr Ala Gln Glu Ile Gln Gln Asp Trp Asp Thr Asn Pro
                        10                        15                        20

cgt tgg aac ggc atc acc cgc gac tac acc gca gac cag gta gct gat 211
Arg Trp Asn Gly Ile Thr Arg Asp Tyr Thr Ala Asp Gln Val Ala Asp
                        25                        30                        35

ctg cag ggt tcc gtc atc gag gag cac act ctt gct cgc cgc ggc tca 259
Leu Gln Gly Ser Val Ile Glu Glu His Thr Leu Ala Arg Arg Gly Ser
                        40                        45                        50

gag atc ctc tgg gac gca gtc acc cag gaa ggt gac gga tac atc aac 307
Glu Ile Leu Trp Asp Ala Val Thr Gln Glu Gly Asp Gly Tyr Ile Asn
                        55                        60                        65

gcg ctt ggc gca ctc acc ggt aac cag gct gtt cag cag gtt cgt gca 355
Ala Leu Gly Ala Leu Thr Gly Asn Gln Ala Val Gln Gln Val Arg Ala
                        70                        75                        80                        85

ggc ctg aag gct gtc tac ctg tcc ggt tgg cag gtc gca ggt gac gcc 403
Gly Leu Lys Ala Val Tyr Leu Ser Gly Trp Gln Val Ala Gly Asp Ala
                        90                        95                        100

aac ctc tcc ggc cac acc tac cct gac cag tcc ctc tac cca gcg aac 451
Asn Leu Ser Gly His Thr Tyr Pro Asp Gln Ser Leu Tyr Pro Ala Asn
                        105                        110                        115

tcc gtt cca agc gtc gtt cgt cgc atc aac aac gca ctg ctg cgt tcc 499
Ser Val Pro Ser Val Val Arg Arg Ile Asn Asn Ala Leu Leu Arg Ser
                        120                        125                        130

gat gaa atc gca cgc acc gaa ggc gac acc tcc gtt gac aac tgg gtt 547
Asp Glu Ile Ala Arg Thr Glu Gly Asp Thr Ser Val Asp Asn Trp Val
                        135                        140                        145

gtc cca atc gtc gcg gac ggc gaa gct ggc ttc ggt gga gca ctc aac 595
Val Pro Ile Val Ala Asp Gly Glu Ala Gly Phe Gly Gly Ala Leu Asn
                        150                        155                        160                        165

gtc tac gaa ctc cag aag gca atg atc gca gct ggc gct gca ggc acc 643
Val Tyr Glu Leu Gln Lys Ala Met Ile Ala Ala Gly Ala Ala Gly Thr
                        170                        175                        180

cac tgg gaa gac cag ctc gct tct gaa aag aag tgt ggc cac ctc ggc 691
His Trp Glu Asp Gln Leu Ala Ser Glu Lys Lys Cys Gly His Leu Gly
                        185                        190                        195

```

09602740-062300



ggc aag gtt ctg atc cca acc cag cag cac atc cgc acc ctg aac tct 739  
 Gly Lys Val Leu Ile Pro Thr Gln Gln His Ile Arg Thr Leu Asn Ser  
 200 205 210

gcc cgc ctt gca gca gac gtt gca aac acc cca act gtt gtt atc gca 787  
 Ala Arg Leu Ala Ala Asp Val Ala Asn Thr Pro Thr Val Val Ile Ala  
 215 220 225

cgt acc gac gct gag gca gca acc ctg atc acc tct gac gtt gat gag 835  
 Arg Thr Asp Ala Glu Ala Ala Thr Leu Ile Thr Ser Asp Val Asp Glu  
 230 235 240 245

cgc gac caa cca ttc atc acc ggt gag cgc acc gca gaa ggc tac tac 883  
 Arg Asp Gln Pro Phe Ile Thr Gly Glu Arg Thr Ala Glu Gly Tyr Tyr  
 250 255 260

cac gtc aag aat ggt ctc gag cca tgt atc gca cgt gca aag tcc tac 931  
 His Val Lys Asn Gly Leu Glu Pro Cys Ile Ala Arg Ala Lys Ser Tyr  
 265 270 275

gca cca tac gca gat atg atc tgg atg gag acc ggc acc cct gac ctg 979  
 Ala Pro Tyr Ala Asp Met Ile Trp Met Glu Thr Gly Thr Pro Asp Leu  
 280 285 290

gag ctc gct aag aag ttc gct gaa ggc gtt cgc tct gag ttc cca gac 1027  
 Glu Leu Ala Lys Lys Phe Ala Glu Gly Val Arg Ser Glu Phe Pro Asp  
 295 300 305

cag ctg ctg tcc tac aac tgc tcc cca tcc ttc aac tgg tct gca cac 1075  
 Gln Leu Leu Ser Tyr Asn Cys Ser Pro Ser Phe Asn Trp Ser Ala His  
 310 315 320 325

ctc gag gca gat gag atc gct aag ttc cag aag gaa ctc ggc gca atg 1123  
 Leu Glu Ala Asp Glu Ile Ala Lys Phe Gln Lys Glu Leu Gly Ala Met  
 330 335 340

ggc ttc aag ttc cag ttc atc acc ctc gca ggc ttc cac tcc ctc aac 1171  
 Gly Phe Lys Phe Gln Phe Ile Thr Leu Ala Gly Phe His Ser Leu Asn  
 345 350 355

tac ggc atg ttc gac ctg gct tac gga tac gct cgc gaa ggc atg acc 1219  
 Tyr Gly Met Phe Asp Leu Ala Tyr Gly Tyr Ala Arg Glu Gly Met Thr  
 360 365 370

tcc ttc gtt gac ctg cag aac cgt gag ttc aag gca gct gaa gag cgt 1267  
 Ser Phe Val Asp Leu Gln Asn Arg Glu Phe Lys Ala Ala Glu Glu Arg  
 375 380 385

ggc ttc acc gct gtt aag cac cag cgt gag gtt ggc gca ggc tac ttc 1315  
 Gly Phe Thr Ala Val Lys His Gln Arg Glu Val Gly Ala Gly Tyr Phe  
 390 395 400 405

gac cag atc gca acc acc gtt gac ccg aac tct tct acc acc gct ttg 1363  
 Asp Gln Ile Ala Thr Thr Val Asp Pro Asn Ser Ser Thr Thr Ala Leu  
 410 415 420

aag ggt tcc act gaa gaa ggc cag ttc cac aac taggacctac aggttctgac 1416  
 Lys Gly Ser Thr Glu Glu Gly Gln Phe His Asn  
 425 430

aat 1419

003290"0420950



&lt;210&gt; 592

&lt;211&gt; 432

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 592

Met	Ser	Asn	Val	Gly	Lys	Pro	Arg	Thr	Ala	Gln	Glu	Ile	Gln	Gln	Asp
1				5					10					15	
Trp	Asp	Thr	Asn	Pro	Arg	Trp	Asn	Gly	Ile	Thr	Arg	Asp	Tyr	Thr	Ala
			20					25					30		
Asp	Gln	Val	Ala	Asp	Leu	Gln	Gly	Ser	Val	Ile	Glu	Glu	His	Thr	Leu
		35					40					45			
Ala	Arg	Arg	Gly	Ser	Glu	Ile	Leu	Trp	Asp	Ala	Val	Thr	Gln	Glu	Gly
	50					55					60				
Asp	Gly	Tyr	Ile	Asn	Ala	Leu	Gly	Ala	Leu	Thr	Gly	Asn	Gln	Ala	Val
65					70					75					80
Gln	Gln	Val	Arg	Ala	Gly	Leu	Lys	Ala	Val	Tyr	Leu	Ser	Gly	Trp	Gln
				85					90					95	
Val	Ala	Gly	Asp	Ala	Asn	Leu	Ser	Gly	His	Thr	Tyr	Pro	Asp	Gln	Ser
			100					105					110		
Leu	Tyr	Pro	Ala	Asn	Ser	Val	Pro	Ser	Val	Val	Arg	Arg	Ile	Asn	Asn
		115					120					125			
Ala	Leu	Leu	Arg	Ser	Asp	Glu	Ile	Ala	Arg	Thr	Glu	Gly	Asp	Thr	Ser
	130					135					140				
Val	Asp	Asn	Trp	Val	Val	Pro	Ile	Val	Ala	Asp	Gly	Glu	Ala	Gly	Phe
145					150					155					160
Gly	Gly	Ala	Leu	Asn	Val	Tyr	Glu	Leu	Gln	Lys	Ala	Met	Ile	Ala	Ala
				165					170					175	
Gly	Ala	Ala	Gly	Thr	His	Trp	Glu	Asp	Gln	Leu	Ala	Ser	Glu	Lys	Lys
			180					185					190		
Cys	Gly	His	Leu	Gly	Gly	Lys	Val	Leu	Ile	Pro	Thr	Gln	Gln	His	Ile
		195					200					205			
Arg	Thr	Leu	Asn	Ser	Ala	Arg	Leu	Ala	Ala	Asp	Val	Ala	Asn	Thr	Pro
	210					215					220				
Thr	Val	Val	Ile	Ala	Arg	Thr	Asp	Ala	Glu	Ala	Ala	Thr	Leu	Ile	Thr
225					230					235					240
Ser	Asp	Val	Asp	Glu	Arg	Asp	Gln	Pro	Phe	Ile	Thr	Gly	Glu	Arg	Thr
				245					250					255	
Ala	Glu	Gly	Tyr	Tyr	His	Val	Lys	Asn	Gly	Leu	Glu	Pro	Cys	Ile	Ala
			260					265					270		
Arg	Ala	Lys	Ser	Tyr	Ala	Pro	Tyr	Ala	Asp	Met	Ile	Trp	Met	Glu	Thr
		275					280					285			

003290"0420960



<400> 593																			
gttttcacaa ccgттаacgg cgtagccaaa caagaaggat tcgcattctt ctggттtagg																		60	
cacaggтcat ctaaaaccца tgctттtaaaa ggagcттca																			
																		atg act gaa cag gaa	115
																		Met Thr Glu Gln Glu	
																		1 5	
ctg ttg tct gct cag act gcc gac aac gct gga act gac agc acc gaa																		163	
Leu Leu Ser Ala Gln Thr Ala Asp Asn Ala Gly Thr Asp Ser Thr Glu																			
																		10 15 20	
cgc gtt gac gcg ggc gga atg cag gtt gca aaa gtt ctc tac gac ttt																		211	
Arg Val Asp Ala Gly Gly Met Gln Val Ala Lys Val Leu Tyr Asp Phe																			
																		25 30 35	
gta acc gaa gcg gta ctc cct cgc gtg ggt gtg gat gcg gaa aag ttc																		259	
Val Thr Glu Ala Val Leu Pro Arg Val Gly Val Asp Ala Glu Lys Phe																			
																		40 45 50	

**096024-4**



[illegible]



Ala	Ala	Val	Asp	Ala	Glu	Asp	Lys	Thr	Leu	Gly	Tyr	Ser	Asn	Trp	Phe	
295						300					305					
gga	ctc	aac	acc	ggc	gaa	ctg	aaa	gaa	gag	atg	tcc	aag	aac	gga	cgc	1075
Gly	Leu	Asn	Thr	Gly	Glu	Leu	Lys	Glu	Glu	Met	Ser	Lys	Asn	Gly	Arg	
310					315					320					325	
atc	ttc	acc	cgt	gag	ctc	aac	aag	gac	cgc	gtc	tac	att	ggc	cgc	aat	1123
Ile	Phe	Thr	Arg	Glu	Leu	Asn	Lys	Asp	Arg	Val	Tyr	Ile	Gly	Arg	Asn	
				330					335					340		
ggt	acc	gag	ctg	ggt	ctg	cac	ggt	cgt	tcc	ctg	ctg	ttc	gtc	cgc	aac	1171
Gly	Thr	Glu	Leu	Val	Leu	His	Gly	Arg	Ser	Leu	Leu	Phe	Val	Arg	Asn	
				345				350					355			
gtt	ggt	cac	ctc	atg	caa	aac	cca	tcc	atc	ttg	att	gat	ggc	gag	gag	1219
Val	Gly	His	Leu	Met	Gln	Asn	Pro	Ser	Ile	Leu	Ile	Asp	Gly	Glu	Glu	
		360					365					370				
atc	ttc	gaa	ggc	atc	atg	gat	gct	gtc	ttg	acc	act	gtt	tgt	gcc	atc	1267
Ile	Phe	Glu	Gly	Ile	Met	Asp	Ala	Val	Leu	Thr	Thr	Val	Cys	Ala	Ile	
		375				380					385					
cca	gga	att	gct	ccg	cag	aac	aag	atg	cgc	aat	tcc	cgc	aag	ggc	tcc	1315
Pro	Gly	Ile	Ala	Pro	Gln	Asn	Lys	Met	Arg	Asn	Ser	Arg	Lys	Gly	Ser	
390					395					400					405	
atc	tac	atc	gtg	aag	cct	aag	cag	cac	ggc	cct	gaa	gaa	gtc	gcg	ttc	1363
Ile	Tyr	Ile	Val	Lys	Pro	Lys	Gln	His	Gly	Pro	Glu	Glu	Val	Ala	Phe	
				410					415					420		
acc	aac	gag	ctc	ttc	ggc	cgc	gtt	gag	gat	ctg	ctt	gat	ctg	cca	cgc	1411
Thr	Asn	Glu	Leu	Phe	Gly	Arg	Val	Glu	Asp	Leu	Leu	Asp	Leu	Pro	Arg	
				425				430					435			
cac	acc	ttg	aag	gtt	ggt	gtt	atg	gat	gag	gag	cgt	cgc	acg	tcc	gtg	1459
His	Thr	Leu	Lys	Val	Gly	Val	Met	Asp	Glu	Glu	Arg	Arg	Thr	Ser	Val	
		440					445					450				
aac	ctg	gat	gcc	agc	atc	atg	gaa	gtt	gct	gac	cgc	ttg	gca	ttc	atc	1507
Asn	Leu	Asp	Ala	Ser	Ile	Met	Glu	Val	Ala	Asp	Arg	Leu	Ala	Phe	Ile	
		455				460					465					
aac	act	ggc	ttc	ctg	gac	cgc	acc	ggc	gat	gaa	atc	cac	acc	tcc	atg	1555
Asn	Thr	Gly	Phe	Leu	Asp	Arg	Thr	Gly	Asp	Glu	Ile	His	Thr	Ser	Met	
470					475					480					485	
gaa	gca	ggc	gcc	atg	gtg	cgc	aag	gct	gat	atg	cag	acc	gca	ccg	tgg	1603
Glu	Ala	Gly	Ala	Met	Val	Arg	Lys	Ala	Asp	Met	Gln	Thr	Ala	Pro	Trp	
				490					495					500		
aag	cag	gcc	tac	gag	aac	aac	aac	gtt	gat	gca	ggt	att	cag	cgt	ggt	1651
Lys	Gln	Ala	Tyr	Glu	Asn	Asn	Asn	Val	Asp	Ala	Gly	Ile	Gln	Arg	Gly	
			505					510					515			
ctt	cct	ggc	aag	gct	cag	atc	ggt	aag	ggc	atg	tgg	gcg	atg	act	gaa	1699
Leu	Pro	Gly	Lys	Ala	Gln	Ile	Gly	Lys	Gly	Met	Trp	Ala	Met	Thr	Glu	
		520					525					530				
ctc	atg	gca	gaa	atg	ctg	gag	aag	aag	atc	ggc	cag	cca	cgc	gaa	ggc	1747
Leu	Met	Ala	Glu	Met	Leu	Glu	Lys	Lys	Ile	Gly	Gln	Pro	Arg	Glu	Gly	

002250" 0420950



535	540	545	
gcc aac act gca tgg gtt cct tca cca act ggt gcg acg ctg cac gca			1795
Ala Asn Thr Ala Trp Val Pro Ser Pro Thr Gly Ala Thr Leu His Ala			
550	555	560	565
acg cac tac cac ttg gtt gat gtg ttc aag gtt caa gac gaa ctg cgt			1843
Thr His Tyr His Leu Val Asp Val Phe Lys Val Gln Asp Glu Leu Arg			
	570	575	580
gct gcc ggc cgc cgc gac agc ctg cgc aac att ctc acc att tca acc			1891
Ala Ala Gly Arg Arg Asp Ser Leu Arg Asn Ile Leu Thr Ile Ser Thr			
	585	590	595
gca cca aac acc aat tgg tct gag gaa gag aag aag gaa gag atg gac			1939
Ala Pro Asn Thr Asn Trp Ser Glu Glu Lys Lys Glu Glu Met Asp			
	600	605	610
aac aac tgc cag tcc atc ctc gga tac gtt gtg cgc tgg gtt gag cac			1987
Asn Asn Cys Gln Ser Ile Leu Gly Tyr Val Val Arg Trp Val Glu His			
	615	620	625
ggt gtt ggt tgc tcc aag gtt cca gac atc cat gac atc gac ctc atg			2035
Gly Val Gly Cys Ser Lys Val Pro Asp Ile His Asp Ile Asp Leu Met			
	630	635	640
gaa gac cgc gca acg ctg cgt att tcc tcg cag atg ctg gcc aac tgg			2083
Glu Asp Arg Ala Thr Leu Arg Ile Ser Ser Gln Met Leu Ala Asn Trp			
	650	655	660
atc cgc cat gat gtt gtc tcg aag gag cag gtc ttg gag tca ctg gaa			2131
Ile Arg His Asp Val Val Ser Lys Glu Gln Val Leu Glu Ser Leu Glu			
	665	670	675
cga atg gca gtg gtc gtc gac aag caa aat gcg ggc gac gag gcc tac			2179
Arg Met Ala Val Val Val Asp Lys Gln Asn Ala Gly Asp Glu Ala Tyr			
	680	685	690
cgc gat atg gcg ccg aag tac gac gcc tcc ctc gcc ttc cag gcg gct			2227
Arg Asp Met Ala Pro Lys Tyr Asp Ala Ser Leu Ala Phe Gln Ala Ala			
	695	700	705
aag gac ttg att ttc gaa ggc acc aag tcc cca tcg ggc tac acc gag			2275
Lys Asp Leu Ile Phe Glu Gly Thr Lys Ser Pro Ser Gly Tyr Thr Glu			
	710	715	720
ccc atc ttg cac gca cgc cgc cgc gag ttc aaa gca aaa aac			2317
Pro Ile Leu His Ala Arg Arg Arg Glu Phe Lys Ala Lys Asn			
	730	735	
taagcacgct tttcgacgct tac			2340

&lt;210&gt; 594

&lt;211&gt; 739

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 594

Met	Thr	Glu	Gln	Glu	Leu	Leu	Ser	Ala	Gln	Thr	Ala	Asp	Asn	Ala	Gly
1					5				10					15	

002250"0420960



Thr Asp Ser Thr Glu Arg Val Asp Ala Gly Gly Met Gln Val Ala Lys  
 20 25 30  
 Val Leu Tyr Asp Phe Val Thr Glu Ala Val Leu Pro Arg Val Gly Val  
 35 40 45  
 Asp Ala Glu Lys Phe Trp Ser Gly Phe Ala Ala Ile Ala Arg Asp Leu  
 50 55 60  
 Thr Pro Arg Asn Arg Glu Leu Leu Ala Arg Arg Asp Glu Leu Gln Met  
 65 70 75 80  
 Leu Ile Asp Asp Tyr His Arg Asn Asn Ser Gly Thr Ile Asp Gln Glu  
 85 90 95  
 Ala Tyr Glu Asp Phe Leu Lys Glu Ile Gly Tyr Leu Val Glu Glu Pro  
 100 105 110  
 Glu Ala Ala Glu Ile Arg Thr Gln Asn Val Asp Thr Glu Ile Ser Ser  
 115 120 125  
 Thr Ala Gly Pro Gln Leu Val Val Pro Ile Leu Asn Ala Arg Phe Ala  
 130 135 140  
 Leu Asn Ala Ala Asn Ala Arg Trp Gly Ser Leu Tyr Asp Ala Leu Tyr  
 145 150 155 160  
 Gly Thr Asn Ala Ile Pro Glu Thr Asp Gly Ala Glu Lys Gly Lys Glu  
 165 170 175  
 Tyr Asn Pro Val Arg Gly Gln Lys Val Ile Glu Trp Gly Arg Glu Phe  
 180 185 190  
 Leu Asp Ser Val Val Pro Leu Asp Gly Ala Ser His Ala Asp Val Glu  
 195 200 205  
 Lys Tyr Asn Ile Thr Asp Gly Lys Leu Ala Ala His Ile Gly Asp Ser  
 210 215 220  
 Val Tyr Arg Leu Lys Asn Arg Glu Ser Tyr Arg Gly Phe Thr Gly Asn  
 225 230 235 240  
 Phe Leu Asp Pro Glu Ala Ile Leu Leu Glu Thr Asn Gly Leu His Ile  
 245 250 255  
 Glu Leu Gln Ile Asp Pro Val His Pro Ile Gly Lys Ala Asp Lys Thr  
 260 265 270  
 Gly Leu Lys Asp Ile Val Leu Glu Ser Ala Ile Thr Thr Ile Met Asp  
 275 280 285  
 Phe Glu Asp Ser Val Ala Ala Val Asp Ala Glu Asp Lys Thr Leu Gly  
 290 295 300  
 Tyr Ser Asn Trp Phe Gly Leu Asn Thr Gly Glu Leu Lys Glu Glu Met  
 305 310 315 320  
 Ser Lys Asn Gly Arg Ile Phe Thr Arg Glu Leu Asn Lys Asp Arg Val  
 325 330 335

002290 0420960



Figure 1 illustrates the steps of the proposed algorithm for finding the minimum spanning tree of a graph. The graphs are represented as grids of nodes and edges. The steps are as follows:

- (a) Initial graph with 10 nodes and 15 edges.
- (b) First edge removed.
- (c) Second edge removed.
- (d) Third edge removed.
- (e) Fourth edge removed.
- (f) Fifth edge removed.
- (g) Sixth edge removed.
- (h) Seventh edge removed.
- (i) Eighth edge removed.
- (j) Ninth edge removed.
- (k) Tenth edge removed.
- (l) Final minimum spanning tree with 9 edges.



```
<210> 595
<211> 2159
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (1)..(2136)
<223> FRXA02404
```

<400> 595																
atg	cag	gtt	gca	aaa	gtt	ctc	tac	gac	ttt	gta	acc	gaa	gcg	gta	ctc	48
Met	Gln	Val	Ala	Lys	Val	Leu	Tyr	Asp	Phe	Val	Thr	Glu	Ala	Val	Leu	
1				5				10						15		
cct	cgc	gtg	ggg	gtg	gat	gcg	gaa	aag	ttc	tgg	tcc	gga	ttc	gcc	gcc	96
Pro	Arg	Val	Gly	Val	Asp	Ala	Glu	Lys	Phe	Trp	Ser	Gly	Phe	Ala	Ala	
		20						25				30				
atc	gcc	cgg	gac	ctc	acc	cca	cgc	aac	cgc	gag	ctg	ctt	gct	cgc	cgc	144
Ile	Ala	Arg	Asp	Leu	Thr	Pro	Arg	Asn	Arg	Glu	Leu	Leu	Ala	Arg	Arg	
		35				40						45				
gat	gaa	ctg	cag	atg	ctt	atc	gac	gac	tac	cac	cgc	aac	aac	tcc	ggc	192
Asp	Glu	Leu	Gln	Met	Leu	Ile	Asp	Asp	Tyr	His	Arg	Asn	Asn	Ser	Gly	
50						55				60						
acc	atc	gac	caa	gag	gcg	tac	gag	gat	ttc	ctc	aaa	gaa	atc	gga	tac	240
Thr	Ile	Asp	Gln	Glu	Ala	Tyr	Glu	Asp	Phe	Leu	Lys	Glu	Ile	Gly	Tyr	
65				70						75				80		
ttg	gtt	gag	gag	cca	gaa	gct	gca	gaa	atc	cggt	acc	caa	aac	gtc	gat	288
Leu	Val	Glu	Glu	Pro	Glu	Ala	Ala	Glu	Ile	Arg	Thr	Gln	Asn	Val	Asp	
				85				90						95		
acg	gaa	atc	tcc	agc	acc	gca	gga	cct	cag	ctg	gtt	gtt	cca	att	ctg	336
Thr	Glu	Ile	Ser	Ser	Thr	Ala	Gly	Pro	Gln	Leu	Val	Val	Pro	Ile	Leu	
		100						105				110				
aac	gca	cgc	ttc	gcg	ctg	aac	gct	gcc	aat	gct	cgc	tgg	ggg	tcc	ctc	384
Asn	Ala	Arg	Phe	Ala	Leu	Asn	Ala	Ala	Asn	Ala	Arg	Trp	Gly	Ser	Leu	
		115				120						125				



tac gat gcg ttg tac ggc acc aac gcc atc cca gaa act gat ggc gct Tyr Asp Ala Leu Tyr Gly Thr Asn Ala Ile Pro Glu Thr Asp Gly Ala 130 135 140	432
gaa aag ggc aag gag tac aac ccg gtc cgc ggc cag aag gtc atc gag Glu Lys Gly Lys Glu Tyr Asn Pro Val Arg Gly Gln Lys Val Ile Glu 145 150 155 160	480
tgg ggt cgt gaa ttc ctc gac agc gtt gtc cca ctg gac ggt gct tcg Trp Gly Arg Glu Phe Leu Asp Ser Val Val Pro Leu Asp Gly Ala Ser 165 170 175	528
cat gcc gat gtt gag aag tac aac atc acc gat gga aag ctt gca gcc His Ala Asp Val Glu Lys Tyr Asn Ile Thr Asp Gly Lys Leu Ala Ala 180 185 190	576
cac att gga gat agc gtc tac cga ctg aaa aac cgt gaa tcc tac cgt His Ile Gly Asp Ser Val Tyr Arg Leu Lys Asn Arg Glu Ser Tyr Arg 195 200 205	624
ggc ttc acc ggc aac ttc ctt gat cca gaa gca atc ctg ctg gaa acc Gly Phe Thr Gly Asn Phe Leu Asp Pro Glu Ala Ile Leu Leu Glu Thr 210 215 220	672
aac ggc ctg cac atc gag ctg cag atc gat cct gtc cac cca atc ggc Asn Gly Leu His Ile Glu Leu Gln Ile Asp Pro Val His Pro Ile Gly 225 230 235 240	720
aag gca gac aag act ggt ctc aaa gac atc gtt ttg gaa tct gcg atc Lys Ala Asp Lys Thr Gly Leu Lys Asp Ile Val Leu Glu Ser Ala Ile 245 250 255	768
acc acg atc atg gac ttc gaa gac tcc gtt gca gct gtt gat gct gaa Thr Thr Ile Met Asp Phe Glu Asp Ser Val Ala Ala Val Asp Ala Glu 260 265 270	816
gac aag acc tta ggt tac tct aac tgg ttc gga ctc aac acc ggc gaa Asp Lys Thr Leu Gly Tyr Ser Asn Trp Phe Gly Leu Asn Thr Gly Glu 275 280 285	864
ctg aaa gaa gag atg tcc aag aac gga cgc atc ttc acc cgt gag ctc Leu Lys Glu Glu Met Ser Lys Asn Gly Arg Ile Phe Thr Arg Glu Leu 290 295 300	912
aac aag gac cgc gtc tac att ggc cgc aat ggt acc gag ctg gtt ctg Asn Lys Asp Arg Val Tyr Ile Gly Arg Asn Gly Thr Glu Leu Val Leu 305 310 315 320	960
cac ggt cgt tcc ctg ctg ttc gtc cgc aac gtt ggt cac ctc atg caa His Gly Arg Ser Leu Leu Phe Val Arg Asn Val Gly His Leu Met Gln 325 330 335	1008
aac cca tcc atc ttg att gat ggc gag gag atc ttc gaa ggc atc atg Asn Pro Ser Ile Leu Ile Asp Gly Glu Glu Ile Phe Glu Gly Ile Met 340 345 350	1056
gat gct gtc ttg acc act gtt tgt gcc atc cca gga att gct ccg cag Asp Ala Val Leu Thr Thr Val Cys Ala Ile Pro Gly Ile Ala Pro Gln 355 360 365	1104
aac aag atg cgc aat tcc cgc aag ggc tcc atc tac atc gtg aag cct	1152

00622740 "062300



Asn	Lys	Met	Arg	Asn	Ser	Arg	Lys	Gly	Ser	Ile	Tyr	Ile	Val	Lys	Pro		
	370					375					380						
aag	cag	cac	ggc	cct	gaa	gaa	gtc	gcg	ttc	acc	aac	gag	ctc	ttc	ggc	1200	
Lys	Gln	His	Gly	Pro	Glu	Glu	Val	Ala	Phe	Thr	Asn	Glu	Leu	Phe	Gly		
385					390					395					400		
cgc	gtt	gag	gat	ctg	ctt	gat	ctg	cca	cgc	cac	acc	ttg	aag	gtt	ggc	1248	
Arg	Val	Glu	Asp	Leu	Leu	Asp	Leu	Pro	Arg	His	Thr	Leu	Lys	Val	Gly		
				405					410					415			
gtt	atg	gat	gag	gag	cgt	cgc	acg	tcc	gtg	aac	ctg	gat	gcc	agc	atc	1296	
Val	Met	Asp	Glu	Glu	Arg	Arg	Thr	Ser	Val	Asn	Leu	Asp	Ala	Ser	Ile		
			420					425					430				
atg	gaa	gtt	gct	gac	cgc	ttg	gca	ttc	atc	aac	act	ggc	ttc	ctg	gac	1344	
Met	Glu	Val	Ala	Asp	Arg	Leu	Ala	Phe	Ile	Asn	Thr	Gly	Phe	Leu	Asp		
		435					440					445					
cgc	acc	ggc	gat	gaa	atc	cac	acc	tcc	atg	gaa	gca	ggc	gcc	atg	gtg	1392	
Arg	Thr	Gly	Asp	Glu	Ile	His	Thr	Ser	Met	Glu	Ala	Gly	Ala	Met	Val		
	450					455					460						
cgc	aag	gct	gat	atg	cag	acc	gca	ccg	tgg	aag	cag	gcc	tac	gag	aac	1440	
Arg	Lys	Ala	Asp	Met	Gln	Thr	Ala	Pro	Trp	Lys	Gln	Ala	Tyr	Glu	Asn		
465					470					475					480		
aac	aac	gtt	gat	gca	ggc	att	cag	cg	ggt	ctt	cct	ggc	aag	gct	cag	1488	
Asn	Asn	Val	Asp	Ala	Gly	Ile	Gln	Arg	Gly	Leu	Pro	Gly	Lys	Ala	Gln		
				485					490					495			
atc	ggt	aag	ggc	atg	tgg	gcg	atg	act	gaa	ctc	atg	gca	gaa	atg	ctg	1536	
Ile	Gly	Lys	Gly	Met	Trp	Ala	Met	Thr	Glu	Leu	Met	Ala	Glu	Met	Leu		
			500					505					510				
gag	aag	aag	atc	ggc	cag	cca	cg	gaa	ggc	gcc	aac	act	gca	tgg	gtt	1584	
Glu	Lys	Lys	Ile	Gly	Gln	Pro	Arg	Glu	Gly	Ala	Asn	Thr	Ala	Trp	Val		
		515					520					525					
cct	tca	cca	act	ggt	gcg	acg	ctg	cac	gca	acg	cac	tac	cac	ttg	gtt	1632	
Pro	Ser	Pro	Thr	Gly	Ala	Thr	Leu	His	Ala	Thr	His	Tyr	His	Leu	Val		
	530					535					540						
gat	gtg	ttc	aag	gtt	caa	gac	gaa	ctg	cg	gct	gcc	ggc	cg	cg	gac	1680	
Asp	Val	Phe	Lys	Val	Gln	Asp	Glu	Leu	Arg	Ala	Ala	Gly	Arg	Arg	Asp		
545					550					555					560		
agc	ctg	cg	aac	att	ctc	acc	att	tca	acc	gca	cca	aac	acc	aat	tgg	1728	
Ser	Leu	Arg	Asn	Ile	Leu	Thr	Ile	Ser	Thr	Ala	Pro	Asn	Thr	Asn	Trp		
				565					570					575			
tct	gag	gaa	gag	aag	aag	gaa	gag	atg	gac	aac	aac	tgc	cag	tcc	atc	1776	
Ser	Glu	Glu	Glu	Lys	Lys	Glu	Glu	Met	Asp	Asn	Asn	Cys	Gln	Ser	Ile		
			580					585					590				
ctc	gga	tac	gtt	gtg	cg	tgg	gtt	gag	cac	ggt	gtt	ggt	tgc	tcc	aag	1824	
Leu	Gly	Tyr	Val	Val	Arg	Trp	Val	Glu	His	Gly	Val	Gly	Cys	Ser	Lys		
		595					600					605					
gtt	cca	gac	atc	cat	gac	atc	gac	ctc	atg	gaa	gac	cg	gca	acg	ctg	1872	
Val	Pro	Asp	Ile	His	Asp	Ile	Asp	Leu	Met	Glu	Asp	Arg	Ala	Thr	Leu		

002290" 0420960



```

        610                615                620
cgt att tcc tcg cag atg ctg gcc aac tgg atc cgc cat gat gtt gtc 1920
Arg Ile Ser Ser Gln Met Leu Ala Asn Trp Ile Arg His Asp Val Val
625                630                635                640

tcg aag gag cag gtc ttg gag tca ctg gaa cga atg gca gtg gtc gtc 1968
Ser Lys Glu Gln Val Leu Glu Ser Leu Glu Arg Met Ala Val Val Val
        645                650                655

gac aag caa aat gcg ggc gac gag gcc tac cgc gat atg gcg ccg aag 2016
Asp Lys Gln Asn Ala Gly Asp Glu Ala Tyr Arg Asp Met Ala Pro Lys
        660                665                670

tac gac gcc tcc ctc gcc ttc cag gcg gct aag gac ttg att ttc gaa 2064
Tyr Asp Ala Ser Leu Ala Phe Gln Ala Ala Lys Asp Leu Ile Phe Glu
        675                680                685

ggc acc aag tcc cca tcg ggc tac acc gag ccc atc ttg cac gca cgc 2112
Gly Thr Lys Ser Pro Ser Gly Tyr Thr Glu Pro Ile Leu His Ala Arg
        690                695                700

cgc cgc gag ttc aaa gca aaa aac taagcacgct tttcgacgct tac 2159
Arg Arg Glu Phe Lys Ala Lys Asn
705                710

<210> 596
<211> 712
<212> PRT
<213> Corynebacterium glutamicum

<400> 596
Met Gln Val Ala Lys Val Leu Tyr Asp Phe Val Thr Glu Ala Val Leu
  1                5                10                15

Pro Arg Val Gly Val Asp Ala Glu Lys Phe Trp Ser Gly Phe Ala Ala
        20                25                30

Ile Ala Arg Asp Leu Thr Pro Arg Asn Arg Glu Leu Leu Ala Arg Arg
        35                40                45

Asp Glu Leu Gln Met Leu Ile Asp Asp Tyr His Arg Asn Asn Ser Gly
        50                55                60

Thr Ile Asp Gln Glu Ala Tyr Glu Asp Phe Leu Lys Glu Ile Gly Tyr
        65                70                75                80

Leu Val Glu Glu Pro Glu Ala Ala Glu Ile Arg Thr Gln Asn Val Asp
        85                90                95

Thr Glu Ile Ser Ser Thr Ala Gly Pro Gln Leu Val Val Pro Ile Leu
        100                105                110

Asn Ala Arg Phe Ala Leu Asn Ala Ala Asn Ala Arg Trp Gly Ser Leu
        115                120                125

Tyr Asp Ala Leu Tyr Gly Thr Asn Ala Ile Pro Glu Thr Asp Gly Ala
        130                135                140

Glu Lys Gly Lys Glu Tyr Asn Pro Val Arg Gly Gln Lys Val Ile Glu

```

09602740-062300



003900-062400



```
<400> 597
aaaaattcgg ttcacaaaag gtttatcagt ccagcttaaa cccatcgcac gggcgggaga 60
attagactca aggcacatca cattgaagga gcttcttata ttg tct cga ttt gct 115
```

# THESE



	Leu	Ser	Arg	Phe	Ala	
	1				5	
gcc aac ctg tca ttg act ttt act gag cta gat ttc ctg gat cgt ttt 163	Ala	Asn	Leu	Ser	Leu	Thr
			10			15
						20
gat gcc gct tcg aag cat gct ttc agt gcc gtg gag ttt cag tac cct 211	Asp	Ala	Ala	Ser	Lys	His
			25			30
						35
tac gat ttc gat gtt caa gag att aaa cag cgt gct gat tcc gca ggt 259	Tyr	Asp	Phe	Asp	Val	Gln
		40			45	50
ctg ccc att gaa ctg ttc aat gcc cca cct ggg gat act ttt ggt ctt 307	Leu	Pro	Ile	Glu	Leu	Phe
	55				60	65
gcg gca ctg gct tcc cct gaa gac ttt caa caa tcc atc gag cag gcc 355	Ala	Ala	Leu	Ala	Ser	Pro
	70			75		80
						85
atc acg tac gcc aca gtg ttg aag cca aag aag atg cat gtc atg gct 403	Ile	Thr	Tyr	Ala	Thr	Val
			90			95
						100
ggc atc gcg gac gta acc tca gaa acc acg gcg cgc tat gtg gag aat 451	Gly	Ile	Ala	Asp	Val	Thr
			105			110
						115
att cgc tgg gct gcg cag caa cta gac aag ctc gac gtt gtc gtt gtt 499	Ile	Arg	Trp	Ala	Ala	Gln
		120			Gln	Leu
					125	130
att gaa cca att aat cac tat tcg gtt ccc ggt tat ttc ctg cac act 547	Ile	Glu	Pro	Ile	Asn	His
	135				140	145
tta gag cag gcg tat tgg ctt atc gac agc att gcc cac ccc aat gtg 595	Leu	Glu	Gln	Ala	Tyr	Trp
	150				155	160
						165
aag atc tta ttc gat act ttc cac ctt cag cag att cat ggc aat ctc 643	Lys	Ile	Leu	Phe	Asp	Thr
			170			175
						180
acc cgc cgc ctg cgc gag gtt cat ggc gca ggt ctt ttg gga cac gtg 691	Thr	Arg	Arg	Leu	Arg	Glu
			185			190
						195
caa gtg gcc tca gtt cct gat cga cac gaa cct ggc act ggc gaa gtc 739	Gln	Val	Ala	Ser	Val	Pro
		200				205
						210
aat gcg gcg tat atc ttc caa ctc cta agc gaa ctg gga tat gac ggt 787	Asn	Ala	Ala	Tyr	Ile	Phe
	215				220	225
gtc atc gct ggc gaa tac cac cct gct ggt gaa act aca gcc ggt ttg 835	Val	Ile	Ala	Gly	Glu	Tyr
					His	Pro
					Ala	Gly

002250 0420960



230                      235                      240                      245

ggc tgg ttg gag ctc tagatcgtaa gtggtgtcgt acc                      873

Gly Trp Leu Glu Leu

250

<210> 598  
 <211> 250  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 598

Leu	Ser	Arg	Phe	Ala	Ala	Asn	Leu	Ser	Leu	Thr	Phe	Thr	Glu	Leu	Asp
1				5					10					15	
Phe	Leu	Asp	Arg	Phe	Asp	Ala	Ala	Ser	Lys	His	Ala	Phe	Ser	Ala	Val
			20					25					30		
Glu	Phe	Gln	Tyr	Pro	Tyr	Asp	Phe	Asp	Val	Gln	Glu	Ile	Lys	Gln	Arg
		35					40					45			
Ala	Asp	Ser	Ala	Gly	Leu	Pro	Ile	Glu	Leu	Phe	Asn	Ala	Pro	Pro	Gly
	50					55					60				
Asp	Thr	Phe	Gly	Leu	Ala	Ala	Leu	Ala	Ser	Pro	Glu	Asp	Phe	Gln	Gln
65					70					75					80
Ser	Ile	Glu	Gln	Ala	Ile	Thr	Tyr	Ala	Thr	Val	Leu	Lys	Pro	Lys	Lys
				85					90					95	
Met	His	Val	Met	Ala	Gly	Ile	Ala	Asp	Val	Thr	Ser	Glu	Thr	Thr	Ala
			100					105					110		
Arg	Tyr	Val	Glu	Asn	Ile	Arg	Trp	Ala	Ala	Gln	Gln	Leu	Asp	Lys	Leu
		115					120					125			
Asp	Val	Val	Val	Val	Ile	Glu	Pro	Ile	Asn	His	Tyr	Ser	Val	Pro	Gly
	130					135					140				
Tyr	Phe	Leu	His	Thr	Leu	Glu	Gln	Ala	Tyr	Trp	Leu	Ile	Asp	Ser	Ile
145					150					155					160
Ala	His	Pro	Asn	Val	Lys	Ile	Leu	Phe	Asp	Thr	Phe	His	Leu	Gln	Gln
				165					170					175	
Ile	His	Gly	Asn	Leu	Thr	Arg	Arg	Leu	Arg	Glu	Val	His	Gly	Ala	Gly
			180					185					190		
Leu	Leu	Gly	His	Val	Gln	Val	Ala	Ser	Val	Pro	Asp	Arg	His	Glu	Pro
		195					200					205			
Gly	Thr	Gly	Glu	Val	Asn	Ala	Ala	Tyr	Ile	Phe	Gln	Leu	Leu	Ser	Glu
	210					215					220				
Leu	Gly	Tyr	Asp	Gly	Val	Ile	Ala	Gly	Glu	Tyr	His	Pro	Ala	Gly	Glu
225					230					235					240
Thr	Thr	Ala	Gly	Leu	Gly	Trp	Leu	Glu	Leu						
				245					250						

09602740.062300



```
<220>
<221> CDS
<222> (101)..(874)
<223> RXA01886
```

0960270-0000



```

att ggc gaa gga aac ctc att gag ctg ctc cgt gag gcg cag cca ttc 691
Ile Gly Glu Gly Asn Leu Ile Glu Leu Leu Arg Glu Ala Gln Pro Phe
      185                      190                      195

atc ggc gaa atc cag gtt gcc gat gtc ccc ggc cgc atg gaa ccc ggc 739
Ile Gly Glu Ile Gln Val Ala Asp Val Pro Gly Arg Met Glu Pro Gly
      200                      205                      210

acc ggc gag atc aac tac cag ggc gtc gcg aaa gct ctc gcc gcg atg 787
Thr Gly Glu Ile Asn Tyr Gln Gly Val Ala Lys Ala Leu Ala Ala Met
      215                      220                      225

ggc tac gac ggc gtc atc ggc atg gag gcg tgg gca tcg ggc gac tcc 835
Gly Tyr Asp Gly Val Ile Gly Met Glu Ala Trp Ala Ser Gly Asp Ser
      230                      235                      240                      245

agc gac gcg ctg cag gcg ttg aag tca gcg ttc acg gtc taaattgctt 884
Ser Asp Ala Leu Gln Ala Leu Lys Ser Ala Phe Thr Val
      250                      255

atcgacgcac ccc 897

```

```

<210> 600
<211> 258
<212> PRT
<213> Corynebacterium glutamicum

```

```

<400> 600
Met Thr Phe Lys Leu Ala Ala Cys Ala Glu Met Ile Tyr Gln Asp Leu
  1              5              10              15

Pro Phe Glu Glu Arg Val Lys Thr Ile Ser Asp Gln Gly Phe Leu Val
      20              25              30

Glu Ile Trp Asp Trp Ser Thr Lys Asp Ile Asp Ala Leu Val Ala Thr
      35              40              45

Gly Ala Glu Phe Ser Ser Met Thr Gly Tyr Leu Arg Gly Asp Leu Ile
      50              55              60

Thr Glu Gln Gly Arg Ala Glu Leu Leu Ala Thr Ala Ser Glu Ser Leu
      65              70              75              80

Ala Val Ala Glu Lys Leu Asn Cys Pro Arg Leu Asn Leu His Gly Thr
      85              90              95

Gly Leu Gly Pro Gln Gly Leu Pro Val Thr Pro Ile Glu Val Val Thr
      100             105             110

Pro Glu Met Trp Leu Tyr Ala Ala Glu Thr Leu Arg Gln Ile Ala Glu
      115             120             125

Leu Gly Glu Arg Ala Gly Lys Val Phe Val Leu Glu Asn Leu Asn Leu
      130             135             140

Ala Val Asp His Pro Gly Thr Pro Phe Ala Lys Ala Thr Asp Thr Leu
      145             150             155             160

Ala Leu Val Lys Ala Val Asn His Pro Asn Leu Arg Leu Asn Leu Asp

```

09602740-062300



<400> 601															
tgtgcaacat tagttcggtta agaagagtca cattccagcc atg att acc cac gaa															55
Met Ile Thr His Glu															
1 1 1 1 5															
gtg cgc acc cac cgt tct gcg gaa gag ttc ccg tac aag aag cac ctg															103
Val Arg Thr His Arg Ser Ala Glu Glu Phe Pro Tyr Lys Lys His Leu															
10 15 20															
gct cac aag atg gct cgc gtt gca gcc gac cca gtt gag gtt gct gcg															151
Ala His Lys Met Ala Arg Val Ala Ala Asp Pro Val Glu Val Ala Ala															
25 30 35															
gac act cag gaa atg atc atc acc cgc atc atc gac aat gca tcg gtg															199
Asp Thr Gln Glu Met Ile Ile Thr Arg Ile Ile Asp Asn Ala Ser Val															
40 45 50															
cag gca gct tcc gtg ttg cgt cga cca gtt agc tct gcc cgt gcg atg															247
Gln Ala Ala Ser Val Leu Arg Arg Pro Val Ser Ser Ala Arg Ala Met															
55 60 65															
gca cag gtc agg cca gtt acc gat ggt cgg ggt gca tct gtt ttc ggt															295
Ala Gln Val Arg Pro Val Thr Asp Gly Arg Gly Ala Ser Val Phe Gly															
70 75 80 85															
ctg cca gga cgt tat gcc gcg gaa tgg gct gcg ctt gct aac ggc act															343
Leu Pro Gly Arg Tyr Ala Ala Glu Trp Ala Ala Leu Ala Asn Gly Thr															
90 95 100															
gcg gtg cgt gag ctt gat ttc cat gac acg ttc ctc gct gcg gaa tac															391

**SECRET**



**SECRET**



```

          345          350          355
ttc gct gtc gcg ctg aag gat cgc gcg tgg cac cac gag cgt tcc tat 1159
Phe Ala Val Ala Leu Lys Asp Arg Ala Trp His His Glu Arg Ser Tyr
          360          365          370

gct cct gag cga gcc cac cgc cga gag acc atc gag ctg tgg aac aag 1207
Ala Pro Glu Arg Ala His Arg Arg Glu Thr Ile Glu Leu Trp Asn Lys
          375          380          385

att tcc acg gtg gag gat cct gaa tgg acc agg cgt tac cac tcc gtt 1255
Ile Ser Thr Val Glu Asp Pro Glu Trp Thr Arg Arg Tyr His Ser Val
          390          395          400          405

gat cct gca gaa aag gcc ttc ggc gca cgc gca gtg atc acc ttc aag 1303
Asp Pro Ala Glu Lys Ala Phe Gly Ala Arg Ala Val Ile Thr Phe Lys
          410          415          420

gat gga acc gtc gtg gaa gat gaa ctg gct gtg gcg aat gcg cat cct 1351
Asp Gly Thr Val Val Glu Asp Glu Leu Ala Val Ala Asn Ala His Pro
          425          430          435

ctg gga gca cgg cct ttc gct agg gag cag tac att cag aaa ttc cgc 1399
Leu Gly Ala Arg Pro Phe Ala Arg Glu Gln Tyr Ile Gln Lys Phe Arg
          440          445          450

acc ttg gct gaa ggt gtt gtg tcc gaa aag gaa cag gat cgc ttc ttg 1447
Thr Leu Ala Glu Gly Val Val Ser Glu Lys Glu Gln Asp Arg Phe Leu
          455          460          465

gat gcg gca cag cgt acg cac gag ctt gag gat ctt tca gaa ctc aac 1495
Asp Ala Ala Gln Arg Thr His Glu Leu Glu Asp Leu Ser Glu Leu Asn
          470          475          480          485

att gaa ttg gat gcc gat att ttg gcc aag gct cct gtg att ccg gaa 1543
Ile Glu Leu Asp Ala Asp Ile Leu Ala Lys Ala Pro Val Ile Pro Glu
          490          495          500

gga ctg ttc tgatggcggg tttgttttcc tct 1575
Gly Leu Phe

```

&lt;210&gt; 602

&lt;211&gt; 504

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 602

```

Met Ile Thr His Glu Val Arg Thr His Arg Ser Ala Glu Glu Phe Pro
  1             5             10             15

```

```

Tyr Lys Lys His Leu Ala His Lys Met Ala Arg Val Ala Ala Asp Pro
      20             25             30

```

```

Val Glu Val Ala Ala Asp Thr Gln Glu Met Ile Ile Thr Arg Ile Ile
      35             40             45

```

```

Asp Asn Ala Ser Val Gln Ala Ala Ser Val Leu Arg Arg Pro Val Ser
      50             55             60

```

003290 0420960



Ser Ala Arg Ala Met Ala Gln Val Arg Pro Val Thr Asp Gly Arg Gly  
 65 70 75 80  
 Ala Ser Val Phe Gly Leu Pro Gly Arg Tyr Ala Ala Glu Trp Ala Ala  
 85 90 95  
 Leu Ala Asn Gly Thr Ala Val Arg Glu Leu Asp Phe His Asp Thr Phe  
 100 105 110  
 Leu Ala Ala Glu Tyr Ser His Pro Gly Asp Asn Ile Pro Pro Ile Leu  
 115 120 125  
 Ala Ala Ala Gln Gln Ala Gly Lys Gly Gly Lys Asp Leu Ile Arg Gly  
 130 135 140  
 Ile Ala Thr Gly Tyr Glu Ile Gln Val Asn Leu Val Arg Gly Met Cys  
 145 150 155 160  
 Leu His Glu His Lys Ile Asp His Val Ala His Leu Gly Pro Ser Ala  
 165 170 175  
 Ala Ala Gly Ile Gly Thr Leu Leu Asp Leu Asp Val Asp Thr Ile Tyr  
 180 185 190  
 Gln Ala Ile Gly Gln Ala Leu His Thr Thr Thr Ala Thr Arg Gln Ser  
 195 200 205  
 Arg Lys Gly Ala Ile Ser Ser Trp Lys Ala Phe Ala Pro Ala Phe Ala  
 210 215 220  
 Gly Lys Met Ser Ile Glu Ala Val Asp Arg Ala Met Arg Gly Glu Gly  
 225 230 235 240  
 Ala Pro Ser Pro Ile Trp Glu Gly Glu Asp Gly Val Ile Ala Trp Leu  
 245 250 255  
 Leu Ser Gly Leu Asp His Ile Tyr Thr Ile Pro Leu Pro Ala Glu Gly  
 260 265 270  
 Glu Ala Lys Arg Ala Ile Leu Asp Thr Tyr Thr Lys Glu His Ser Ala  
 275 280 285  
 Glu Tyr Gln Ser Gln Ala Pro Ile Asp Leu Ala Arg Ser Met Gly Glu  
 290 295 300  
 Lys Leu Ala Ala Gln Gly Leu Asp Leu Arg Asp Val Asp Ser Ile Val  
 305 310 315 320  
 Leu His Thr Ser His His Thr His Tyr Val Ile Gly Thr Gly Ser Asn  
 325 330 335  
 Asp Pro Gln Lys Phe Asp Pro Asp Ala Ser Arg Glu Thr Leu Asp His  
 340 345 350  
 Ser Ile Met Tyr Ile Phe Ala Val Ala Leu Lys Asp Arg Ala Trp His  
 355 360 365  
 His Glu Arg Ser Tyr Ala Pro Glu Arg Ala His Arg Arg Glu Thr Ile  
 370 375 380  
 Glu Leu Trp Asn Lys Ile Ser Thr Val Glu Asp Pro Glu Trp Thr Arg

09602740, 062300



```
<210> 603
<211> 975
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (1)..(975)  
<223> FRXA00406
```

<400> 603																
gac	cca	gtt	gag	gtt	gct	gcg	gac	act	cag	gaa	atg	atc	atc	acc	cgc	48
Asp	Pro	Val	Glu	Val	Ala	Ala	Asp	Thr	Gln	Glu	Met	Ile	Ile	Thr	Arg	
1				5					10					15		
atc	atc	gac	aat	gca	tcg	gtg	cag	gca	gct	tcc	gtg	ttg	cgt	cga	cca	96
Ile	Ile	Asp	Asn	Ala	Ser	Val	Gln	Ala	Ala	Ser	Val	Leu	Arg	Arg	Pro	
			20					25					30			
gtt	agc	tct	gcc	cgt	gcg	atg	gca	cag	gtc	agg	cca	gtt	acc	gat	ggc	144
Val	Ser	Ser	Ala	Arg	Ala	Met	Ala	Gln	Val	Arg	Pro	Val	Thr	Asp	Gly	
		35					40					45				
cgg	ggc	gca	tct	gtt	ttc	ggc	ctg	cca	gga	cgt	tat	gcc	gcg	gaa	tgg	192
Arg	Gly	Ala	Ser	Val	Phe	Gly	Leu	Pro	Gly	Arg	Tyr	Ala	Ala	Glu	Trp	
	50					55					60					
gct	gcg	ctt	gct	aac	ggc	act	gcg	gtg	cgt	gag	ctt	gat	ttc	cat	gac	240
Ala	Ala	Leu	Ala	Asn	Gly	Thr	Ala	Val	Arg	Glu	Leu	Asp	Phe	His	Asp	
65					70					75					80	
acg	ttc	ctc	gct	gcg	gaa	tac	tcc	cac	cca	gga	gat	aac	att	cct	ccg	288
Thr	Phe	Leu	Ala	Ala	Glu	Tyr	Ser	His	Pro	Gly	Asp	Asn	Ile	Pro	Pro	
				85					90					95		
att	ttg	gct	gca	gca	cag	cag	gct	gga	aaa	ggc	ggc	aag	gat	ctg	atc	336
Ile	Leu	Ala	Ala	Ala	Gln	Gln	Ala	Gly	Lys	Gly	Gly	Lys	Asp	Leu	Ile	

1. The first part of the document discusses the importance of maintaining accurate records of all transactions and activities. It emphasizes that proper record-keeping is essential for transparency and accountability, particularly in the context of public administration and financial management.

2. The second part of the document outlines the various methods and tools used to collect, analyze, and report data. It highlights the need for standardized procedures and the use of modern technology to ensure the reliability and accuracy of the information gathered.

3. The third part of the document focuses on the role of the data in decision-making processes. It explains how the collected information is used to identify trends, assess risks, and develop effective strategies to address challenges and improve performance.

4. The fourth part of the document discusses the importance of communication and collaboration in the data management process. It stresses that sharing information and working together across different departments and levels of the organization are crucial for achieving the desired outcomes.

5. The fifth part of the document concludes by summarizing the key points and reiterating the commitment to continuous improvement and innovation in data management practices.



100										105					110					
cgt	ggc	atc	gct	act	ggg	tat	gag	att	cag	gtt	aac	ttg	gtg	cgt	gga	384				
Arg	Gly	Ile	Ala	Thr	Gly	Tyr	Glu	Ile	Gln	Val	Asn	Leu	Val	Arg	Gly					
		115					120					125								
atg	tgc	ctg	cat	gag	cac	aag	att	gat	cac	gtt	gct	cat	ctt	gga	cca	432				
Met	Cys	Leu	His	Glu	His	Lys	Ile	Asp	His	Val	Ala	His	Leu	Gly	Pro					
	130					135					140									
tca	gcg	gct	gct	ggg	atc	gga	acc	ttg	cta	gac	cta	gat	gtg	gac	acc	480				
Ser	Ala	Ala	Ala	Gly	Ile	Gly	Thr	Leu	Leu	Asp	Leu	Asp	Val	Asp	Thr					
145					150					155					160					
atc	tac	cag	gca	att	ggg	cag	gca	ttg	cac	acc	acc	acg	gcg	acg	agg	528				
Ile	Tyr	Gln	Ala	Ile	Gly	Gln	Ala	Leu	His	Thr	Thr	Thr	Ala	Thr	Arg					
				165					170					175						
cag	tcc	cgt	aaa	ggg	gcg	att	tct	tca	tgg	aag	gca	ttt	gct	cct	gcg	576				
Gln	Ser	Arg	Lys	Gly	Ala	Ile	Ser	Ser	Trp	Lys	Ala	Phe	Ala	Pro	Ala					
			180					185					190							
ttt	gcg	ggc	aag	atg	tcc	atc	gag	gca	gta	gat	cgc	gca	atg	cgt	ggc	624				
Phe	Ala	Gly	Lys	Met	Ser	Ile	Glu	Ala	Val	Asp	Arg	Ala	Met	Arg	Gly					
		195					200					205								
gag	ggc	gca	ccg	tca	cca	atc	tgg	gaa	ggc	gaa	gac	ggc	gta	atc	gcg	672				
Glu	Gly	Ala	Pro	Ser	Pro	Ile	Trp	Glu	Gly	Glu	Asp	Gly	Val	Ile	Ala					
	210					215					220									
tgg	ctg	ctg	tcc	ggg	ctt	gat	cac	atc	tac	acc	att	cct	ttg	cct	gca	720				
Trp	Leu	Leu	Ser	Gly	Leu	Asp	His	Ile	Tyr	Thr	Ile	Pro	Leu	Pro	Ala					
225					230					235					240					
gaa	ggg	gaa	gcc	aaa	cga	gca	atc	ttg	gat	acc	tac	acc	aag	gaa	cac	768				
Glu	Gly	Glu	Ala	Lys	Arg	Ala	Ile	Leu	Asp	Thr	Tyr	Thr	Lys	Glu	His					
				245					250					255						
tcg	gcg	gaa	tac	cag	tca	cag	gca	ccg	atc	gac	ttg	gcg	cgc	agc	atg	816				
Ser	Ala	Glu	Tyr	Gln	Ser	Gln	Ala	Pro	Ile	Asp	Leu	Ala	Arg	Ser	Met					
			260					265					270							
ggg	gag	aag	ctg	gca	gca	cag	ggc	ttg	gac	ctg	cgt	gat	gtg	gac	tcc	864				
Gly	Glu	Lys	Leu	Ala	Ala	Gln	Gly	Leu	Asp	Leu	Arg	Asp	Val	Asp	Ser					
		275					280					285								
atc	gtt	ttg	cac	acc	tcc	cac	cac	act	cac	tac	gtg	atc	ggc	acc	gga	912				
Ile	Val	Leu	His	Thr	Ser	His	His	Thr	His	Tyr	Val	Ile	Gly	Thr	Gly					
		290					295				300									
tct	aat	gat	cca	cag	aag	ttc	gat	cca	gat	gca	tcg	cga	gaa	acc	ctt	960				
Ser	Asn	Asp	Pro	Gln	Lys	Phe	Asp	Pro	Asp	Ala	Ser	Arg	Glu	Thr	Leu					
305					310					315					320					
gat	cac	tcc	atc	atg												975				
Asp	His	Ser	Ile	Met																
				325																

&lt;210&gt; 604

&lt;211&gt; 325

09602740 "062300



&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 604

```

Asp Pro Val Glu Val Ala Ala Asp Thr Gln Glu Met Ile Ile Thr Arg
 1           5           10           15

Ile Ile Asp Asn Ala Ser Val Gln Ala Ala Ser Val Leu Arg Arg Pro
          20           25           30

Val Ser Ser Ala Arg Ala Met Ala Gln Val Arg Pro Val Thr Asp Gly
          35           40           45

Arg Gly Ala Ser Val Phe Gly Leu Pro Gly Arg Tyr Ala Ala Glu Trp
 50           55           60

Ala Ala Leu Ala Asn Gly Thr Ala Val Arg Glu Leu Asp Phe His Asp
 65           70           75           80

Thr Phe Leu Ala Ala Glu Tyr Ser His Pro Gly Asp Asn Ile Pro Pro
          85           90           95

Ile Leu Ala Ala Ala Gln Gln Ala Gly Lys Gly Gly Lys Asp Leu Ile
          100          105          110

Arg Gly Ile Ala Thr Gly Tyr Glu Ile Gln Val Asn Leu Val Arg Gly
 115          120          125

Met Cys Leu His Glu His Lys Ile Asp His Val Ala His Leu Gly Pro
 130          135          140

Ser Ala Ala Ala Gly Ile Gly Thr Leu Leu Asp Leu Asp Val Asp Thr
 145          150          155          160

Ile Tyr Gln Ala Ile Gly Gln Ala Leu His Thr Thr Thr Ala Thr Arg
          165          170          175

Gln Ser Arg Lys Gly Ala Ile Ser Ser Trp Lys Ala Phe Ala Pro Ala
          180          185          190

Phe Ala Gly Lys Met Ser Ile Glu Ala Val Asp Arg Ala Met Arg Gly
          195          200          205

Glu Gly Ala Pro Ser Pro Ile Trp Glu Gly Glu Asp Gly Val Ile Ala
 210          215          220

Trp Leu Leu Ser Gly Leu Asp His Ile Tyr Thr Ile Pro Leu Pro Ala
 225          230          235          240

Glu Gly Glu Ala Lys Arg Ala Ile Leu Asp Thr Tyr Thr Lys Glu His
          245          250          255

Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile Asp Leu Ala Arg Ser Met
          260          265          270

Gly Glu Lys Leu Ala Ala Gln Gly Leu Asp Leu Arg Asp Val Asp Ser
          275          280          285

Ile Val Leu His Thr Ser His His Thr His Tyr Val Ile Gly Thr Gly
 290          295          300

```

09602740 062300



Ser Asn Asp Pro Gln Lys Phe Asp Pro Asp Ala Ser Arg Glu Thr Leu  
305 310 315 320

Asp His Ser Ile Met  
325

<210> 605

<211> 431

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(408)

<223> FRXA00514

<400> 605

cac gag cgt tcc tat gct cct gag cga gcc ctc cgc cga gag acc atc 48  
His Glu Arg Ser Tyr Ala Pro Glu Arg Ala Leu Arg Arg Glu Thr Ile  
1 5 10 15

gag ctg tgg aac aag att tcc acg gtg gag gat cct gaa tgg acc agg 96  
Glu Leu Trp Asn Lys Ile Ser Thr Val Glu Asp Pro Glu Trp Thr Arg  
20 25 30

cgt tac cac tcc gtt gat cct gca gaa aag gcc ttc ggc gca cgc gca 144  
Arg Tyr His Ser Val Asp Pro Ala Glu Lys Ala Phe Gly Ala Arg Ala  
35 40 45

gtg atc acc ttc aag gat gga acc gtc gtg gaa gat gaa ctg gct gtg 192  
Val Ile Thr Phe Lys Asp Gly Thr Val Val Glu Asp Glu Leu Ala Val  
50 55 60

gcg aat gcg cat cct ctg gga gca cgg cct ttc gct agg gag cag tac 240  
Ala Asn Ala His Pro Leu Gly Ala Arg Pro Phe Ala Arg Glu Gln Tyr  
65 70 75 80

att cag aaa ttc cgc acc ttg gct gaa ggt gtt gtg tcc gaa aag gaa 288  
Ile Gln Lys Phe Arg Thr Leu Ala Glu Gly Val Val Ser Glu Lys Glu  
85 90 95

cag gat cgc ttc ttg gat gcg gca cag cgt acg cac gag ctt gag gat 336  
Gln Asp Arg Phe Leu Asp Ala Ala Gln Arg Thr His Glu Leu Glu Asp  
100 105 110

ctt tca gaa ctc aac att gaa ttg gat gcc gat att ttg gcc aag gct 384  
Leu Ser Glu Leu Asn Ile Glu Leu Asp Ala Asp Ile Leu Ala Lys Ala  
115 120 125

cct gtg att ccg gaa gga ctg ttc tgatggcggg tttgttttcc tct 431  
Pro Val Ile Pro Glu Gly Leu Phe  
130 135

<210> 606

<211> 136

<212> PRT

<213> Corynebacterium glutamicum

<400> 606

09602740 062300



His Glu Arg Ser Tyr Ala Pro Glu Arg Ala Leu Arg Arg Glu Thr Ile  
 1 5 10 15  
 Glu Leu Trp Asn Lys Ile Ser Thr Val Glu Asp Pro Glu Trp Thr Arg  
 20 25 30  
 Arg Tyr His Ser Val Asp Pro Ala Glu Lys Ala Phe Gly Ala Arg Ala  
 35 40 45  
 Val Ile Thr Phe Lys Asp Gly Thr Val Val Glu Asp Glu Leu Ala Val  
 50 55 60  
 Ala Asn Ala His Pro Leu Gly Ala Arg Pro Phe Ala Arg Glu Gln Tyr  
 65 70 75 80  
 Ile Gln Lys Phe Arg Thr Leu Ala Glu Gly Val Val Ser Glu Lys Glu  
 85 90 95  
 Gln Asp Arg Phe Leu Asp Ala Ala Gln Arg Thr His Glu Leu Glu Asp  
 100 105 110  
 Leu Ser Glu Leu Asn Ile Glu Leu Asp Ala Asp Ile Leu Ala Lys Ala  
 115 120 125  
 Pro Val Ile Pro Glu Gly Leu Phe  
 130 135

<210> 607  
 <211> 718  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(718)  
 <223> RXA00512

<400> 607  
 tacaacgagt acaacgcttt cgaccagcaa gtattcacct attccgctga cagctacaag 60  
 cccatcttct aaccgccta tatataagga gtgaatcacc atg tcc agc gcc aca 115  
 Met Ser Ser Ala Thr 5  
 acc act gat gtt cgc aaa ggg ctc tac gga gtc atc gcc gat tac acg 163  
 Thr Thr Asp Val Arg Lys Gly Leu Tyr Gly Val Ile Ala Asp Tyr Thr 20  
 gcc gtt tcc aaa gtc atg cca gag acc aat tca ctg acc tac cgt ggc 211  
 Ala Val Ser Lys Val Met Pro Glu Thr Asn Ser Leu Thr Tyr Arg Gly 25 30 35  
 tac gcg gtg gaa gat ttg gtg gaa aac tgc agc ttc gag gag gtg ttt 259  
 Tyr Ala Val Glu Asp Leu Val Glu Asn Cys Ser Phe Glu Glu Val Phe 40 45 50  
 tac ctc ctg tgg cac ggc gag ctg ccc act gcg caa caa ctt gcg gag 307  
 Tyr Leu Leu Trp His Gly Glu Leu Pro Thr Ala Gln Gln Leu Ala Glu 55 60 65

09602740-062300



```
tcc ctg atc cac tct ttg ccc aaa gaa gcc cac ccg atg gat gtt atg 403
Ser Leu Ile His Ser Leu Pro Lys Glu Ala His Pro Met Asp Val Met
          90                      95                      100
```

cgc acc gcg gtg tcc tac atg ggc acc aag gat tcc gag tat ttc acc 451  
 Arg Thr Ala Val Ser Tyr Met Gly Thr Lys Asp Ser Glu Tyr Phe Thr  
 105 110 115

acc gat tct gag cac atc cgc aaa gtt ggc cac acc ttg ttg gcg cag 499  
Thr Asp Ser Glu His Ile Arg Lys Val Gly His Thr Leu Leu Ala Gln  
120 125 130

ctt ccg atg gtg cta gcc atg gat att cgt cgc cgc aag ggc ctc gat 547  
Leu Pro Met Val Leu Ala Met Asp Ile Arg Arg Arg Lys Gly Leu Asp  
135 140 145

atc atc gcc cct gac tcc agc aag tca gtc gcc gaa aac ctg ctg tct 595  
Ile Ile Ala Pro Asp Ser Ser Lys Ser Val Ala Glu Asn Leu Leu Ser  
150 155 160 165

atg gtg ttt ggt act ggc ccg gaa tca cct gca tcc aac cca gct gac 643  
Met Val Phe Gly Thr Gly Pro Glu Ser Pro Ala Ser Asn Pro Ala Asp  
170 175 180

gtc cgc gat ttt gag aaa tca ctg atc ctc tac gcc gag cac tcc ttc 691  
Val Arg Asp Phe Glu Lys Ser Leu Ile Leu Tyr Ala Glu His Ser Phe  
185 190 195

aac gcc tcc acc ttc acc gcc cgc gtg	718
Asn Ala Ser Thr Phe Thr Ala Arg Val	
200	205

<213> Corynebacterium glutamicum

Met Ser Ser Ala Thr Thr Thr Asp Val Arg Lys Gly Leu Tyr Gly Val  
1 5 10 15

Ile Ala Asp Tyr Thr Ala Val Ser Lys Val Met Pro Glu Thr Asn Ser  
20 25 30

Leu Thr Tyr Arg Gly Tyr Ala Val Glu Asp Leu Val Glu Asn Cys Ser  
35 40 45

Phe Glu Glu Val Phe Tyr Leu Leu Trp His Gly Glu Leu Pro Thr Ala  
50 55 60

Gln Gln Leu Ala Glu Phe Asn Glu Arg Gly Arg Ser Tyr Arg Ser Leu  
65 70 75 80

Asp Ala Gly Leu Ile Ser Leu Ile His Ser Leu Pro Lys Glu Ala His  
85 90 95



```
<210> 609
<211> 320
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (1) .. (297)  
<223> RXA00518
```

<400> 609																
gtc	ctt	ccg	gta	tta	gct	gcc	cgc	cac	gac	ggc	gaa	aag	tgg	gtt	gcc	48
Val	Leu	Pro	Val	Leu	Ala	Ala	Arg	His	Asp	Gly	Glu	Lys	Trp	Val	Ala	
1				5				10				15				
atg	tat	gaa	aac	atg	cgc	gac	gcc	atg	gac	gcc	cgc	acc	ggc	atc	aag	96
Met	Tyr	Glu	Asn	Met	Arg	Asp	Ala	Met	Asp	Ala	Arg	Thr	Gly	Ile	Lys	
20				25				30								
ccg	aat	ctc	gat	ttc	cct	gct	ggc	cct	gcc	tac	cac	ctg	ctc	ggt	ttc	144
Pro	Asn	Leu	Asp	Phe	Pro	Ala	Gly	Pro	Ala	Tyr	His	Leu	Leu	Gly	Phe	
35				40				45								
ccg	gtc	gat	ttc	ttc	acc	ccg	ctg	ttc	gtc	atc	gcc	cgc	gtc	gcc	ggc	192
Pro	Val	Asp	Phe	Phe	Thr	Pro	Leu	Phe	Val	Ile	Ala	Arg	Val	Ala	Gly	
50				55				60								
tgg	acg	gcc	cac	atc	gtg	gag	cag	tac	gaa	aac	aac	tcg	ctc	atc	cgc	240
Trp	Thr	Ala	His	Ile	Val	Glu	Gln	Tyr	Glu	Asn	Asn	Ser	Leu	Ile	Arg	
65				70				75				80				
cca	ctg	tcc	gag	tac	aac	ggc	gag	gag	cag	cgc	gag	gtc	gcg	ccc	att	288
Pro	Leu	Ser	Glu	Tyr	Asn	Gly	Glu	Glu	Gln	Arg	Glu	Val	Ala	Pro	Ile	
85				90				95								
gaa aag cgc taaaagattt tcgcttttcg acg																320
Glu Lys Arg																







aaa acc agt ccg gaa cgt gca gca ttt ttc aac agc gca tta agc cgc 355  
 Lys Thr Ser Pro Glu Arg Ala Ala Phe Phe Asn Ser Ala Leu Ser Arg  
 70 75 80 85

tac ctc gac ttc atg gac gcc tac cta gca aag ggc gaa acc aac cac 403  
 Tyr Leu Asp Phe Met Asp Ala Tyr Leu Ala Lys Gly Glu Thr Asn His  
 90 95 100

ccc tcg gat aac ttc gga gca gtg ctc gct gca gcc gaa agc gtt ggc 451  
 Pro Ser Asp Asn Phe Gly Ala Val Leu Ala Ala Ala Glu Ser Val Gly  
 105 110 115

gcc tct gga aaa gac ctg ctc acc gca ttc gcc gtg gcc tac cag gta 499  
 Ala Ser Gly Lys Asp Leu Leu Thr Ala Phe Ala Val Ala Tyr Gln Val  
 120 125 130

cac acc aga ctt tca gat gtc gca cca gtt cgc gcc aaa ggt ttc gat 547  
 His Thr Arg Leu Ser Asp Val Ala Pro Val Arg Ala Lys Gly Phe Asp  
 135 140 145

cac acc acc caa gga gca ttc gca gcg ggc gca tct gct gcc aag gca 595  
 His Thr Thr Gln Gly Ala Phe Ala Ala Gly Ala Ser Ala Ala Lys Ala  
 150 155 160 165

ctg ggt ttg cca gct gat caa atc gcc aac gca ctg gcc atc gca gga 643  
 Leu Gly Leu Pro Ala Asp Gln Ile Ala Asn Ala Leu Ala Ile Ala Gly  
 170 175 180

aca gcc aat gtt gca ctt cgt gtc act cgc act gga aac ttg agc cac 691  
 Thr Ala Asn Val Ala Leu Arg Val Thr Arg Thr Gly Asn Leu Ser His  
 185 190 195

tgg aaa ggc ctt gcc tac cca cac gtg tcc aaa gaa gga acc tgg gca 739  
 Trp Lys Gly Leu Ala Tyr Pro His Val Ser Lys Glu Gly Thr Trp Ala  
 200 205 210

gca ctg ctc gca agc cga ggt att acc ggt ccg gaa gaa gtc ttc gaa 787  
 Ala Leu Leu Ala Ser Arg Gly Ile Thr Gly Pro Glu Glu Val Phe Glu  
 215 220 225

ggc aac aag gga ttc aaa gag tcc gtc tcc gga ccg ttc gag atc gat 835  
 Gly Asn Lys Gly Phe Lys Glu Ser Val Ser Gly Pro Phe Glu Ile Asp  
 230 235 240 245

tgg tcc aag gaa gac ttg gaa agc gtt aag cgc acc atc atc aag aaa 883  
 Trp Ser Lys Glu Asp Leu Glu Ser Val Lys Arg Thr Ile Ile Lys Lys  
 250 255 260

cac aac gcg gaa att cac tcg cag tca gcg ctt gat gca gcc caa gaa 931  
 His Asn Ala Glu Ile His Ser Gln Ser Ala Leu Asp Ala Ala Gln Glu  
 265 270 275

ata cgc gca caa gaa ggc ttc aat gtg gac aac att gaa aag att cac 979  
 Ile Arg Ala Gln Glu Gly Phe Asn Val Asp Asn Ile Glu Lys Ile His  
 280 285 290

ctg act act ttc gac gtt gcc tac tcc atc att ggc ggc ggc gaa gaa 1027  
 Leu Thr Thr Phe Asp Val Ala Tyr Ser Ile Ile Gly Gly Gly Glu Glu  
 295 300 305

09602740-062300



<400> 612															
Met	Thr	Glu	Ser	Gln	Asp	Leu	Ala	Ala	Phe	Val	Glu	Ala	Ala	Lys	Leu
1				5					10					15	
Asn	Asp	Ala	Ser	Pro	Glu	Ala	Val	Glu	Gln	Leu	Lys	Ile	Arg	Val	Leu
			20					25					30		
Asp	Thr	Val	Gly	Val	Ala	Ile	Gly	Ala	Leu	Asp	Ala	Glu	Pro	Ile	Val
		35					40					45			
Ala	Ile	Arg	Gly	Leu	Leu	Glu	Asp	Leu	Gly	Gly	Thr	Glu	Gln	Ser	Thr
	50					55					60				
Leu	Ile	Gly	Gly	Gly	Lys	Thr	Ser	Pro	Glu	Arg	Ala	Ala	Phe	Phe	Asn
65					70					75					80

**SECRET**



Ser	Ala	Leu	Ser	Arg 85	Tyr	Leu	Asp	Phe	Met 90	Asp	Ala	Tyr	Leu	Ala	Lys
Gly	Glu	Thr	Asn 100	His	Pro	Ser	Asp	Asn 105	Phe	Gly	Ala	Val	Leu 110	Ala	Ala
Ala	Glu	Ser 115	Val	Gly	Ala	Ser	Gly 120	Lys	Asp	Leu	Leu	Thr 125	Ala	Phe	Ala
Val	Ala 130	Tyr	Gln	Val	His	Thr 135	Arg	Leu	Ser	Asp	Val 140	Ala	Pro	Val	Arg
Ala 145	Lys	Gly	Phe	Asp	His 150	Thr	Thr	Gln	Gly	Ala 155	Phe	Ala	Ala	Gly	Ala 160
Ser	Ala	Ala	Lys 165	Ala	Leu	Gly	Leu	Pro	Ala 170	Asp	Gln	Ile	Ala 175	Asn	Ala
Leu	Ala	Ile	Ala 180	Gly	Thr	Ala	Asn	Val 185	Ala	Leu	Arg	Val	Thr 190	Arg	Thr
Gly	Asn 195	Leu	Ser	His	Trp	Lys	Gly 200	Leu	Ala	Tyr	Pro	His 205	Val	Ser	Lys
Glu	Gly 210	Thr	Trp	Ala	Ala	Leu 215	Leu	Ala	Ser	Arg	Gly 220	Ile	Thr	Gly	Pro
Glu 225	Glu	Val	Phe	Glu	Gly 230	Asn	Lys	Gly	Phe	Lys 235	Glu	Ser	Val	Ser	Gly 240
Pro	Phe	Glu	Ile	Asp 245	Trp	Ser	Lys	Glu	Asp 250	Leu	Glu	Ser	Val	Lys 255	Arg
Thr	Ile	Ile	Lys 260	Lys	His	Asn	Ala	Glu 265	Ile	His	Ser	Gln	Ser 270	Ala	Leu
Asp	Ala	Ala 275	Gln	Glu	Ile	Arg	Ala 280	Gln	Glu	Gly	Phe	Asn 285	Val	Asp	Asn
Ile 290	Glu	Lys	Ile	His	Leu	Thr 295	Thr	Phe	Asp	Val 300	Ala	Tyr	Ser	Ile	Ile
Gly 305	Gly	Gly	Glu	Glu	Gly 310	Asp	Lys	Gln	Leu	Ile 315	Arg	Thr	Lys	Glu	Glu 320
Ala	Asp	His	Ser	Leu 325	Pro	Trp	Met	Leu	Ala 330	Val	Val	Leu	Leu	Asp 335	Gly
Gln	Leu	Asn 340	Pro	Glu	Gln	Tyr	Glu 345	Pro	Ser	Arg	Ile	Val 350	Ala	Asp	Asp
Val	Gln	Thr 355	Leu	Met	Lys	Lys	Ile 360	Glu	Ile	Thr	Pro	Ser 365	Asp	Glu	Phe
Ser	Asp 370	Arg	Phe	Pro	Asp	His 375	Met	Pro	Ala	Asp	Leu 380	Glu	Val	Thr	Leu
Asn 385	Asp	Gly	Ser	Val	Phe 390	Lys	Ala	Ser	Gln	Asp 395	Ser	Tyr	Leu	Gly	Phe 400



<400> 613																
acc	acg	acg	gct	acc	agg	cag	tcg	cga	aaa	ggt	gag	att	tcc	agc	tgg	48
Thr	Thr	Thr	Ala	Thr	Arg	Gln	Ser	Arg	Lys	Gly	Glu	Ile	Ser	Ser	Trp	
1				5					10					15		
aag	gcg	ttc	gcg	cca	gcg	ttt	gcg	gga	aag	atg	gcc	att	gag	gcg	atg	96
Lys	Ala	Phe	Ala	Pro	Ala	Phe	Ala	Gly	Lys	Met	Ala	Ile	Glu	Ala	Met	
			20					25					30			
gat	cgt	gcg	atg	cgt	ggg	gag	ggt	tcg	ccc	gca	ccg	att	tgg	gag	ggc	144
Asp	Arg	Ala	Met	Arg	Gly	Glu	Gly	Ser	Pro	Ala	Pro	Ile	Trp	Glu	Gly	
			35				40					45				
gaa	gac	ggg	gtc	atc	gcg	tgg	ctg	tta	tcg	ggc	aaa	gat	cat	gtt	tat	192
Glu	Asp	Gly	Val	Ile	Ala	Trp	Leu	Leu	Ser	Gly	Lys	Asp	His	Val	Tyr	
50						55					60					
cat	gtg	cca	ttg	ccg	gaa	cac	ggc	gag	ccc	aag	ctg	ggg	att	cta	gag	240
His	Val	Pro	Leu	Pro	Glu	His	Gly	Glu	Pro	Lys	Leu	Gly	Ile	Leu	Glu	
65					70					75					80	
act	tac	aca	aag	gaa	cat	tca	gcg	gaa	tat	caa	tcg	cag	gca	ccg	att	288
Thr	Tyr	Thr	Lys	Glu	His	Ser	Ala	Glu	Tyr	Gln	Ser	Gln	Ala	Pro	Ile	
				85					90					95		
gat	ctg	gcg	cgc	agg	atg	aag	cca	ctg	gtt	gac	gcg	gct	ggc	gga	acg	336
Asp	Leu	Ala	Arg	Arg	Met	Lys	Pro	Leu	Val	Asp	Ala	Ala	Gly	Gly	Thr	
			100					105					110			
gaa	cac	att	gca	gag	att	gtg	ctg	cgc	acc	agt	cac	cac	acg	cat	tat	384
Glu	His	Ile	Ala	Glu	Ile	Val	Leu	Arg	Thr	Ser	His	His	Thr	His	Tyr	
115						120					125					
gtg	att	ggc	act	ggg	gcg	aac	gat	ccg	cag	aag	atg	gat	ccg	cag	gcc	432
Val	Ile	Gly	Thr	Gly	Ala	Asn	Asp	Pro	Gln	Lys	Met	Asp	Pro	Gln	Ala	
130						135					140					
tcg	cgt	gaa	acc	ctg	gat	cat	tcc	atc	atg	tac	att	ttc	gcc	gtc	gcg	480

**SECRET**



<400> 614															
Thr	Thr	Thr	Ala	Thr	Arg	Gln	Ser	Arg	Lys	Gly	Glu	Ile	Ser	Ser	Trp
1				5					10					15	
Lys	Ala	Phe	Ala	Pro	Ala	Phe	Ala	Gly	Lys	Met	Ala	Ile	Glu	Ala	Met
			20					25					30		
Asp	Arg	Ala	Met	Arg	Gly	Glu	Gly	Ser	Pro	Ala	Pro	Ile	Trp	Glu	Gly
		35					40					45			
Glu	Asp	Gly	Val	Ile	Ala	Trp	Leu	Leu	Ser	Gly	Lys	Asp	His	Val	Tyr
	50					55					60				
His	Val	Pro	Leu	Pro	Glu	His	Gly	Glu	Pro	Lys	Leu	Gly	Ile	Leu	Glu



65				70				75				80				
Thr	Tyr	Thr	Lys	Glu	His	Ser	Ala	Glu	Tyr	Gln	Ser	Gln	Ala	Pro	Ile	
				85					90					95		
Asp	Leu	Ala	Arg	Arg	Met	Lys	Pro	Leu	Val	Asp	Ala	Ala	Gly	Gly	Thr	
				100					105					110		
Glu	His	Ile	Ala	Glu	Ile	Val	Leu	Arg	Thr	Ser	His	His	Thr	His	Tyr	
				115					120					125		
Val	Ile	Gly	Thr	Gly	Ala	Asn	Asp	Pro	Gln	Lys	Met	Asp	Pro	Gln	Ala	
				130					135					140		
Ser	Arg	Glu	Thr	Leu	Asp	His	Ser	Ile	Met	Tyr	Ile	Phe	Ala	Val	Ala	
				145					150					155		
Leu	Gln	Asp	Gly	Val	Trp	His	His	Glu	Phe	Ser	Tyr	Thr	Arg	Lys	Arg	
				165					170					175		
Ser	Thr	Arg	Pro	Glu	Thr	Val	Glu	Leu	Trp	His	Lys	Ile	Arg	Thr	Val	
				180					185					190		
Glu	Asp	Pro	Glu	Trp	Thr	Arg	Arg	Tyr	His	Ser	Asp	Asp	Pro	Ala	Lys	
				195					200					205		
Lys	Ala	Phe	Gly	Ala	Lys	Ala	Val	Ile	Thr	Met	Ala	Asp	Gly	Thr	Val	
				210					215					220		
Ile	Glu	Asp	Glu	Leu	Ala	Val	Ala	Asp	Ala	His	Pro	Leu	Gly	Ala	Arg	
				225					230					235		
Pro	Phe	Ala	Arg	Glu	Asn	Tyr	Ile	Glu	Lys	Phe	Arg	Thr	Leu	Ala	Gln	
				245					250					255		
Gly	Ile	Val	Ile	Asp	Ser	Glu	Gln	Glu	Arg	Phe	Leu	His	Ala	Val	Gln	
				260					265					270		
Ser	Leu	Pro	Asp	Leu	Asp	Asp	Leu	Asp	Gln	Leu	Asn	Ile	Glu	Val	Asp	
				275					280					285		
Ile	Ser	Asn	Gln	Ala	Ala	Thr	Lys	Ala	Gly	Leu	Leu					
				290					295					300		

```
<210> 615
<211> 511
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(511)  
<223> FRXA02322
```

<400> 615  
cgcgcagagc taaactgcgt gaggttggtg cctgtcacac ataatcggcc tagggtggga 60

ctttaaggaa acagtgcaca aataaatctc aaggagcccc atg cgc atc cac gat 115  
Met Arg Ile His Asp  
1 5

[illegible]



```

<400> 616
Met Arg Ile His Asp Val Tyr Thr His Leu Ser Ala Asp Asn Phe Pro
  1          5          10          15

Lys Ala Glu His Leu Ala Trp Lys Phe Ser Glu Leu Ala Thr Asp Pro
          20          25          30

Val Glu Val Thr Pro Asp Val Ser Glu Met Ile Ile Asn Arg Ile Ile
  35          40          45

Asp Asn Ala Ala Val Ser Ala Ala Ser Val Leu Arg Arg Pro Val Thr
  50          55          60

Val Ala Arg Gln Gln Ala Gln Ser His Pro Arg Glu Lys Gly Gly Lys
  65          70          75          80

Val Phe Gly Ile Ser Gly Ser Tyr Ser Pro Glu Trp Ala Ala Phe Ala
          85          90          95

```

[illegible]



Ala Gln Ala Gln Arg Ser Ser Gly Arg  
130 135

```
<220>  
<221> CDS  
<222> (1)..(603)  
<223> RXA02329
```

<400> 617																
acg	gct	acc	agg	cag	tcg	cga	aaa	ggt	gag	att	tcc	agc	tgg	aag	gcg	48
Thr	Ala	Thr	Arg	Gln	Ser	Arg	Lys	Gly	Glu	Ile	Ser	Ser	Trp	Lys	Ala	
1				5					10					15		
ttc	gcg	cca	gcg	ttt	gcg	gga	aag	atg	gcc	att	gag	gcg	atg	gat	cgt	96
Phe	Ala	Pro	Ala	Phe	Ala	Gly	Lys	Met	Ala	Ile	Glu	Ala	Met	Asp	Arg	
			20					25					30			
gcg	atg	cgt	ggg	gag	ggt	tcg	ccc	gca	ccg	att	tgg	gag	ggc	gaa	gac	144
Ala	Met	Arg	Gly	Glu	Gly	Ser	Pro	Ala	Pro	Ile	Trp	Glu	Gly	Glu	Asp	
		35					40					45				
ggg	gtc	atc	gcg	tgg	ctg	tta	tcg	ggc	aaa	gat	cat	gtt	tat	cat	gtg	192
Gly	Val	Ile	Ala	Trp	Leu	Leu	Ser	Gly	Lys	Asp	His	Val	Tyr	His	Val	
	50					55					60					
cca	ttg	ccg	gaa	cac	ggc	gag	ccc	aag	ctg	ggg	att	cta	gag	act	tac	240
Pro	Leu	Pro	Glu	His	Gly	Glu	Pro	Lys	Leu	Gly	Ile	Leu	Glu	Thr	Tyr	
65					70				75						80	
aca	aag	gaa	cat	tca	gcg	gaa	tat	caa	tcg	cag	gca	ccg	att	gat	ctg	288
Thr	Lys	Glu	His	Ser	Ala	Glu	Tyr	Gln	Ser	Gln	Ala	Pro	Ile	Asp	Leu	
				85				90						95		
gcg	cgc	agg	atg	aag	cca	ctg	gtt	gac	gcg	gct	ggc	gga	acg	gaa	cac	336
Ala	Arg	Arg	Met	Lys	Pro	Leu	Val	Asp	Ala	Ala	Gly	Gly	Thr	Glu	His	
			100					105					110			
att	gca	gag	att	gtg	ctg	cgc	acc	agt	cac	cac	acg	cat	tat	gtg	att	384
Ile	Ala	Glu	Ile	Val	Leu	Arg	Thr	Ser	His	His	Thr	His	Tyr	Val	Ile	
		115					120					125				
ggc	act	ggg	gcg	aac	gat	ccg	cag	aag	atg	gat	ccg	cag	gcc	tcg	cgt	432
Gly	Thr	Gly	Ala	Asn	Asp	Pro	Gln	Lys	Met	Asp	Pro	Gln	Ala	Ser	Arg	
	130					135					140					
gaa	acc	ctg	gat	cat	tcc	atc	atg	tac	att	ttc	gcc	gtc	gcg	ctt	caa	480
Glu	Thr	Leu	Asp	His	Ser	Ile	Met	Tyr	Ile	Phe	Ala	Val	Ala	Leu	Gln	
145					150					155					160	







<211> 1266  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1243)  
 <223> RXA02332

<400> 619

```

gaccgcatgc aacaccgcag cagattatat gagctcctgc gatacgaaga ctacaacgtc 60

tttgaccagc acattttcac ctacagaaaa ggagaaaaca atg agt gac agc caa 115
              Met Ser Asp Ser Gln
              1              5

gtc cgc aaa gga ctc aac ggc gtc atc tct gac tac aca agc att tcc 163
Val Arg Lys Gly Leu Asn Gly Val Ile Ser Asp Tyr Thr Ser Ile Ser
              10              15              20

aaa gtg atg cca gag agc aac tcg ctg act tac cgt ggc tac gcc gtg 211
Lys Val Met Pro Glu Ser Asn Ser Leu Thr Tyr Arg Gly Tyr Ala Val
              25              30              35

gag gat ttg gtg gaa aac tgc agc ttt gaa gaa gtg atc tac ctc ctg 259
Glu Asp Leu Val Glu Asn Cys Ser Phe Glu Glu Val Ile Tyr Leu Leu
              40              45              50

tgg ttt ggg gag ctg ccc acc act gaa caa ctc cgg acc ttc aac acg 307
Trp Phe Gly Glu Leu Pro Thr Thr Glu Gln Leu Arg Thr Phe Asn Thr
              55              60              65

aca ggt cga agc tac cgc tca ctc gac gcc gga ctg att tcc ctc atc 355
Thr Gly Arg Ser Tyr Arg Ser Leu Asp Ala Gly Leu Ile Ser Leu Ile
              70              75              80              85

cac tcc tta ccc aac acc tgc cac ccc atg gac gtg ctg cgc acc gca 403
His Ser Leu Pro Asn Thr Cys His Pro Met Asp Val Leu Arg Thr Ala
              90              95              100

gtg tcc tac atg ggt acc ttt gat ccc gat ccg ttt acc cgc gat gcc 451
Val Ser Tyr Met Gly Thr Phe Asp Pro Asp Pro Phe Thr Arg Asp Ala
              105              110              115

gat cat atc cga agc att gga cac aac ctg ctt gcg cag ctt ccc atg 499
Asp His Ile Arg Ser Ile Gly His Asn Leu Leu Ala Gln Leu Pro Met
              120              125              130

gtg gtt gcc atg gat atc cgc agg cga agt ggg gaa gag atc atc gca 547
Val Val Ala Met Asp Ile Arg Arg Arg Ser Gly Glu Glu Ile Ile Ala
              135              140              145

cct gac cac aac aaa ggt atc gct tcg aat ttc tta tcc atg gtg ttt 595
Pro Asp His Asn Lys Gly Ile Ala Ser Asn Phe Leu Ser Met Val Phe
              150              155              160              165

ggc aat gat gat ggt tct gta gcc aac tcc gca gat gac atc cgc gat 643
Gly Asn Asp Asp Gly Ser Val Ala Asn Ser Ala Asp Asp Ile Arg Asp
              170              175              180

ttt gaa cgc tcc ctc atc ctc tac gcc gag cac tcc ttc aac gcc tcc 691

```

09602740-062300



```
<210> 620
<211> 381
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 620  
Met Ser Asp Ser Gln Val Arg Lys Gly Leu Asn Gly Val Ile Ser Asp  
1 5 10 15



[illegible]



	340		345		350
Gln Phe Glu Asn Asn Ala Leu Ile Arg Pro Leu Ser Ala Tyr Asn Gly					
	355		360		365
Val Glu Glu Arg Glu Val Val Pro Ile Ser Glu Arg Thr					
	370		375		380

<210> 621  
 <211> 1038  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1015)  
 <223> RXN02333

<400> 621  
 tcttgcatgc cgtgcaaagc ctgcctgacc tggatgatct tgcacagctc aacatcgaag 60  
 tcgacataag caaccaggcc ggcacgaaag cggggctggt atg aat ctc ttt tcg 115  
 Met Asn Leu Phe Ser  
 1 5  
 aat ggt gtt gat gtg ggg agg cgt cga caa gca ttt aaa gcg gca ctc 163  
 Asn Gly Val Asp Val Gly Arg Arg Arg Gln Ala Phe Lys Ala Ala Leu  
 10 15 20  
 gcc gca ccc cac atc gcc cgg ctg ccc ggc gca ttc tcc cct ctg att 211  
 Ala Ala Pro His Ile Ala Arg Leu Pro Gly Ala Phe Ser Pro Leu Ile  
 25 30 35  
 gcg cgc tcc atc gaa gaa gcc ggc ttc gaa ggc gtc tac gtt tcc ggc 259  
 Ala Arg Ser Ile Glu Glu Ala Gly Phe Glu Gly Val Tyr Val Ser Gly  
 40 45 50  
 gcc gtc ata gct gct gac ctg gca cta ccc gat atc ggc ttg acg acg 307  
 Ala Val Ile Ala Ala Asp Leu Ala Leu Pro Asp Ile Gly Leu Thr Thr  
 55 60 65  
 ctg acc gaa gtc gcc cac cgc gcg cgg caa att gcg cgc gtc aca gac 355  
 Leu Thr Glu Val Ala His Arg Ala Arg Gln Ile Ala Arg Val Thr Asp  
 70 75 80 85  
 cta gga gtg ctt gtc gac gcc gac acc ggc ttt ggc gaa ccc atg tcg 403  
 Leu Gly Val Leu Val Asp Ala Asp Thr Gly Phe Gly Glu Pro Met Ser  
 90 95 100  
 gcc gca cgc acc gtc gcc gaa ttg gag gac gcc ggt gtg gcc gga tgc 451  
 Ala Ala Arg Thr Val Ala Glu Leu Glu Asp Ala Gly Val Ala Gly Cys  
 105 110 115  
 cac ctt gaa gac caa gtc aac ccc aaa cgt tgc ggc cac ttg gac ggc 499  
 His Leu Glu Asp Gln Val Asn Pro Lys Arg Cys Gly His Leu Asp Gly  
 120 125 130  
 aaa gaa gtc gtg cgc aca gac gtg atg gtt cga cgc atc gca gcc gcc 547  
 Lys Glu Val Val Arg Thr Asp Val Met Val Arg Arg Ile Ala Ala Ala  
 135 140 145

09602740 062300



gtc tcg gcc cgg cgc gac ccg aac ttt gtc atc tgc gcc cgc acc gac 595  
 Val Ser Ala Arg Arg Asp Pro Asn Phe Val Ile Cys Ala Arg Thr Asp  
 150 155 160 165  
  
 gcc gct gga gtg gaa gga atc gac gcc gcc att gag cgc gcg aaa gcc 643  
 Ala Ala Gly Val Glu Gly Ile Asp Ala Ala Ile Glu Arg Ala Lys Ala  
 170 175 180  
  
 tac tta gat gcg ggc gcc gac atg att ttc acc gaa gcc ctc cac agc 691  
 Tyr Leu Asp Ala Gly Ala Asp Met Ile Phe Thr Glu Ala Leu His Ser  
 185 190 195  
  
 gaa gcc gac ttc cga tac ttc ccg cac gcc atc cct gat gcc ttg ttg 739  
 Glu Ala Asp Phe Arg Tyr Phe Arg His Ala Ile Pro Asp Ala Leu Leu  
 200 205 210  
  
 ctg gcg aat atg acc gaa ttt ggc aaa acg acg ctg ctg tca gcc gac 787  
 Leu Ala Asn Met Thr Glu Phe Gly Lys Thr Thr Leu Leu Ser Ala Asp  
 215 220 225  
  
 gtg ttg gaa gag att ggc tac aac gcc gtg atc tac ccc gtg acc acg 835  
 Val Leu Glu Glu Ile Gly Tyr Asn Ala Val Ile Tyr Pro Val Thr Thr  
 230 235 240 245  
  
 ctg cgt att gcc atg gga caa gta gaa caa gca cta gcc gaa atc aaa 883  
 Leu Arg Ile Ala Met Gly Gln Val Glu Gln Ala Leu Ala Glu Ile Lys  
 250 255 260  
  
 gaa cac ggt acc caa gaa gga tgg ctg gac cgc atg caa cac cgc agc 931  
 Glu His Gly Thr Gln Glu Gly Trp Leu Asp Arg Met Gln His Arg Ser  
 265 270 275  
  
 aga tta tat gag ctc ctg cga tac gaa gac tac aac gtc ttt gac cag 979  
 Arg Leu Tyr Glu Leu Leu Arg Tyr Glu Asp Tyr Asn Val Phe Asp Gln  
 280 285 290  
  
 cac att ttc acc tac aga aaa gga gaa aac aat gag tgacagccaa 1025  
 His Ile Phe Thr Tyr Arg Lys Gly Glu Asn Asn Glu  
 295 300 305  
  
 gtccgcaaag gac 1038

&lt;210&gt; 622

&lt;211&gt; 305

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 622

Met Asn Leu Phe Ser Asn Gly Val Asp Val Gly Arg Arg Arg Gln Ala  
 1 5 10 15

Phe Lys Ala Ala Leu Ala Ala Pro His Ile Ala Arg Leu Pro Gly Ala  
 20 25 30

Phe Ser Pro Leu Ile Ala Arg Ser Ile Glu Glu Ala Gly Phe Glu Gly  
 35 40 45

Val Tyr Val Ser Gly Ala Val Ile Ala Ala Asp Leu Ala Leu Pro Asp  
 50 55 60

09602740-062300



[illegible]

```
<210> 623
<211> 242
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(219)
<223> FRXA02333

<400> 623
```



ctctctgcac aatgtttctt tcggaactat tctggcgacc atg cga att gaa atc 115  
Met Arg Ile Glu Ile  
1 5

[illegible]



aca agc gta ttt gtt gat gac cag gcc aaa gca ctc gat ttc tac acc 163  
 Thr Ser Val Phe Val Asp Asp Gln Ala Lys Ala Leu Asp Phe Tyr Thr  
                     10                    15                    20

acg aag ctc gga ttt gag ctc aaa cac gat gta act gct ggt gac tac 211  
 Thr Lys Leu Gly Phe Glu Leu Lys His Asp Val Thr Ala Gly Asp Tyr  
                     25                    30                    35

cgc tgg ttg act gtt gtt gat cca gaa aac cca gat ggt gtg cag ctt 259  
 Arg Trp Leu Thr Val Val Asp Pro Glu Asn Pro Asp Gly Val Gln Leu  
                     40                    45                    50

ttg ttg gaa cca aac cag cac cca gat gca gcg act tac caa gct gga 307  
 Leu Leu Glu Pro Asn Gln His Pro Asp Ala Ala Thr Tyr Gln Ala Gly  
                     55                    60                    65

att aaa cga gac ggt att ccc gct aca cag ttt tat gtt gat gat gtg 355  
 Ile Lys Arg Asp Gly Ile Pro Ala Thr Gln Phe Tyr Val Asp Asp Val  
                     70                    75                    80                    85

cag gaa gaa tat gac agc ctc aag gat aaa ggc gtg gat ttc atc atg 403  
 Gln Glu Glu Tyr Asp Ser Leu Lys Asp Lys Gly Val Asp Phe Ile Met  
                     90                    95                    100

gaa cca acc gat gtg ggc cct tca gtg att gcc att ctc gat gac acc 451  
 Glu Pro Thr Asp Val Gly Pro Ser Val Ile Ala Ile Leu Asp Asp Thr  
                     105                    110                    115

gta gga aac cta att cag att gtt caa ttg aag cag aac taacccccgtg 500  
 Val Gly Asn Leu Ile Gln Ile Val Gln Leu Lys Gln Asn  
                     120                    125                    130

gaatgacaaa atc 513

&lt;210&gt; 626

&lt;211&gt; 130

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 626

Met Arg Ile Glu Ile Thr Ser Val Phe Val Asp Asp Gln Ala Lys Ala  
   1                    5                    10                    15

Leu Asp Phe Tyr Thr Thr Lys Leu Gly Phe Glu Leu Lys His Asp Val  
                     20                    25                    30

Thr Ala Gly Asp Tyr Arg Trp Leu Thr Val Val Asp Pro Glu Asn Pro  
                     35                    40                    45

Asp Gly Val Gln Leu Leu Leu Glu Pro Asn Gln His Pro Asp Ala Ala  
                     50                    55                    60

Thr Tyr Gln Ala Gly Ile Lys Arg Asp Gly Ile Pro Ala Thr Gln Phe  
                     65                    70                    75                    80

Tyr Val Asp Asp Val Gln Glu Glu Tyr Asp Ser Leu Lys Asp Lys Gly  
                     85                    90                    95

Val Asp Phe Ile Met Glu Pro Thr Asp Val Gly Pro Ser Val Ile Ala

00602740-062300



atg	gcc	ggc	gtg	gcg	att	gat	tcg	att	ttg	gat	atg	cgt	cag	ctg	ttt	547
Met	Ala	Gly	Val	Ala	Ile	Asp	Ser	Ile	Leu	Asp	Met	Arg	Gln	Leu	Phe	
	135					140					145					

[illegible]



gat ggc att gat ttg tcc agc gtg tcg gtg tcg atg acc atg aat ggc	595
Asp Gly Ile Asp Leu Ser Ser Val Ser Val Ser Met Thr Met Asn Gly	
150 155 160 165	
gct gtg ctg ccg att ctt gcg ttc tat atc gtg gcg gct gag gaa caa	643
Ala Val Leu Pro Ile Leu Ala Phe Tyr Ile Val Ala Ala Glu Glu Gln	
170 175 180	
ggg gtg ggt ccg gag cag ctt gcg ggc acg atc cag aat gac atc ttg	691
Gly Val Gly Pro Glu Gln Leu Ala Gly Thr Ile Gln Asn Asp Ile Leu	
185 190 195	
aaa gaa ttt atg gtg cgc aac acc tat att tat ccg ccg aag ccg tcg	739
Lys Glu Phe Met Val Arg Asn Thr Tyr Ile Tyr Pro Pro Lys Pro Ser	
200 205 210	
atg cgc atc att tcc aac atc ttt gag tac acc tcc ttg aag atg cca	787
Met Arg Ile Ile Ser Asn Ile Phe Glu Tyr Thr Ser Leu Lys Met Pro	
215 220 225	
cgt ttt aac tcc att tcg att tct ggc tat cac atc cag gaa gcg gga	835
Arg Phe Asn Ser Ile Ser Ile Ser Gly Tyr His Ile Gln Glu Ala Gly	
230 235 240 245	
gcg act gcc gat ttg gag ctg gcc tac act ctg gcg gat ggt att gaa	883
Ala Thr Ala Asp Leu Glu Leu Ala Tyr Thr Leu Ala Asp Gly Ile Glu	
250 255 260	
tac atc cgt gca ggt aaa gag gta ggc ctt gac gtg gat aag ttc gcg	931
Tyr Ile Arg Ala Gly Lys Glu Val Gly Leu Asp Val Asp Lys Phe Ala	
265 270 275	
cct cgt ctg tcc ttc ttc tgg ggt att tct atg tac acc ttc atg gag	979
Pro Arg Leu Ser Phe Phe Trp Gly Ile Ser Met Tyr Thr Phe Met Glu	
280 285 290	
atc gca aag ctg cgt gcg gga cga ctg ctg tgg agc gag ttg gtg gca	1027
Ile Ala Lys Leu Arg Ala Gly Arg Leu Leu Trp Ser Glu Leu Val Ala	
295 300 305	
aaa ttc gat ccg aaa aac gcc aag tcc cag tcg ctg cgc acg cac tcg	1075
Lys Phe Asp Pro Lys Asn Ala Lys Ser Gln Ser Leu Arg Thr His Ser	
310 315 320 325	
cag acc tct ggt tgg tcg ttg acc gcg cag gat gtg tac aac aac gtc	1123
Gln Thr Ser Gly Trp Ser Leu Thr Ala Gln Asp Val Tyr Asn Asn Val	
330 335 340	
gcc cgc acc gcg att gag gcg atg gct gca acc cag ggc cac acc cag	1171
Ala Arg Thr Ala Ile Glu Ala Met Ala Ala Thr Gln Gly His Thr Gln	
345 350 355	
tcg ctg cac acc aat gca ctt gat gag gcg ttg gcg ctg ccc acc gat	1219
Ser Leu His Thr Asn Ala Leu Asp Glu Ala Leu Ala Leu Pro Thr Asp	
360 365 370	
ttc tct gct cgt atc gcc cga aac acc cag ctg ttg ctg cag cag gaa	1267
Phe Ser Ala Arg Ile Ala Arg Asn Thr Gln Leu Leu Leu Gln Gln Glu	
375 380 385	

09602740-062300



0960740-0630000



Asp Val Gly Pro Leu Phe Gln Thr Pro Ala Glu Ala Ala Arg Ala Ala  
 630 635 640 645  
 gtg gac gcc gat gtt cac gtg gtg ggt atg tct tcg ctg gca gca ggc 2083  
 Val Asp Ala Asp Val His Val Val Gly Met Ser Ser Leu Ala Ala Gly  
 650 655 660  
 cac ctc acc ttg ctg ccc gag ctg aag aaa gaa ctt gca gct ctt ggc 2131  
 His Leu Thr Leu Leu Pro Glu Leu Lys Lys Glu Leu Ala Ala Leu Gly  
 665 670 675  
 cgc gat gac att ctg gtc acc gtg ggc ggc gtc att ccg ccg ggc gat 2179  
 Arg Asp Asp Ile Leu Val Thr Val Gly Gly Val Ile Pro Pro Gly Asp  
 680 685 690  
 ttc cag gat ctc tac gat atg ggt gcc gcc gcg att tac cct tca gga 2227  
 Phe Gln Asp Leu Tyr Asp Met Gly Ala Ala Ala Ile Tyr Pro Ser Gly  
 695 700 705  
 acc gtc atc gcg gag tcg gcg atc gat ctg atc acc cga ctc gcc gca 2275  
 Thr Val Ile Ala Glu Ser Ala Ile Asp Leu Ile Thr Arg Leu Ala Ala  
 710 715 720 725  
 cac ctg ggc ttt gac ctg gat gtg gat gtg aat gaa tgatcacggt 2321  
 His Leu Gly Phe Asp Leu Asp Val Asp Val Asn Glu  
 730 735  
 ttcctagaag aca 2334  
  
 <210> 628  
 <211> 737  
 <212> PRT  
 <213> Corynebacterium glutamicum  
  
 <400> 628  
 Met Thr Ser Ile Pro Asn Phe Ser Asp Ile Pro Leu Thr Ala Glu Thr  
 1 5 10 15  
 Arg Ala Ser Glu Ser His Asn Val Asp Ala Gly Lys Val Trp Asn Thr  
 20 25 30  
 Pro Glu Gly Ile Asp Val Lys Arg Val Phe Thr Gln Ala Asp Arg Asp  
 35 40 45  
 Glu Ala Gln Ala Ala Gly His Pro Val Asp Ser Leu Pro Gly Gln Lys  
 50 55 60  
 Pro Phe Met Arg Gly Pro Tyr Pro Thr Met Tyr Thr Asn Gln Pro Trp  
 65 70 75 80  
 Thr Ile Arg Gln Tyr Ala Gly Phe Ser Thr Ala Ala Glu Ser Asn Ala  
 85 90 95  
 Phe Tyr Arg Arg Asn Leu Ala Ala Gly Gln Lys Gly Leu Ser Val Ala  
 100 105 110  
 Phe Asp Leu Ala Thr His Arg Gly Tyr Asp Ser Asp Asn Glu Arg Val  
 115 120 125  
 Val Gly Asp Val Gly Met Ala Gly Val Ala Ile Asp Ser Ile Leu Asp

09602740-062300



130					135					140					
Met	Arg	Gln	Leu	Phe	Asp	Gly	Ile	Asp	Leu	Ser	Ser	Val	Ser	Val	Ser
145					150					155					160
Met	Thr	Met	Asn	Gly	Ala	Val	Leu	Pro	Ile	Leu	Ala	Phe	Tyr	Ile	Val
				165					170					175	
Ala	Ala	Glu	Glu	Gln	Gly	Val	Gly	Pro	Glu	Gln	Leu	Ala	Gly	Thr	Ile
			180					185					190		
Gln	Asn	Asp	Ile	Leu	Lys	Glu	Phe	Met	Val	Arg	Asn	Thr	Tyr	Ile	Tyr
		195					200					205			
Pro	Pro	Lys	Pro	Ser	Met	Arg	Ile	Ile	Ser	Asn	Ile	Phe	Glu	Tyr	Thr
	210					215					220				
Ser	Leu	Lys	Met	Pro	Arg	Phe	Asn	Ser	Ile	Ser	Ile	Ser	Gly	Tyr	His
225					230					235					240
Ile	Gln	Glu	Ala	Gly	Ala	Thr	Ala	Asp	Leu	Glu	Leu	Ala	Tyr	Thr	Leu
				245					250					255	
Ala	Asp	Gly	Ile	Glu	Tyr	Ile	Arg	Ala	Gly	Lys	Glu	Val	Gly	Leu	Asp
			260					265					270		
Val	Asp	Lys	Phe	Ala	Pro	Arg	Leu	Ser	Phe	Phe	Trp	Gly	Ile	Ser	Met
		275					280					285			
Tyr	Thr	Phe	Met	Glu	Ile	Ala	Lys	Leu	Arg	Ala	Gly	Arg	Leu	Leu	Trp
	290					295					300				
Ser	Glu	Leu	Val	Ala	Lys	Phe	Asp	Pro	Lys	Asn	Ala	Lys	Ser	Gln	Ser
305					310					315					320
Leu	Arg	Thr	His	Ser	Gln	Thr	Ser	Gly	Trp	Ser	Leu	Thr	Ala	Gln	Asp
				325					330					335	
Val	Tyr	Asn	Asn	Val	Ala	Arg	Thr	Ala	Ile	Glu	Ala	Met	Ala	Ala	Thr
			340					345					350		
Gln	Gly	His	Thr	Gln	Ser	Leu	His	Thr	Asn	Ala	Leu	Asp	Glu	Ala	Leu
		355					360					365			
Ala	Leu	Pro	Thr	Asp	Phe	Ser	Ala	Arg	Ile	Ala	Arg	Asn	Thr	Gln	Leu
	370					375					380				
Leu	Leu	Gln	Gln	Glu	Ser	Gly	Thr	Val	Arg	Pro	Val	Asp	Pro	Trp	Ala
385					390					395					400
Gly	Ser	Tyr	Tyr	Val	Glu	Trp	Leu	Thr	Asn	Glu	Leu	Ala	Asn	Arg	Ala
				405					410					415	
Arg	Lys	His	Ile	Asp	Glu	Val	Glu	Glu	Ala	Gly	Gly	Met	Ala	Gln	Ala
			420					425					430		
Thr	Ala	Gln	Gly	Ile	Pro	Lys	Leu	Arg	Ile	Glu	Glu	Ser	Ala	Ala	Arg
	435						440					445			
Thr	Gln	Ala	Arg	Ile	Asp	Ser	Gly	Arg	Gln	Ala	Leu	Ile	Gly	Val	Asn
450						455					460				

09602740-062300



Arg Tyr Val Ala Glu Glu Asp Glu Glu Ile Glu Val Leu Lys Val Asp  
 465 470 475 480  
 Asn Thr Lys Val Arg Ala Glu Gln Leu Ala Lys Leu Ala Gln Leu Lys  
 485 490 495  
 Ala Glu Arg Asn Asp Ala Glu Val Lys Ala Ala Leu Asp Ala Leu Thr  
 500 505 510  
 Ala Ala Ala Arg Asn Glu His Lys Glu Pro Gly Asp Leu Asp Gln Asn  
 515 520 525  
 Leu Leu Lys Leu Ala Val Asp Ala Ala Arg Ala Lys Ala Thr Ile Gly  
 530 535 540  
 Glu Ile Ser Asp Ala Leu Glu Val Val Phe Gly Arg His Glu Ala Glu  
 545 550 555 560  
 Ile Arg Thr Leu Ser Gly Val Tyr Lys Asp Glu Val Gly Lys Glu Gly  
 565 570 575  
 Thr Val Ser Asn Val Glu Arg Ala Ile Ala Leu Ala Asp Ala Phe Glu  
 580 585 590  
 Ala Glu Glu Gly Arg Arg Pro Arg Ile Phe Ile Ala Lys Met Gly Gln  
 595 600 605  
 Asp Gly His Asp Arg Gly Gln Lys Val Val Ala Ser Ala Tyr Ala Asp  
 610 615 620  
 Leu Gly Met Asp Val Asp Val Gly Pro Leu Phe Gln Thr Pro Ala Glu  
 625 630 635 640  
 Ala Ala Arg Ala Ala Val Asp Ala Asp Val His Val Val Gly Met Ser  
 645 650 655  
 Ser Leu Ala Ala Gly His Leu Thr Leu Leu Pro Glu Leu Lys Lys Glu  
 660 665 670  
 Leu Ala Ala Leu Gly Arg Asp Asp Ile Leu Val Thr Val Gly Gly Val  
 675 680 685  
 Ile Pro Pro Gly Asp Phe Gln Asp Leu Tyr Asp Met Gly Ala Ala Ala  
 690 695 700  
 Ile Tyr Pro Ser Gly Thr Val Ile Ala Glu Ser Ala Ile Asp Leu Ile  
 705 710 715 720  
 Thr Arg Leu Ala Ala His Leu Gly Phe Asp Leu Asp Val Asp Val Asn  
 725 730 735  
 Glu

&lt;210&gt; 629

&lt;211&gt; 2098

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

09602740 "062300" 002290



&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(2098)

&lt;223&gt; FRXA00148

&lt;400&gt; 629

```

ctttgagggc agcgcgcatg cgcccgatgg ttatttgaac atgacaattg atgccgcggc 60

gacgctggct gacctgctag atgctttggg agcttaaatac atg acg tcg atc cct 115
Met Thr Ser Ile Pro
1 5

aat ttt tca gac atc cca ttg act gct gag aca cgt gca tcg gag tca 163
Asn Phe Ser Asp Ile Pro Leu Thr Ala Glu Thr Arg Ala Ser Glu Ser
10 15 20

cac aac gtt gac gcc ggc aag gtg tgg aac act ccc gaa ggc att gat 211
His Asn Val Asp Ala Gly Lys Val Trp Asn Thr Pro Glu Gly Ile Asp
25 30 35

gtc aag cgc gta ttc acg cag gct gac cgc gac gag gcg caa gcg gcg 259
Val Lys Arg Val Phe Thr Gln Ala Asp Arg Asp Glu Ala Gln Ala Ala
40 45 50

gga cat ccg gtg gat tct ttg cca ggt caa aag cca ttt atg cgc ggg 307
Gly His Pro Val Asp Ser Leu Pro Gly Gln Lys Pro Phe Met Arg Gly
55 60 65

ccg tac cca act atg tac acc aat cag ccg tgg acg att cgc cag tac 355
Pro Tyr Pro Thr Met Tyr Thr Asn Gln Pro Trp Thr Ile Arg Gln Tyr
70 75 80 85

gca ggc ttt tca acc gcc gcg gaa tcc aat gcg ttt tat cgg agg aac 403
Ala Gly Phe Ser Thr Ala Ala Glu Ser Asn Ala Phe Tyr Arg Arg Asn
90 95 100

ctt gct gcg ggt caa aaa ggt ttg tcg gtt gcg ttc gat cta gcg acc 451
Leu Ala Ala Gly Gln Lys Gly Leu Ser Val Ala Phe Asp Leu Ala Thr
105 110 115

cac cgc ggt tat gac tcg gat aat gag cgc gtg gtc ggc gat gtg ggt 499
His Arg Gly Tyr Asp Ser Asp Asn Glu Arg Val Val Gly Asp Val Gly
120 125 130

atg gcc ggc gtg gcg att gat tcg att ttg gat atg cgt cag ctg ttt 547
Met Ala Gly Val Ala Ile Asp Ser Ile Leu Asp Met Arg Gln Leu Phe
135 140 145

gat ggc att gat ttg tcc agc gtg tcg gtg tcg atg acc atg aat ggc 595
Asp Gly Ile Asp Leu Ser Ser Val Ser Val Ser Met Thr Met Asn Gly
150 155 160 165

gct gtg ctg ccg att ctt gcg ttc tat atc gtg gcg gct gag gaa caa 643
Ala Val Leu Pro Ile Leu Ala Phe Tyr Ile Val Ala Ala Glu Glu Gln
170 175 180

ggg gtg ggt ccg gag cag ctt gcg ggc acg atc cag aat gac atc ttg 691
Gly Val Gly Pro Glu Gln Leu Ala Gly Thr Ile Gln Asn Asp Ile Leu
185 190 195

aaa gaa ttt atg gtg cgc aac acc tat att tat ccg ccg aag ccg tcg 739

```

09602740-062300



Lys	Glu	Phe	Met	Val	Arg	Asn	Thr	Tyr	Ile	Tyr	Pro	Pro	Lys	Pro	Ser		
		200					205					210					
atg	cgc	atc	att	tcc	aac	atc	ttt	gag	tac	acc	tcc	ttg	aag	atg	cca	787	
Met	Arg	Ile	Ile	Ser	Asn	Ile	Phe	Glu	Tyr	Thr	Ser	Leu	Lys	Met	Pro		
	215					220					225						
cgt	ttt	aac	tcc	att	tcg	att	tct	ggc	tat	cac	atc	cag	gaa	gcg	gga	835	
Arg	Phe	Asn	Ser	Ile	Ser	Ile	Ser	Gly	Tyr	His	Ile	Gln	Glu	Ala	Gly		
230					235					240					245		
gcg	act	gcc	gat	ttg	gag	ctg	gcc	tac	act	ctg	gcg	gat	ggt	att	gaa	883	
Ala	Thr	Ala	Asp	Leu	Glu	Leu	Ala	Tyr	Thr	Leu	Ala	Asp	Gly	Ile	Glu		
			250						255					260			
tac	atc	cgt	gca	ggt	aaa	gag	gta	ggc	ctt	gac	gtg	gat	aag	ttc	gcg	931	
Tyr	Ile	Arg	Ala	Gly	Lys	Glu	Val	Gly	Leu	Asp	Val	Asp	Lys	Phe	Ala		
			265					270					275				
cct	cgt	ctg	tcc	ttc	ttc	tgg	ggt	att	tct	atg	tac	acc	ttc	atg	gag	979	
Pro	Arg	Leu	Ser	Phe	Phe	Trp	Gly	Ile	Ser	Met	Tyr	Thr	Phe	Met	Glu		
		280					285					290					
atc	gca	aag	ctg	cgt	gcg	gga	cga	ctg	ctg	tgg	agc	gag	ttg	gtg	gca	1027	
Ile	Ala	Lys	Leu	Arg	Ala	Gly	Arg	Leu	Leu	Trp	Ser	Glu	Leu	Val	Ala		
	295					300					305						
aaa	ttc	gat	ccg	aaa	aac	gcc	aag	tcc	cag	tcg	ctg	cgc	acg	cac	tcg	1075	
Lys	Phe	Asp	Pro	Lys	Asn	Ala	Lys	Ser	Gln	Ser	Leu	Arg	Thr	His	Ser		
310					315					320					325		
cag	acc	tct	ggt	tgg	tcg	ttg	acc	gcg	cag	gat	gtg	tac	aac	aac	gtc	1123	
Gln	Thr	Ser	Gly	Trp	Ser	Leu	Thr	Ala	Gln	Asp	Val	Tyr	Asn	Asn	Val		
				330					335					340			
gcc	cgc	acc	gcg	att	gag	gcg	atg	gct	gca	acc	cag	ggc	cac	acc	cag	1171	
Ala	Arg	Thr	Ala	Ile	Glu	Ala	Met	Ala	Ala	Thr	Gln	Gly	His	Thr	Gln		
			345					350					355				
tcg	ctg	cac	acc	aat	gca	ctt	gat	gag	gcg	ttg	gcg	ctg	ccc	acc	gat	1219	
Ser	Leu	His	Thr	Asn	Ala	Leu	Asp	Glu	Ala	Leu	Ala	Leu	Pro	Thr	Asp		
			360				365					370					
ttc	tct	gct	cgt	atc	gcc	cga	aac	acc	cag	ctg	ttg	ctg	cag	cag	gaa	1267	
Phe	Ser	Ala	Arg	Ile	Ala	Arg	Asn	Thr	Gln	Leu	Leu	Leu	Gln	Gln	Glu		
	375					380					385						
tct	ggc	acg	gtg	cgt	cca	ggt	gat	cca	tgg	gcg	ggc	tcc	tat	tac	gtg	1315	
Ser	Gly	Thr	Val	Arg	Pro	Val	Asp	Pro	Trp	Ala	Gly	Ser	Tyr	Tyr	Val		
390					395				400						405		
gag	tgg	ttg	acc	aat	gag	ctg	gct	aac	cgc	gcg	cgc	aag	cac	atc	gat	1363	
Glu	Trp	Leu	Thr	Asn	Glu	Leu	Ala	Asn	Arg	Ala	Arg	Lys	His	Ile	Asp		
				410				415						420			
gag	gtg	gag	gaa	gcc	ggc	gga	atg	gcg	cag	gcc	acc	gcg	cag	gga	att	1411	
Glu	Val	Glu	Glu	Ala	Gly	Gly	Met	Ala	Gln	Ala	Thr	Ala	Gln	Gly	Ile		
			425					430					435				
cct	aag	ctg	cgc	att	gag	gaa	tca	gcg	gca	cgc	acc	cag	gct	cgc	att	1459	
Pro	Lys	Leu	Arg	Ile	Glu	Glu	Ser	Ala	Ala	Arg	Thr	Gln	Ala	Arg	Ile		

002290"0420960



440	445	450	
gat tcc ggc cgc cag gcg ctg atc ggc gtg aat cgc tac gtg gcg gaa Asp Ser Gly Arg Gln Ala Leu Ile Gly Val Asn Arg Tyr Val Ala Glu 455 460 465			1507
gaa gat gag gaa att gaa gtc ctc aag gtt gac aac acc aag gtt cgc Glu Asp Glu Glu Ile Glu Val Leu Lys Val Asp Asn Thr Lys Val Arg 470 475 480 485			1555
gca gaa cag ttg gct aaa ctc gcg caa ctg aaa gca gag cgc aac gat Ala Glu Gln Leu Ala Lys Leu Ala Gln Leu Lys Ala Glu Arg Asn Asp 490 495 500			1603
gcg gaa gtc aag gct gcg ctg gat gcg ttg aca gct gct gcc cgc aac Ala Glu Val Lys Ala Ala Leu Asp Ala Leu Thr Ala Ala Arg Asn 505 510 515			1651
gag cat aaa gag cca ggg gat ttg gat cag aac ctg ctc aaa ctt gcc Glu His Lys Glu Pro Gly Asp Leu Asp Gln Asn Leu Leu Lys Leu Ala 520 525 530			1699
gtc gat gct gcg cgc gca aaa gct acc att gga gag atc tcc gat gct Val Asp Ala Ala Arg Ala Lys Ala Thr Ile Gly Glu Ile Ser Asp Ala 535 540 545			1747
ttg gaa gtt gtc ttt ggc cgc cac gaa gca gaa atc agg acg ctg tct Leu Glu Val Val Phe Gly Arg His Glu Ala Glu Ile Arg Thr Leu Ser 550 555 560 565			1795
ggc gtg tac aag gat gag gtt gga aag gaa ggc aca gtg agc aac gtc Gly Val Tyr Lys Asp Glu Val Gly Lys Glu Gly Thr Val Ser Asn Val 570 575 580			1843
gaa cgc gcg atc gcc ctg gct gac gcc ttt gag gct gag gaa ggc cgc Glu Arg Ala Ile Ala Leu Ala Asp Ala Phe Glu Ala Glu Glu Gly Arg 585 590 595			1891
cgc cca cgt atc ttt att gcc aag atg ggc cag gat gga cat gac cgt Arg Pro Arg Ile Phe Ile Ala Lys Met Gly Gln Asp Gly His Asp Arg 600 605 610			1939
gga cag aag gtt gtc gcg tct gcc tat gct gac ctg ggc atg gac gtg Gly Gln Lys Val Val Ala Ser Ala Tyr Ala Asp Leu Gly Met Asp Val 615 620 625			1987
gat gtt gga ccg ctg ttt caa act cca gcc gaa gct gcc cgc gcc gcc Asp Val Gly Pro Leu Phe Gln Thr Pro Ala Glu Ala Ala Arg Ala Ala 630 635 640 645			2035
gtg gac gcc gat gtt cac gtg gtg ggt atg tct tcg ctg gca gca ggc Val Asp Ala Asp Val His Val Val Gly Met Ser Ser Leu Ala Ala Gly 650 655 660			2083
cac ctc acc ttg ctg His Leu Thr Leu Leu 665			2098

&lt;210&gt; 630

&lt;211&gt; 666

09502740 062300



&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 630

```

Met Thr Ser Ile Pro Asn Phe Ser Asp Ile Pro Leu Thr Ala Glu Thr
 1           5           10           15

Arg Ala Ser Glu Ser His Asn Val Asp Ala Gly Lys Val Trp Asn Thr
          20           25           30

Pro Glu Gly Ile Asp Val Lys Arg Val Phe Thr Gln Ala Asp Arg Asp
          35           40           45

Glu Ala Gln Ala Ala Gly His Pro Val Asp Ser Leu Pro Gly Gln Lys
 50           55           60

Pro Phe Met Arg Gly Pro Tyr Pro Thr Met Tyr Thr Asn Gln Pro Trp
 65           70           75           80

Thr Ile Arg Gln Tyr Ala Gly Phe Ser Thr Ala Ala Glu Ser Asn Ala
          85           90           95

Phe Tyr Arg Arg Asn Leu Ala Ala Gly Gln Lys Gly Leu Ser Val Ala
          100          105          110

Phe Asp Leu Ala Thr His Arg Gly Tyr Asp Ser Asp Asn Glu Arg Val
          115          120          125

Val Gly Asp Val Gly Met Ala Gly Val Ala Ile Asp Ser Ile Leu Asp
          130          135          140

Met Arg Gln Leu Phe Asp Gly Ile Asp Leu Ser Ser Val Ser Val Ser
          145          150          155          160

Met Thr Met Asn Gly Ala Val Leu Pro Ile Leu Ala Phe Tyr Ile Val
          165          170          175

Ala Ala Glu Glu Gln Gly Val Gly Pro Glu Gln Leu Ala Gly Thr Ile
          180          185          190

Gln Asn Asp Ile Leu Lys Glu Phe Met Val Arg Asn Thr Tyr Ile Tyr
          195          200          205

Pro Pro Lys Pro Ser Met Arg Ile Ile Ser Asn Ile Phe Glu Tyr Thr
          210          215          220

Ser Leu Lys Met Pro Arg Phe Asn Ser Ile Ser Ile Ser Gly Tyr His
          225          230          235          240

Ile Gln Glu Ala Gly Ala Thr Ala Asp Leu Glu Leu Ala Tyr Thr Leu
          245          250          255

Ala Asp Gly Ile Glu Tyr Ile Arg Ala Gly Lys Glu Val Gly Leu Asp
          260          265          270

Val Asp Lys Phe Ala Pro Arg Leu Ser Phe Phe Trp Gly Ile Ser Met
          275          280          285

Tyr Thr Phe Met Glu Ile Ala Lys Leu Arg Ala Gly Arg Leu Leu Trp
          290          295          300

```

09602740 062300



Ser Glu Leu Val Ala Lys Phe Asp Pro Lys Asn Ala Lys Ser Gln Ser  
 305 310 315 320  
 Leu Arg Thr His Ser Gln Thr Ser Gly Trp Ser Leu Thr Ala Gln Asp  
 325 330 335  
 Val Tyr Asn Asn Val Ala Arg Thr Ala Ile Glu Ala Met Ala Ala Thr  
 340 345 350  
 Gln Gly His Thr Gln Ser Leu His Thr Asn Ala Leu Asp Glu Ala Leu  
 355 360 365  
 Ala Leu Pro Thr Asp Phe Ser Ala Arg Ile Ala Arg Asn Thr Gln Leu  
 370 375 380  
 Leu Leu Gln Gln Glu Ser Gly Thr Val Arg Pro Val Asp Pro Trp Ala  
 385 390 395 400  
 Gly Ser Tyr Tyr Val Glu Trp Leu Thr Asn Glu Leu Ala Asn Arg Ala  
 405 410 415  
 Arg Lys His Ile Asp Glu Val Glu Glu Ala Gly Gly Met Ala Gln Ala  
 420 425 430  
 Thr Ala Gln Gly Ile Pro Lys Leu Arg Ile Glu Glu Ser Ala Ala Arg  
 435 440 445  
 Thr Gln Ala Arg Ile Asp Ser Gly Arg Gln Ala Leu Ile Gly Val Asn  
 450 455 460  
 Arg Tyr Val Ala Glu Glu Asp Glu Glu Ile Glu Val Leu Lys Val Asp  
 465 470 475 480  
 Asn Thr Lys Val Arg Ala Glu Gln Leu Ala Lys Leu Ala Gln Leu Lys  
 485 490 495  
 Ala Glu Arg Asn Asp Ala Glu Val Lys Ala Ala Leu Asp Ala Leu Thr  
 500 505 510  
 Ala Ala Ala Arg Asn Glu His Lys Glu Pro Gly Asp Leu Asp Gln Asn  
 515 520 525  
 Leu Leu Lys Leu Ala Val Asp Ala Ala Arg Ala Lys Ala Thr Ile Gly  
 530 535 540  
 Glu Ile Ser Asp Ala Leu Glu Val Val Phe Gly Arg His Glu Ala Glu  
 545 550 555 560  
 Ile Arg Thr Leu Ser Gly Val Tyr Lys Asp Glu Val Gly Lys Glu Gly  
 565 570 575  
 Thr Val Ser Asn Val Glu Arg Ala Ile Ala Leu Ala Asp Ala Phe Glu  
 580 585 590  
 Ala Glu Glu Gly Arg Arg Pro Arg Ile Phe Ile Ala Lys Met Gly Gln  
 595 600 605  
 Asp Gly His Asp Arg Gly Gln Lys Val Val Ala Ser Ala Tyr Ala Asp  
 610 615 620  
 Leu Gly Met Asp Val Asp Val Gly Pro Leu Phe Gln Thr Pro Ala Glu

09602740 062300



```
<210> 631
<211> 1971
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101) .. (1948)  
<223> RXA00149
```

<400> 631																	
ttttcgtagg taaacacagg tgaaggcttt acaagcttgt gaactcccta cacaaaagca 60																	
atccaatagc tatccataag caagagaaaag taagtctacg										ttg	act	gat	ctc	aca	115		
										Leu	Thr	Asp	Leu	Thr	5		
										1							
aag	act	gcg	gtg	ccc	gag	gaa	ctt	tca	gag	aac	ctc	gaa	act	tgg	tac	163	
Lys	Thr	Ala	Val	Pro	Glu	Glu	Leu	Ser	Glu	Asn	Leu	Glu	Thr	Trp	Tyr		
				10					15								
aag	gct	gtg	gcc	ggg	gtt	ttc	gcg	cg	aca	cag	aaa	aaa	gac	atc	ggc	211	
Lys	Ala	Val	Ala	Gly	Val	Phe	Ala	Arg	Thr	Gln	Lys	Lys	Asp	Ile	Gly		
				25					30								
gac	att	gcc	gta	gat	gtg	tgg	aag	aaa	ctc	atc	gtc	act	aca	ccg	gat	259	
Asp	Ile	Ala	Val	Asp	Val	Trp	Lys	Lys	Leu	Ile	Val	Thr	Thr	Pro	Asp		
		40					45					50					
ggg	gtt	gat	atc	aat	ccg	ctg	tac	acc	aga	gca	gat	gag	tcc	cag	agg	307	
Gly	Val	Asp	Ile	Asn	Pro	Leu	Tyr	Thr	Arg	Ala	Asp	Glu	Ser	Gln	Arg		
		55					60					65					
aaa	ttc	act	gag	gtt	cct	ggg	gag	ttt	ccc	ttc	act	agg	gga	acc	act	355	
Lys	Phe	Thr	Glu	Val	Pro	Gly	Glu	Phe	Pro	Phe	Thr	Arg	Gly	Thr	Thr		
70					75					80					85		
gtt	gat	ggg	gaa	cgc	gtt	ggg	tgg	ggg	gtt	act	gag	act	ttc	gga	cat	403	
Val	Asp	Gly	Glu	Arg	Val	Gly	Trp	Gly	Val	Thr	Glu	Thr	Phe	Gly	His		
				90					95					100			
gac	agc	ccg	aag	aat	atc	aac	gct	gcg	gtg	ctg	aat	gct	ctg	aat	tct	451	
Asp	Ser	Pro	Lys	Asn	Ile	Asn	Ala	Ala	Val	Leu	Asn	Ala	Leu	Asn	Ser		
			105					110					115				
ggc	acc	acc	aca	ttg	ggg	ttt	gag	ttc	tct	gag	gaa	ttc	acg	gca	gct	499	
Gly	Thr	Thr	Thr	Leu	Gly	Phe	Glu	Phe	Ser	Glu	Glu	Phe	Thr	Ala	Ala		
		120					125					130					
gat	ctt	aaa	gtt	gct	ctc	gaa	ggc	gtg	tat	ctc	aac	atg	gct	ccg	ttg	547	
Asp	Leu	Lys	Val	Ala	Leu	Glu	Gly	Val	Tyr	Leu	Asn	Met	Ala	Pro	Leu		
		135					140					145					

**000000000000**



ctg att cat gcg ggt gga tcc acg tca gag gtt gca gcg gcg ttg tat	595
Leu Ile His Ala Gly Gly Ser Thr Ser Glu Val Ala Ala Ala Leu Tyr	
150 155 160 165	
acg ttg gcg gag gaa gcc gga acg ttt ttt gct gcg ttg acc ttg ggt	643
Thr Leu Ala Glu Ala Gly Thr Phe Phe Ala Ala Leu Thr Leu Gly	
170 175 180	
tct cgt cct ttg acg gcg cag gtt gat ggt tcg cac agt gac acc att	691
Ser Arg Pro Leu Thr Ala Gln Val Asp Gly Ser His Ser Asp Thr Ile	
185 190 195	
gaa gaa gca gtt cag ttg gca gtg aat gct tcc aag cgt gcg aat gtg	739
Glu Glu Ala Val Gln Leu Ala Val Asn Ala Ser Lys Arg Ala Asn Val	
200 205 210	
cgc gct atc ttg gtg gat ggt tcc agt ttt tcc aac cag ggc gcg tcg	787
Arg Ala Ile Leu Val Asp Gly Ser Ser Phe Ser Asn Gln Gly Ala Ser	
215 220 225	
gat gct caa gaa att ggt cta agt atc gcc gcc ggt gtg gat tat gtc	835
Asp Ala Gln Glu Ile Gly Leu Ser Ile Ala Ala Gly Val Asp Tyr Val	
230 235 240 245	
cgt cgc ttg gtc gat gca ggc ctt tcc acg gaa gct gca ctt aag cag	883
Arg Arg Leu Val Asp Ala Gly Leu Ser Thr Glu Ala Ala Leu Lys Gln	
250 255 260	
gtg gcg ttc cgt ttt gcg gtc acc gat gag cag ttc gcg cag att tct	931
Val Ala Phe Arg Phe Ala Val Thr Asp Glu Gln Phe Ala Gln Ile Ser	
265 270 275	
aag ctg cgt gtg gct cga cgt ctg tgg gcc agg gtg tgt gag gtg ctt	979
Lys Leu Arg Val Ala Arg Arg Leu Trp Ala Arg Val Cys Glu Val Leu	
280 285 290	
ggg ttt cca gag ctg gcc gta gca cca cag cat gcg gtg act gca cga	1027
Gly Phe Pro Glu Leu Ala Val Ala Pro Gln His Ala Val Thr Ala Arg	
295 300 305	
gcg atg ttt agc cag cgt gat ccg tgg gtg aat atg ctg cgc agt act	1075
Ala Met Phe Ser Gln Arg Asp Pro Trp Val Asn Met Leu Arg Ser Thr	
310 315 320 325	
gtt gca gct ttc gct gca ggc gtc ggt gga gca acc gat gtg gag gtt	1123
Val Ala Ala Phe Ala Ala Gly Val Gly Gly Ala Thr Asp Val Glu Val	
330 335 340	
cgt act ttt gat gat gcg atc cca gat gga gtt cct gga gtg tcg agg	1171
Arg Thr Phe Asp Asp Ala Ile Pro Asp Gly Val Pro Gly Val Ser Arg	
345 350 355	
aat ttc gct cac cgc atc gcg cgc aat act aat ttg ttg ttg cta gaa	1219
Asn Phe Ala His Arg Ile Ala Arg Asn Thr Asn Leu Leu Leu Leu Glu	
360 365 370	
gag tca cat ctt ggt cac gtg gtt gat cct gct ggt gga tca tat ttc	1267
Glu Ser His Leu Gly His Val Val Asp Pro Ala Gly Gly Ser Tyr Phe	
375 380 385	

09602740-062300



Parameter	Value	Unit
Temperature	25.0	°C
Pressure	1.0	atm
Flow rate	1.0	L/min
Concentration	0.1	mol/L
pH	7.0	
Time	10.0	min
Volume	10.0	L
Mass	10.0	g
Energy	10.0	J
Power	10.0	W
Frequency	10.0	Hz
Wavelength	10.0	nm
Angle	10.0	°
Distance	10.0	m
Area	10.0	m²
Volume	10.0	m³
Mass	10.0	kg
Energy	10.0	J
Power	10.0	W
Frequency	10.0	Hz
Wavelength	10.0	nm
Angle	10.0	°
Distance	10.0	m
Area	10.0	m²
Volume	10.0	m³
Mass	10.0	kg
Energy	10.0	J
Power	10.0	W
Frequency	10.0	Hz
Wavelength	10.0	nm
Angle	10.0	°
Distance	10.0	m
Area	10.0	m²
Volume	10.0	m³
Mass	10.0	kg
Energy	10.0	J
Power	10.0	W
Frequency	10.0	Hz
Wavelength	10.0	nm
Angle	10.0	°
Distance	10.0	m
Area	10.0	m²
Volume	10.0	m³
Mass	10.0	kg
Energy	10.0	J
Power	10.0	W
Frequency	10.0	Hz
Wavelength	10.0	nm
Angle	10.0	°
Distance	10.0	m
Area	10.0	m²
Volume	10.0	m³
Mass	10.0	kg
Energy	10.0	J
Power	10.0	W
Frequency	10.0	Hz
Wavelength	10.0	nm
Angle	10.0	°
Distance	10.0	m
Area	10.0	m²
Volume	10.0	m³
Mass	10.0	kg
Energy	10.0	J
Power	10.0	W
Frequency	10.0	Hz
Wavelength	10.0	nm
Angle	10.0	°
Distance	10.0	m
Area	10.0	m²
Volume	10.0	m³
Mass	10.0	kg
Energy	10.0	J
Power	10.0	W
Frequency	10.0	Hz
Wavelength	10.0	nm
Angle	10.0	°
Distance	10.0	m
Area	10.0	m²
Volume	10.0	m³
Mass	10.0	kg
Energy	10.0	J
Power	10.0	W
Frequency	10.0	Hz
Wavelength	10.0	nm
Angle	10.0	°
Distance	10.0	m
Area	10.0	m²
Volume	10.0	m³
Mass	10.0	kg
Energy	10.0	J
Power	10.0	W
Frequency	10.0	Hz
Wavelength	10.0	nm
Angle	10.0	°
Distance	10.0	m
Area	10.0	m²
Volume	10.0	m³
Mass	10.0	kg
Energy	10.0	J
Power	10.0	W
Frequency	10.0	Hz
Wavelength	10.0	nm
Angle	10.0	°
Distance	10.0	m
Area	10.0	m²
Volume	10.0	m³
Mass	10.0	kg
Energy	10.0	J
Power	10.0	W
Frequency	10.0	Hz
Wavelength	10.0	nm
Angle	10.0	°
Distance	10.0	m
Area	10.0	m²
Volume	10.0	m³
Mass	10.0	kg
Energy	10.0	J
Power	10.0	W
Frequency	10.0	Hz
Wavelength	10.0	nm
Angle	10.0	°
Distance	10.0	m
Area	10.0	m²
Volume	10.0	m³
Mass	10.0	kg
Energy	10.0	J
Power	10.0	W
Frequency	10.0	Hz
Wavelength	10.0	nm
Angle	10.0	°
Distance	10.0	m
Area</		



&lt;210&gt; 632

&lt;211&gt; 616

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 632

Leu Thr Asp Leu Thr Lys Thr Ala Val Pro Glu Glu Leu Ser Glu Asn  
 1 5 10 15

Leu Glu Thr Trp Tyr Lys Ala Val Ala Gly Val Phe Ala Arg Thr Gln  
 20 25 30

Lys Lys Asp Ile Gly Asp Ile Ala Val Asp Val Trp Lys Lys Leu Ile  
 35 40 45

Val Thr Thr Pro Asp Gly Val Asp Ile Asn Pro Leu Tyr Thr Arg Ala  
 50 55 60

Asp Glu Ser Gln Arg Lys Phe Thr Glu Val Pro Gly Glu Phe Pro Phe  
 65 70 75 80

Thr Arg Gly Thr Thr Val Asp Gly Glu Arg Val Gly Trp Gly Val Thr  
 85 90 95

Glu Thr Phe Gly His Asp Ser Pro Lys Asn Ile Asn Ala Ala Val Leu  
 100 105 110

Asn Ala Leu Asn Ser Gly Thr Thr Thr Leu Gly Phe Glu Phe Ser Glu  
 115 120 125

Glu Phe Thr Ala Ala Asp Leu Lys Val Ala Leu Glu Gly Val Tyr Leu  
 130 135 140

Asn Met Ala Pro Leu Leu Ile His Ala Gly Gly Ser Thr Ser Glu Val  
 145 150 155 160

Ala Ala Ala Leu Tyr Thr Leu Ala Glu Glu Ala Gly Thr Phe Phe Ala  
 165 170 175

Ala Leu Thr Leu Gly Ser Arg Pro Leu Thr Ala Gln Val Asp Gly Ser  
 180 185 190

His Ser Asp Thr Ile Glu Glu Ala Val Gln Leu Ala Val Asn Ala Ser  
 195 200 205

Lys Arg Ala Asn Val Arg Ala Ile Leu Val Asp Gly Ser Ser Phe Ser  
 210 215 220

Asn Gln Gly Ala Ser Asp Ala Gln Glu Ile Gly Leu Ser Ile Ala Ala  
 225 230 235 240

Gly Val Asp Tyr Val Arg Arg Leu Val Asp Ala Gly Leu Ser Thr Glu  
 245 250 255

Ala Ala Leu Lys Gln Val Ala Phe Arg Phe Ala Val Thr Asp Glu Gln  
 260 265 270

Phe Ala Gln Ile Ser Lys Leu Arg Val Ala Arg Arg Leu Trp Ala Arg  
 275 280 285

Val Cys Glu Val Leu Gly Phe Pro Glu Leu Ala Val Ala Pro Gln His

09602740-062300



290	295	300
Ala Val Thr Ala Arg 305	Ala Met Phe Ser Gln Arg 310	Asp Pro Trp Val Asn 315 320
Met Leu Arg Ser Thr Val Ala Ala Phe Ala Ala Gly Val Gly Gly Ala 325 330 335		
Thr Asp Val Glu Val Arg Thr Phe Asp Asp Ala Ile Pro Asp Gly Val 340 345 350		
Pro Gly Val Ser Arg Asn Phe Ala His Arg Ile Ala Arg Asn Thr Asn 355 360 365		
Leu Leu Leu Leu Glu Glu Ser His Leu Gly His Val Val Asp Pro Ala 370 375 380		
Gly Gly Ser Tyr Phe Val Glu Ser Phe Thr Asp Asp Leu Ala Glu Lys 385 390 395 400		
Ala Trp Ala Val Phe Ser Gly Ile Glu Ala Glu Gly Gly Tyr Ser Ala 405 410 415		
Ala Cys Ala Ser Gly Thr Val Thr Ala Met Leu Asp Gln Thr Trp Glu 420 425 430		
Gln Thr Arg Ala Asp Val Ala Ser Arg Lys Lys Lys Leu Thr Gly Ile 435 440 445		
Asn Glu Phe Pro Asn Leu Ala Glu Ser Pro Leu Pro Ala Asp Arg Arg 450 455 460		
Val Glu Pro Ala Gly Val Arg Arg Trp Ala Ala Asp Phe Glu Ala Leu 465 470 475 480		
Arg Asn Arg Ser Asp Ala Phe Leu Glu Lys Asn Gly Ala Arg Pro Gln 485 490 495		
Ile Thr Met Ile Pro Leu Gly Pro Leu Ser Lys His Asn Ile Arg Thr 500 505 510		
Gly Phe Thr Ser Asn Leu Leu Ala Ser Gly Gly Ile Glu Ala Ile Asn 515 520 525		
Pro Gly Gln Leu Val Pro Gly Thr Asp Ala Phe Ala Glu Ala Ala Gln 530 535 540		
Ala Ala Gly Ile Val Val Val Cys Gly Thr Asp Gln Glu Tyr Ala Glu 545 550 555 560		
Thr Gly Glu Gly Ala Val Glu Lys Leu Arg Glu Ala Gly Val Glu Arg 565 570 575		
Ile Leu Leu Ala Gly Ala Pro Lys Ser Phe Glu Gly Ser Ala His Ala 580 585 590		
Pro Asp Gly Tyr Leu Asn Met Thr Ile Asp Ala Ala Ala Thr Leu Ala 595 600 605		
Asp Leu Leu Asp Ala Leu Gly Ala 610 615		

09602740 062300



```
<220>  
<221> CDS  
<222> (101)..(754)  
<223> RXN00317
```

1101 1102 1103 1104 1105 1106 1107 1108 1109 1110 1111 1112 1113 1114 1115 1116 1117 1118 1119 1120 1121 1122 1123 1124 1125 1126 1127 1128 1129 1130 1131 1132 1133 1134 1135 1136 1137 1138 1139 1140 1141 1142 1143 1144 1145 1146 1147 1148 1149 1150 1151 1152 1153 1154 1155 1156 1157 1158 1159 1160 1161 1162 1163 1164 1165 1166 1167 1168 1169 1170 1171 1172 1173 1174 1175 1176 1177 1178 1179 1180 1181 1182 1183 1184 1185 1186 1187 1188 1189 1190 1191 1192 1193 1194 1195 1196 1197 1198 1199 1200 1201 1202 1203 1204 1205 1206 1207 1208 1209 1210 1211 1212 1213 1214 1215 1216 1217 1218 1219 1220 1221 1222 1223 1224 1225 1226 1227 1228 1229 1230 1231 1232 1233 1234 1235 1236 1237 1238 1239 1240 1241 1242 1243 1244 1245 1246 1247 1248 1249 1250 1251 1252 1253 1254 1255 1256 1257 1258 1259 1260 1261 1262 1263 1264 1265 1266 1267 1268 1269 1270 1271 1272 1273 1274 1275 1276 1277 1278 1279 1280 1281 1282 1283 1284 1285 1286 1287 1288 1289 1290 1291 1292 1293 1294 1295 1296 1297 1298 1299 1300 1301 1302 1303 1304 1305 1306 1307 1308 1309 1310 1311 1312 1313 1314 1315 1316 1317 1318 1319 1320 1321 1322 1323 1324 1325 1326 1327 1328 1329 1330 1331 1332 1333 1334 1335 1336 1337 1338 1339 1340 1341 1342 1343 1344 1345 1346 1347 1348 1349 1350 1351 1352 1353 1354 1355 1356 1357 1358 1359 1360 1361 1362 1363 1364 1365 1366 1367 1368 1369 1370 1371 1372 1373 1374 1375 1376 1377 1378 1379 1380 1381 1382 1383 1384 1385 1386 1387 1388 1389 1390 1391 1392 1393 1394 1395 1396 1397 1398 1399 1400 1401 1402 1403 1404 1405 1406 1407 1408 1409 1410 1411 1412 1413 1414 1415 1416 1417 1418 1419 1420 1421 1422 1423 1424 1425 1426 1427 1428 1429 1430 1431 1432 1433 1434 1435 1436 1437 1438 1439 1440 1441 1442 1443 1444 1445 1446 1447 1448 1449 1450 1451 1452 1453 1454 1455 1456 1457 1458 1459 1460 1461 1462 1463 1464 1465 1466 1467 1468 1469 1470 1471 1472 1473 1474 1475 1476 1477 1478 1479 1480 1481 1482 1483 1484 1485 1486 1487 1488 1489 1490 1491 1492 1493 1494 1495 1496 1497 1498 1499 1500 1501 1502 1503 1504 1505 1506 1507 1508 1509 1510 1511 1512 1513 1514 1515 1516 1517 1518 1519 1520 1521 1522 1523 1524 1525 1526 1527 1528 1529 1530 1531 1532 1533 1534 1535 1536 1537 1538 1539 1540 1541 1542 1543 1544 1545 1546 1547 1548 1549 1550 1551 1552 1553 1554 1555 1556 1557 1558 1559 1560 1561 1562 1563 1564 1565 1566 1567 1568 1569 1570 1571 1572 1573 1574 1575 1576 1577 1578 1579 1580 1581 1582 1583 1584 1585 1586 1587 1588 1589 1590 1591 1592 1593 1594 1595 1596 1597 1598 1599 1600 1601 1602 1603 1604 1605 1606 1607 1608 1609 1610 1611 1612 1613 1614 1615 1616 1617 1618 1619 1620 1621 1622 1623 1624 1625 1626 1627 1628 1629 1630 1631 1632 1633 1634 1635 1636 1637 1638 1639 1640 1641 1642 1643 1644 1645 1646 1647 1648 1649 1650 1651 1652 1653 1654 1655 1656 1657 1658 1659 1660 1661 1662 1663 1664 1665 1666 1667 1668 1669 1670 1671 1672 1673 1674 1675 1676 1677 1678 1679 1680 1681 1682 1683 1684 1685 1686 1687 1688 1689 1690 1691 1692 1693 1694 1695 1696 1697 1698 1699 1700 1701 1702 1703 1704 1705 1706 1707 1708 1709 1710 1711 1712 1713 1714 1715 1716 1717 1718 1719 1720 1721 1722 1723 1724 1725 1726 1727 1728 1729 1730 1731 1732 1733 1734 1735 1736 1737 1738 1739 1740 1741 1742 1743 1744 1745 1746 1747 1748 1749 1750 1751 1752 1753 1754 1755 1756 1757 1758 1759 1760 1761 1762 1763 1764 1765 1766 1767 1768 1769 1770 1771 1772 1773 1774 1775 1776 1777 1778 1779 1780 1781 1782 1783 1784 1785 1786 1787 1788 1789 1790 1791 1792 1793 1794 1795 1796 1797 1798 1799 1800 1801 1802 1803 1804 1805 1806 1807 1808 1809 1810 1811 1812 1813 1814 1815 1816 1817 1818 1819 1820 1821 1822 1823 1824 1825 1826 1827 1828 1829 1830 1831 1832 1833 1834 1835 1836 1837 1838 1839 1840 1841 1842 1843 1844 1845 1846 1847 1848 1849 1850 1851 1852 1853 1854 1855 1856 1857 1858 1859 1860 1861 1862 1863 1864 1865 1866 1867 1868 1869 1870 1871 1872 1873 1874 1875 1876 1877 1878 1879 1880 1881 1882 1883 1884 1885 1886 1887 1888 1889 1890 1891 1892 1893 1894 1895 1896 1897 1898 1899 1900 1901 1902 1903 1904 1905 1906 1907 1908 1909 1910 1911 1912 1913 1914 1915 1916 1917 1918 1919



170										175					180					
atc	gat	tgt	gtt	gcc	gta	acc	tgg	ggc	tac	ggc	agc	aaa	act	gaa	tgg	691				
Ile	Asp	Cys	Val	Ala	Val	Thr	Trp	Gly	Tyr	Gly	Ser	Lys	Thr	Glu	Trp					
			185					190					195							
gac	gct	gcc	cgc	tac	acc	gtg	agc	acc	gca	gaa	gaa	tta	gaa	agg	atc	739				
Asp	Ala	Ala	Arg	Tyr	Thr	Val	Ser	Thr	Ala	Glu	Glu	Leu	Glu	Arg	Ile					
		200					205					210								
atc	cat	gac	tgg	gcc	taaaacttcg	ctacctgtgg	aaa									777				
Ile	His	Asp	Trp	Ala																
		215																		

&lt;210&gt; 634

&lt;211&gt; 218

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 634

Val	Thr	Thr	Pro	Ser	Lys	Lys	Thr	Leu	Leu	Phe	Asp	Leu	Asp	Gly	Thr	
1				5					10					15		
Leu	Val	Asp	Ser	Phe	Pro	Gly	Ile	Arg	Thr	Ser	Phe	Leu	His	Thr	Leu	
			20					25					30			
His	Glu	Lys	Asn	Trp	Glu	Ile	Pro	Ser	Glu	Glu	Arg	Ile	Ser	Gln	Val	
		35					40					45				
Pro	Gly	Pro	Pro	Met	Glu	Trp	Thr	Phe	Gln	Asp	Leu	Gly	Met	Thr	Pro	
	50					55					60					
Glu	Gln	Ala	Gln	Asp	Ala	Leu	Gln	Thr	Tyr	Leu	Glu	His	Tyr	Gly	Gln	
	65				70					75					80	
Val	Gly	Trp	Asp	Leu	Ser	Glu	Ala	Phe	Pro	Gly	Met	Arg	Asp	Leu	Leu	
				85					90					95		
Ile	Arg	Leu	Lys	Tyr	Glu	Gly	Phe	Arg	Leu	Cys	Thr	Ala	Thr	Ser	Lys	
			100					105					110			
Gly	Glu	Phe	Phe	Ala	Glu	Lys	Val	Leu	Arg	Lys	Phe	Glu	Met	Phe	Asp	
		115					120					125				
Leu	Phe	Glu	Phe	Met	Gly	Ala	Ala	Thr	Asp	Ser	Gly	Asn	Arg	Arg	Ser	
	130					135					140					
Lys	Ser	Ala	Val	Ile	Lys	His	Val	Leu	Asp	Ser	Val	Gly	Leu	Asp	Glu	
145					150	?				155					160	
Pro	Asn	Asp	Ile	Leu	Met	Ile	Gly	Asp	Arg	Ser	His	Asp	Ile	Glu	Gly	
				165					170					175		
Ser	Ser	Glu	Phe	Gly	Ile	Asp	Cys	Val	Ala	Val	Thr	Trp	Gly	Tyr	Gly	
			180					185					190			
Ser	Lys	Thr	Glu	Trp	Asp	Ala	Ala	Arg	Tyr	Thr	Val	Ser	Thr	Ala	Glu	
		195					200					205				
Glu	Leu	Glu	Arg	Ile	Ile	His	Asp	Trp	Ala							

09602740.062300



215

<400> 635  
caacggttac atcactcacg cattacctcc cctggttggt accgcatggt cgtttccaa 60

gaa ggt ttt cgt ctg tgc acc gcc acc ttt caa ggg 439  
Glu Gly Phe Arg Leu Cys Thr Ala Thr Phe Gln Gly  
105 110

Leu Val Asp Ser Phe Pro Gly Ile Arg Thr Ser Phe Leu His Thr Leu  
20 25 30

[illegible]



Gly

```
<220>  
<221> CDS  
<222> (101)..(793)  
<223> RXA02196
```

Figure 1. Schematic representation of the experimental design. The subjects were divided into two groups: the control group and the experimental group. The control group was divided into two subgroups: the control group and the control group. The experimental group was divided into two subgroups: the experimental group and the experimental group. The control group was divided into two subgroups: the control group and the control group. The experimental group was divided into two subgroups: the experimental group and the experimental group.







[illegible]



```
<210> 640
<211> 136
<212> PRT
<213> Corynebacterium glutamicum
```

```
<210> 641
<211> 1662
<212> DNA
<213> Corynebacterium glutamicum
```

[illegible]



<223> RXN01744

tcttattggt tcttcgtttt gtatcgataa atacaatcgg tttcctggct taataaggct 60

```

atc gca cgg tgg caa ttc gga att acc acc gtc tat cac ttc att ttt    163
Ile Ala Arg Trp Gln Phe Gly Ile Thr Thr Val Tyr His Phe Ile Phe
          10                      15                      20

```

gtc cca ctg acc att ggc tta gcg ccg ctg gtc gca atc atg caa acg 211  
Val Pro Leu Thr Ile Gly Leu Ala Pro Leu Val Ala Ile Met Gln Thr  
25 30 35

ttt tgg caa gtt acc ggc aaa gag cac tgg tat cgg gcc aca aga ttt 259  
Phe Trp Gln Val Thr Gly Lys Glu His Trp Tyr Arg Ala Thr Arg Phe  
40 45 50

ttt ggc act gtg ctg ctc atc aac ttc gcg gtt ggt gta gca acg ggc 307  
Phe Gly Thr Val Leu Leu Ile Asn Phe Ala Val Gly Val Ala Thr Gly  
55 60 65

att gtg cag gag ttc cag ttc ggt atg aac tgg tcg gaa tat tcg cgt 355  
Ile Val Gln Glu Phe Gln Phe Gly Met Asn Trp Ser Glu Tyr Ser Arg  
70 75 80 85

ttc	gtc	ggg	gat	gtt	ttc	ggc	gga	ccg	ctg	gct	ttg	gag	ggg	ctt	atc	403
Phe	Val	Gly	Asp	Val	Phe	Gly	Gly	Pro	Leu	Ala	Leu	Glu	Gly	Leu	Ile	
				90					95					100		

gcg ttc ttc ctt gag tct gta ttc ctg gga ctg tgg att ttc gga tgg 451  
Ala Phe Phe Leu Glu Ser Val Phe Leu Gly Leu Trp Ile Phe Gly Trp  
105 110 115

ggg aag att cct ggt tgg ttg cac act gca tcc att tgg atc gtt gct 499  
Gly Lys Ile Pro Gly Trp Leu His Thr Ala Ser Ile Trp Ile Val Ala  
120 125 130

att gcg acg aat att tct gcc tat ttc atc atc gtg gcc aac tcg ttt 547  
Ile Ala Thr Asn Ile Ser Ala Tyr Phe Ile Ile Val Ala Asn Ser Phe  
135 140 145

atg cag cat ccg gtg ggt gct gag tat aac cct gag act ggt cgt gcg 595  
Met Gln His Pro Val Gly Ala Glu Tyr Asn Pro Glu Thr Gly Arg Ala  
150 155 160 165

gag ctt act gat ttt tgg gct ctt ctc aca aac tcc acc gcg ctg gct 643  
Glu Leu Thr Asp Phe Trp Ala Leu Leu Thr Asn Ser Thr Ala Leu Ala  
170 175 180

gcg ttc ccg cat gct gtt gcc ggt ggt ttt tta aca gct gga act ttc 691  
Ala Phe Pro His Ala Val Ala Gly Gly Phe Leu Thr Ala Gly Thr Phe  
185 190 195

ggt ctc gga att tcg ggt tgg tgg att att cgt gcg cac cgt cag gcc 739  
Val Leu Gly Ile Ser Gly Trp Trp Ile Ile Arg Ala His Arg Gln Ala  
200 205 210

**00000000000000000000000000000000**



aag aag gct gag tcg gaa atc gag tcg aag cat tcg atg cac agg ccc 787  
Lys Lys Ala Glu Ser Glu Ile Glu Ser Lys His Ser Met His Arg Pro  
215 220 225

gcg ttg tgg gtt ggt tgg tgg acc aca gtt gtc tct tcc gtg gcg ctg 835  
Ala Leu Trp Val Gly Trp Trp Thr Thr Val Val Ser Ser Val Ala Leu  
230 235 240 245

ttc atc act ggc gat atc cag gcg aag ctc atg ttc gtg caa cag cca 883  
Phe Ile Thr Gly Asp Ile Gln Ala Lys Leu Met Phe Val Gln Gln Pro  
250 255 260

atg aag atg gcg tcg gcg gaa tcc ttg tgt gaa acc gcc aca gat cca 931  
Met Lys Met Ala Ser Ala Glu Ser Leu Cys Glu Thr Ala Thr Asp Pro  
265 270 275

aac ttc tcc att ctg aca att ggt acg cac aac aac tgc gat acg gta 979  
Asn Phe Ser Ile Leu Thr Ile Gly Thr His Asn Asn Cys Asp Thr Val  
280 285 290

acc cac ctg atc gat gtt ccg ttt gtg ctt cca ttc ttg gct gaa gga 1027  
Thr His Leu Ile Asp Val Pro Phe Val Leu Pro Phe Leu Ala Glu Gly  
295 300 305

aaa ttc acc ggt gtg act ttg cag ggt gta aac cag ctc caa gct gca 1075  
Lys Phe Thr Gly Val Thr Leu Gln Gly Val Asn Gln Leu Gln Ala Ala  
310 315 320 325

gcg gag caa gca tac ggt cct ggc aac tac tcc cct aac ttg ttt gtc 1123  
Ala Glu Gln Ala Tyr Gly Pro Gly Asn Tyr Ser Pro Asn Leu Phe Val  
330 335 340

acc tac tgg tca ttc cgc gca atg atc ggc ctg atg ctt ggt tct ttg 1171  
Thr Tyr Trp Ser Phe Arg Ala Met Ile Gly Leu Met Leu Gly Ser Leu  
345 350 355

gct atc gct gcg att gcg tgg ctg ttg ctg cgt aag aag cgc aca cca 1219  
Ala Ile Ala Ala Ile Ala Trp Leu Leu Leu Arg Lys Lys Arg Thr Pro  
360 365 370

act gga aag att gct cgt ctg ttc cag atc ggc agc ctc att gct atc 1267  
Thr Gly Lys Ile Ala Arg Leu Phe Gln Ile Gly Ser Leu Ile Ala Ile  
375 380 385

ccg ttc cca ttc ttg gcc aac tct gct ggt tgg atc ttc acc gag atg 1315  
Pro Phe Pro Phe Leu Ala Asn Ser Ala Gly Trp Ile Phe Thr Glu Met  
390 395 400 405

ggc cgc cag cct tgg gtg gtg cac ccg aac cct gaa tct gcc ggc gat 1363  
Gly Arg Gln Pro Trp Val Val His Pro Asn Pro Glu Ser Ala Gly Asp  
410 415 420

gcc cga aca gag atg atc cgg atg act gtt gat atg ggt gta tct gat 1411  
Ala Arg Thr Glu Met Ile Arg Met Thr Val Asp Met Gly Val Ser Asp  
425 430 435

cat gcg cca tgg caa gtc tgg ctg act ctc att ggc ttc acg att ctc 1459  
His Ala Pro Trp Gln Val Trp Leu Thr Leu Ile Gly Phe Thr Ile Leu  
440 445 450

003290"0420966



tat ctc att ttg ttc gtg gtg tgg gtg tgg ctg att cgc cgc gca gtt 1507  
 Tyr Leu Ile Leu Phe Val Val Trp Val Trp Leu Ile Arg Arg Ala Val  
 455 460 465

ctg atc gga cca cca gag gaa ggc gct cca tcc gtg gag gca aag act 1555  
 Leu Ile Gly Pro Pro Glu Glu Gly Ala Pro Ser Val Glu Ala Lys Thr  
 470 475 480 485

gga ccg gca acc ccg att ggt tca gat atg ccc atg aca ccg ctg caa 1603  
 Gly Pro Ala Thr Pro Ile Gly Ser Asp Met Pro Met Thr Pro Leu Gln  
 490 495 500

ttt act gcc gct gcc cca acc aca ggt gaa aag gaa taaccatgga 1649  
 Phe Thr Ala Ala Ala Pro Thr Thr Gly Glu Lys Glu  
 505 510

tctcaatacc ttt 1662

<210> 642

<211> 513

<212> PRT

<213> Corynebacterium glutamicum

<400> 642

Val Asp Val Val Asp Ile Ala Arg Trp Gln Phe Gly Ile Thr Thr Val  
 1 5 10 15

Tyr His Phe Ile Phe Val Pro Leu Thr Ile Gly Leu Ala Pro Leu Val  
 20 25 30

Ala Ile Met Gln Thr Phe Trp Gln Val Thr Gly Lys Glu His Trp Tyr  
 35 40 45

Arg Ala Thr Arg Phe Phe Gly Thr Val Leu Leu Ile Asn Phe Ala Val  
 50 55 60

Gly Val Ala Thr Gly Ile Val Gln Glu Phe Gln Phe Gly Met Asn Trp  
 65 70 75 80

Ser Glu Tyr Ser Arg Phe Val Gly Asp Val Phe Gly Gly Pro Leu Ala  
 85 90 95

Leu Glu Gly Leu Ile Ala Phe Phe Leu Glu Ser Val Phe Leu Gly Leu  
 100 105 110

Trp Ile Phe Gly Trp Gly Lys Ile Pro Gly Trp Leu His Thr Ala Ser  
 115 120 125

Ile Trp Ile Val Ala Ile Ala Thr Asn Ile Ser Ala Tyr Phe Ile Ile  
 130 135 140

Val Ala Asn Ser Phe Met Gln His Pro Val Gly Ala Glu Tyr Asn Pro  
 145 150 155 160

Glu Thr Gly Arg Ala Glu Leu Thr Asp Phe Trp Ala Leu Leu Thr Asn  
 165 170 175

Ser Thr Ala Leu Ala Ala Phe Pro His Ala Val Ala Gly Gly Phe Leu  
 180 185 190

002230" 0420960



Thr Ala Gly Thr Phe Val Leu Gly Ile Ser Gly Trp Trp Ile Ile Arg  
 195 200 205  
 Ala His Arg Gln Ala Lys Lys Ala Glu Ser Glu Ile Glu Ser Lys His  
 210 215 220  
 Ser Met His Arg Pro Ala Leu Trp Val Gly Trp Trp Thr Thr Val Val  
 225 230 235 240  
 Ser Ser Val Ala Leu Phe Ile Thr Gly Asp Ile Gln Ala Lys Leu Met  
 245 250 255  
 Phe Val Gln Gln Pro Met Lys Met Ala Ser Ala Glu Ser Leu Cys Glu  
 260 265 270  
 Thr Ala Thr Asp Pro Asn Phe Ser Ile Leu Thr Ile Gly Thr His Asn  
 275 280 285  
 Asn Cys Asp Thr Val Thr His Leu Ile Asp Val Pro Phe Val Leu Pro  
 290 295 300  
 Phe Leu Ala Glu Gly Lys Phe Thr Gly Val Thr Leu Gln Gly Val Asn  
 305 310 315 320  
 Gln Leu Gln Ala Ala Ala Glu Gln Ala Tyr Gly Pro Gly Asn Tyr Ser  
 325 330 335  
 Pro Asn Leu Phe Val Thr Tyr Trp Ser Phe Arg Ala Met Ile Gly Leu  
 340 345 350  
 Met Leu Gly Ser Leu Ala Ile Ala Ala Ile Ala Trp Leu Leu Leu Arg  
 355 360 365  
 Lys Lys Arg Thr Pro Thr Gly Lys Ile Ala Arg Leu Phe Gln Ile Gly  
 370 375 380  
 Ser Leu Ile Ala Ile Pro Phe Pro Phe Leu Ala Asn Ser Ala Gly Trp  
 385 390 395 400  
 Ile Phe Thr Glu Met Gly Arg Gln Pro Trp Val Val His Pro Asn Pro  
 405 410 415  
 Glu Ser Ala Gly Asp Ala Arg Thr Glu Met Ile Arg Met Thr Val Asp  
 420 425 430  
 Met Gly Val Ser Asp His Ala Pro Trp Gln Val Trp Leu Thr Leu Ile  
 435 440 445  
 Gly Phe Thr Ile Leu Tyr Leu Ile Leu Phe Val Val Trp Val Trp Leu  
 450 455 460  
 Ile Arg Arg Ala Val Leu Ile Gly Pro Pro Glu Glu Gly Ala Pro Ser  
 465 470 475 480  
 Val Glu Ala Lys Thr Gly Pro Ala Thr Pro Ile Gly Ser Asp Met Pro  
 485 490 495  
 Met Thr Pro Leu Gln Phe Thr Ala Ala Ala Pro Thr Thr Gly Glu Lys  
 500 505 510  
 Glu

0062290" 04220960



```
<210> 643
<211> 238
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(238)  
<223> FRXA00055
```

<400> 643																
tcttattggt	tcttcgtttt	gtatcgataa	atacaatcgg	tttctctggct	taataaggct	60										
gttcctgtca acctgcaatg gaagaggaag tgtacctagc							gtg	gat	gtc	gtc	gac	115				
							Val	Asp	Val	Val	Asp					
							1				5					
atc	gca	cgg	tgg	caa	ttc	gga	att	acc	acc	gtc	tat	cac	ttc	att	ttt	163
Ile	Ala	Arg	Trp	Gln	Phe	Gly	Ile	Thr	Thr	Val	Tyr	His	Phe	Ile	Phe	
				10					15					20		
gtc	cca	ctg	acc	att	ggc	tta	gca	ccg	ctg	gtc	gcg	atc	atg	caa	acg	211
Val	Pro	Leu	Thr	Ile	Gly	Leu	Ala	Pro	Leu	Val	Ala	Ile	Met	Gln	Thr	
			25				30				35					
ttt	tgg	caa	gtt	acc	ggc	aaa	gag	cac								238
Phe	Trp	Gln	Val	Thr	Gly	Lys	Glu	His								
			40				45									

```
<210> 644
<211> 46
<212> PRT
<213> Corynebacterium glutamicum
```

```

<400> 644
Val Asp Val Val Asp Ile Ala Arg Trp Gln Phe Gly Ile Thr Thr Val
  1          5          10          15

Tyr His Phe Ile Phe Val Pro Leu Thr Ile Gly Leu Ala Pro Leu Val
          20          25          30

Ala Ile Met Gln Thr Phe Trp Gln Val Thr Gly Lys Glu His
  35          40          45

```

```
<210> 645
<211> 1325
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (1)..(1302)
<223> FRXA01744
```

<400> 645  
tgg tcg gaa tat tcg cgt ttc gtc ggt gat gtt ttc ggc gga ccg ctg 48

[illegible]



Trp 1	Ser	Glu	Tyr	Ser 5	Arg	Phe	Val	Gly	Asp 10	Val	Phe	Gly	Gly	Pro 15	Leu	
gct	ttg	gag	ggt	ctt	atc	gcg	ttc	ttc	ctt	gag	tct	gta	ttc	ctg	gga	96
Ala	Leu	Glu	Gly 20	Leu	Ile	Ala	Phe	Phe 25	Leu	Glu	Ser	Val	Phe 30	Leu	Gly	
ctg	tgg	att	ttc	gga	tgg	ggg	aag	att	cct	ggt	tgg	ttg	cac	act	gca	144
Leu	Trp	Ile 35	Phe	Gly	Trp	Gly	Lys 40	Ile	Pro	Gly	Trp	Leu	His 45	Thr	Ala	
tcc	att	tgg	atc	gtt	gct	att	gcg	acg	aat	att	tct	gcc	tat	ttc	atc	192
Ser	Ile 50	Trp	Ile	Val	Ala	Ile 55	Ala	Thr	Asn	Ile	Ser	Ala	Tyr	Phe	Ile	
atc	gtg	gcc	aac	tcg	ttt	atg	cag	cat	ccg	gtg	ggt	gct	gag	tat	aac	240
Ile	Val	Ala	Asn	Ser	Phe 70	Met	Gln	His	Pro	Val 75	Gly	Ala	Glu	Tyr	Asn 80	
cct	gag	act	ggt	cgt	gcg	gag	ctt	act	gat	ttt	tgg	gct	ctt	ctc	aca	288
Pro	Glu	Thr	Gly	Arg 85	Ala	Glu	Leu	Thr	Asp 90	Phe	Trp	Ala	Leu	Leu	Thr 95	
aac	tcc	acc	gcg	ctg	gct	gcg	ttc	ccg	cat	gct	gtt	gcc	ggt	ggt	ttt	336
Asn	Ser	Thr	Ala 100	Leu	Ala	Ala	Phe	Pro 105	His	Ala	Val	Ala	Gly 110	Gly	Phe	
tta	aca	gct	gga	act	ttc	gtt	ctc	gga	att	tcg	ggt	tgg	tgg	att	att	384
Leu	Thr	Ala 115	Gly	Thr	Phe	Val	Leu 120	Gly	Ile	Ser	Gly	Trp	Trp	Ile	Ile	
cgt	gcg	cac	cgt	cag	gcc	aag	aag	gct	gag	tcg	gaa	atc	gag	tcg	aag	432
Arg	Ala	His	Arg	Gln	Ala 130	Lys	Lys 135	Ala	Glu	Ser	Glu 140	Ile	Glu	Ser	Lys	
cat	tcg	atg	cac	agg	ccc	gcg	ttg	tgg	gtt	ggt	tgg	tgg	acc	aca	gtt	480
His	Ser	Met	His	Arg	Pro 145	Ala	Leu 150	Trp	Val	Gly 155	Trp	Trp	Thr	Thr	Val 160	
gtc	tct	tcc	gtg	gcg	ctg	ttc	atc	act	ggc	gat	atc	cag	gcg	aag	ctc	528
Val	Ser	Ser	Val	Ala 165	Leu	Phe	Ile	Thr	Gly 170	Asp	Ile	Gln	Ala	Lys 175	Leu	
atg	ttc	gtg	caa	cag	cca	atg	aag	atg	gcg	tcg	gcg	gaa	tcc	ttg	tgt	576
Met	Phe	Val	Gln 180	Gln	Pro	Met	Lys 185	Met	Ala	Ser	Ala	Glu	Ser 190	Leu	Cys	
gaa	acc	gcc	aca	gat	cca	aac	ttc	tcc	att	ctg	aca	att	ggt	acg	cac	624
Glu	Thr	Ala 195	Thr	Asp	Pro	Asn	Phe 200	Ser	Ile	Leu	Thr	Ile 205	Gly	Thr	His	
aac	aac	tgc	gat	acg	gta	acc	cac	ctg	atc	gat	gtt	ccg	ttt	gtg	ctt	672
Asn	Asn	Cys 210	Asp	Thr	Val	Thr 215	His	Leu	Ile	Asp	Val 220	Pro	Phe	Val	Leu	
cca	ttc	ttg	gct	gaa	gga	aaa	ttc	acc	ggt	gtg	act	ttg	cag	ggt	gta	720
Pro	Phe	Leu	Ala	Glu	Gly 225	Lys	Phe 230	Thr	Gly	Val 235	Thr	Leu	Gln	Gly	Val 240	
aac	cag	ctc	caa	gct	gca	gcg	gag	caa	gca	tac	ggt	cct	ggc	aac	tac	768
Asn	Gln	Leu	Gln	Ala	Ala	Ala	Glu	Gln	Ala	Tyr	Gly	Pro	Gly	Asn	Tyr	

005290"0420960



	245	250	255	
tcc cct aac ttg ttt gtc acc tac tgg tca ttc cgc gca atg atc ggc				816
Ser Pro Asn Leu Phe Val Thr Tyr Trp Ser Phe Arg Ala Met Ile Gly				
	260	265	270	
ctg atg ctt ggt tct ttg gct atc gct gcg att gcg tgg ctg ttg ctg				864
Leu Met Leu Gly Ser Leu Ala Ile Ala Ala Ile Ala Trp Leu Leu Leu				
	275	280	285	
cgt aag aag cgc aca cca act gga aag att gct cgt ctg ttc cag atc				912
Arg Lys Lys Arg Thr Pro Thr Gly Lys Ile Ala Arg Leu Phe Gln Ile				
	290	295	300	
ggc agc ctc att gct atc ccg ttc cca ttc ttg gcc aac tct gct ggt				960
Gly Ser Leu Ile Ala Ile Pro Phe Pro Phe Leu Ala Asn Ser Ala Gly				
	305	310	315	320
tgg atc ttc acc gag atg ggc cgc cag cct tgg gtg gtg cac ccg aac				1008
Trp Ile Phe Thr Glu Met Gly Arg Gln Pro Trp Val Val His Pro Asn				
	325	330	335	
cct gaa tct gcc ggc gat gcc cga aca gag atg atc cgg atg act gtt				1056
Pro Glu Ser Ala Gly Asp Ala Arg Thr Glu Met Ile Arg Met Thr Val				
	340	345	350	
gat atg ggt gta tct gat cat gcg cca tgg caa gtc tgg ctg act ctc				1104
Asp Met Gly Val Ser Asp His Ala Pro Trp Gln Val Trp Leu Thr Leu				
	355	360	365	
att ggc ttc acg att ctc tat ctc att ttg ttc gtg gtg tgg gtg tgg				1152
Ile Gly Phe Thr Ile Leu Tyr Leu Ile Leu Phe Val Val Trp Val Trp				
	370	375	380	
ctg att cgc cgc gca gtt ctg atc gga cca cca gag gaa ggc gct cca				1200
Leu Ile Arg Arg Ala Val Leu Ile Gly Pro Pro Glu Glu Gly Ala Pro				
	385	390	395	400
tcc gtg gag gca aag act gga ccg gca acc ccg att ggt tca gat atg				1248
Ser Val Glu Ala Lys Thr Gly Pro Ala Thr Pro Ile Gly Ser Asp Met				
	405	410	415	
ccc atg aca ccg ctg caa ttt act gcc gct gcc cca acc aca ggt gaa				1296
Pro Met Thr Pro Leu Gln Phe Thr Ala Ala Ala Pro Thr Thr Gly Glu				
	420	425	430	
aag gaa taaccatgga tctcaataacc ttt				1325
Lys Glu				

&lt;210&gt; 646

&lt;211&gt; 434

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 646

Trp	Ser	Glu	Tyr	Ser	Arg	Phe	Val	Gly	Asp	Val	Phe	Gly	Gly	Pro	Leu
1				5				10						15	

Ala Leu Glu Gly Leu Ile Ala Phe Phe Leu Glu Ser Val Phe Leu Gly

09602740.062300



		20						25				30				
Leu	Trp	Ile 35	Phe	Gly	Trp	Gly	Lys 40	Ile	Pro	Gly	Trp	Leu 45	His	Thr	Ala	
Ser	Ile 50	Trp	Ile	Val	Ala	Ile 55	Ala	Thr	Asn	Ile	Ser 60	Ala	Tyr	Phe	Ile	
Ile 65	Val	Ala	Asn	Ser	Phe 70	Met	Gln	His	Pro	Val 75	Gly	Ala	Glu	Tyr	Asn 80	
Pro	Glu	Thr	Gly	Arg 85	Ala	Glu	Leu	Thr	Asp 90	Phe	Trp	Ala	Leu	Leu 95	Thr	
Asn	Ser	Thr	Ala 100	Leu	Ala	Ala	Phe	Pro 105	His	Ala	Val	Ala	Gly 110	Gly	Phe	
Leu	Thr	Ala 115	Gly	Thr	Phe	Val	Leu 120	Gly	Ile	Ser	Gly	Trp 125	Trp	Ile	Ile	
Arg	Ala 130	His	Arg	Gln	Ala	Lys 135	Lys	Ala	Glu	Ser	Glu 140	Ile	Glu	Ser	Lys	
His 145	Ser	Met	His	Arg	Pro 150	Ala	Leu	Trp	Val	Gly 155	Trp	Trp	Thr	Thr	Val 160	
Val	Ser	Ser	Val	Ala 165	Leu	Phe	Ile	Thr	Gly 170	Asp	Ile	Gln	Ala	Lys 175	Leu	
Met	Phe	Val	Gln 180	Gln	Pro	Met	Lys	Met 185	Ala	Ser	Ala	Glu	Ser 190	Leu	Cys	
Glu	Thr	Ala 195	Thr	Asp	Pro	Asn	Phe 200	Ser	Ile	Leu	Thr	Ile 205	Gly	Thr	His	
Asn	Asn 210	Cys	Asp	Thr	Val	Thr 215	His	Leu	Ile	Asp	Val 220	Pro	Phe	Val	Leu	
Pro 225	Phe	Leu	Ala	Glu	Gly 230	Lys	Phe	Thr	Gly	Val 235	Thr	Leu	Gln	Gly	Val 240	
Asn	Gln	Leu	Gln 245	Ala	Ala	Ala	Glu	Gln	Ala 250	Tyr	Gly	Pro	Gly	Asn 255	Tyr	
Ser	Pro	Asn	Leu 260	Phe	Val	Thr	Tyr	Trp 265	Ser	Phe	Arg	Ala	Met 270	Ile	Gly	
Leu	Met 275	Leu	Gly	Ser	Leu	Ala	Ile 280	Ala	Ala	Ile	Ala	Trp 285	Leu	Leu	Leu	
Arg	Lys 290	Lys	Arg	Thr	Pro	Thr 295	Gly	Lys	Ile	Ala	Arg 300	Leu	Phe	Gln	Ile	
Gly 305	Ser	Leu	Ile	Ala	Ile 310	Pro	Phe	Pro	Phe	Leu 315	Ala	Asn	Ser	Ala	Gly 320	
Trp	Ile	Phe	Thr	Glu 325	Met	Gly	Arg	Gln	Pro 330	Trp	Val	Val	His	Pro 335	Asn	
Pro	Glu	Ser	Ala 340	Gly	Asp	Ala	Arg	Thr 345	Glu	Met	Ile	Arg	Met 350	Thr	Val	



Asp Met Gly Val Ser Asp His Ala Pro Trp Gln Val Trp Leu Thr Leu  
355 360 365

Ile Gly Phe Thr Ile Leu Tyr Leu Ile Leu Phe Val Val Trp Val Trp  
370 375 380

Leu Ile Arg Arg Ala Val Leu Ile Gly Pro Pro Glu Glu Gly Ala Pro  
385 390 395 400

Ser Val Glu Ala Lys Thr Gly Pro Ala Thr Pro Ile Gly Ser Asp Met  
405 410 415

Pro Met Thr Pro Leu Gln Phe Thr Ala Ala Ala Pro Thr Thr Gly Glu  
420 425 430

Lys Glu

<210> 647

<211> 307

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(307)

<223> RXA00379

<400> 647

cgtgctggat aaacagcacc gccccgcagc agtgttcttg cgcgaagtca cctccaaaga 60

tgtgttggat gttgcgttgc cattggtaga tgaggcctaa atg tct gag att gtg 115  
Met Ser Glu Ile Val  
1 5

gta gcc caa agc atc ggc cag cag ttt gct gac gtc gca gct tcc ggg 163  
Val Ala Gln Ser Ile Gly Gln Gln Phe Ala Asp Val Ala Ala Ser Gly  
10 15 20

cca ctg ttc ctt ggc atc ctt gcc gca gcg ctc gca ggt ctg gtg tct 211  
Pro Leu Phe Leu Gly Ile Leu Ala Ala Leu Ala Gly Leu Val Ser  
25 30 35

ttt gcc agc ccg tgt gtt gtg ccg ttg gtg cca gga tat att tcc tac 259  
Phe Ala Ser Pro Cys Val Val Pro Leu Val Pro Gly Tyr Ile Ser Tyr  
40 45 50

ctc gcc ggc gtg gtc ggt ggg gaa gtg gaa tac agc gct cat gcc acc 307  
Leu Ala Gly Val Val Gly Gly Glu Val Glu Tyr Ser Ala His Ala Thr  
55 60 65

<210> 648

<211> 69

<212> PRT

<213> Corynebacterium glutamicum

<400> 648

Met Ser Glu Ile Val Val Ala Gln Ser Ile Gly Gln Gln Phe Ala Asp

002290 04230960



<400> 649																
ctt	ggc	gga	gtg	ttc	gct	ctc	ggt	tgg	acc	cct	tgt	ttg	ggc	ccc	acc	48
Leu	Gly	Gly	Val	Phe	Ala	Leu	Gly	Trp	Thr	Pro	Cys	Leu	Gly	Pro	Thr	
1				5					10					15		
<400> 96																
ctg	gct	gcg	atc	atc	tcc	att	tct	gca	ggg	act	gaa	ggc	atg	acc	gct	96
Leu	Ala	Ala	Ile	Ile	Ser	Ile	Ser	Ala	Gly	Thr	Glu	Gly	Met	Thr	Ala	
			20					25					30			
<400> 144																
gcg	cgt	ggc	gtg	atc	tta	att	gtg	ggg	tac	tgc	ctc	gga	ctg	ggg	ctg	144
Ala	Arg	Gly	Val	Ile	Leu	Ile	Val	Gly	Tyr	Cys	Leu	Gly	Leu	Gly	Leu	
		35					40					45				
<400> 192																
ccg	ttc	ctg	ctg	atc	gcg	ttg	ggc	tcc	agc	aag	gca	ctc	acc	gga	gtc	192
Pro	Phe	Leu	Leu	Ile	Ala	Leu	Gly	Ser	Ser	Lys	Ala	Leu	Thr	Gly	Val	
	50					55					60					
<400> 240																
gag	tgg	ttg	cgc	aag	cat	tcc	cgc	acc	ctg	caa	att	atc	ggc	ggg	gtg	240
Glu	Trp	Leu	Arg	Lys	His	Ser	Arg	Thr	Leu	Gln	Ile	Ile	Gly	Gly	Val	
65				70						75					80	
<400> 288																
ttt	ttg	atc	ttg	gtc	gga	gta	gcg	ttg	ctc	tct	ggc	tca	tgg	gca	att	288
Phe	Leu	Ile	Leu	Val	Gly	Val	Ala	Leu	Leu	Ser	Gly	Ser	Trp	Ala	Ile	
				85					90					95		
<400> 336																
ttt	atc	aac	tgg	gtc	cgt	cag	tgg	acc	gtt	gaa	tac	ggc	gca	aca	ctg	336
Phe	Ile	Asn	Trp	Val	Arg	Gln	Trp	Thr	Val	Glu	Tyr	Gly	Ala	Thr	Leu	
			100					105					110			
<400> 362																
ctc	tagaaaaaga	cttttagtag				gaa										362
Leu																

$\langle 210 \rangle$	650
$\langle 211 \rangle$	113



<213> Corynebacterium glutamicum

Leu Gly Gly Val Phe Ala Leu Gly Trp Thr Pro Cys Leu Gly Pro Thr  
1 5 10 15

Leu Ala Ala Ile Ile Ser Ile Ser Ala Gly Thr Glu Gly Met Thr Ala  
20 25 30

Ala Arg Gly Val Ile Leu Ile Val Gly Tyr Cys Leu Gly Leu Gly Leu  
35 40 45

Pro Phe Leu Leu Ile Ala Leu Gly Ser Ser Lys Ala Leu Thr Gly Val  
50 55 60

Glu Trp Leu Arg Lys His Ser Arg Thr Leu Gln Ile Ile Gly Gly Val  
65 70 75 80

Phe Leu Ile Leu Val Gly Val Ala Leu Leu Ser Gly Ser Trp Ala Ile  
85 90 95

Phe Ile Asn Trp Val Arg Gln Trp Thr Val Glu Tyr Gly Ala Thr Leu  
100 105 110

Leu

<211> 901

<213> Corynebacterium glutamicum

&lt;221&gt; CDS

<223> RXA01743

aggcaaagac tggaccggca accccgattg gttcagatat gcccatgaca ccgctgcaat 60

ttactgccgc tgccccaacc acaggtgaaa aggaataacc atg gat ctc aat acc 115  
Met Asp Leu Asn Thr  
1 5

ttt tgg ttt att ctc atc gca ttt ttg ttt gcg gga tac ttt ctc ctc 163  
Phe Trp Phe Ile Leu Ile Ala Phe Leu Phe Ala Gly Tyr Phe Leu Leu  
10 15 20

gaa gga ttc gac ttc ggc gtc gga att ttg gca ccc atc atc ggt aaa 211  
Glu Gly Phe Asp Phe Gly Val Gly Ile Leu Ala Pro Ile Ile Gly Lys  
25 30 35

gat tca gcg gct agg aac aca gtg atc cgt acg att ggc cct gtc tgg 259  
Asp Ser Ala Ala Arg Asn Thr Val Ile Arg Thr Ile Gly Pro Val Trp  
40 45 50

gac gga aat gaa gtg tgg ctg atc gtg gca ggt ggc gct ttg ttt gct 307  
Asp Gly Asn Glu Val Trp Leu Ile Val Ala Gly Gly Ala Leu Phe Ala  
55 60 65

[illegible]







```
<220>
<221> CDS
<222> (101)..(1756)
<223> RXN02480
```



acctatgacc gctgtggcgc ctagggtcga cgggcacgtc gccctcaga ggcccgaacc 60

tac gat cca gct aac ggc ggc tcc ctc ctg tgg cag cac ctg ttc tgg 787  
Tyr Asp Pro Ala Asn Gly Gly Ser Leu Leu Trp Gln His Leu Phe Trp

[illegible]



**SECRET**



tac ggt gag ctc gtt acc gtt gat gat cct tgg ggt tac ggc aac tcc 1555  
 Tyr Gly Glu Leu Val Thr Val Asp Asp Pro Trp Gly Tyr Gly Asn Ser  
 470 475 480 485

ctg gag tgg gca acc tcc tgc cct cct cct cgc cac aac ttc gca tcc 1603  
 Leu Glu Trp Ala Thr Ser Cys Pro Pro Pro Arg His Asn Phe Ala Ser  
 490 495 500

ttg cct cgt atc cgc tcc gag cgc cct gcg ttc gag ctg cac tac ccg 1651  
 Leu Pro Arg Ile Arg Ser Glu Arg Pro Ala Phe Glu Leu His Tyr Pro  
 505 510 515

cac atg att gaa cgc atg cgc gca gag gca cac act gga cat cac gat 1699  
 His Met Ile Glu Arg Met Arg Ala Glu Ala His Thr Gly His His Asp  
 520 525 530

gat att aat gct cca gaa ttg ggt acc gcc cca gcc ctt gca tct gac 1747  
 Asp Ile Asn Ala Pro Glu Leu Gly Thr Ala Pro Ala Leu Ala Ser Asp  
 535 540 545

tcc agc cgc taaaagcgtc tgatttaagt cgg 1779  
 Ser Ser Arg  
 550

<210> 654

<211> 552

<212> PRT

<213> Corynebacterium glutamicum

<400> 654

Met Thr Thr Thr Asp His Lys Gln Leu Gly Ile Met Tyr Ile Ile Met  
 1 5 10 15

Ser Phe Ser Phe Phe Phe Leu Gly Gly Leu Met Ala Leu Leu Ile Arg  
 20 25 30

Ala Glu Leu Phe Thr Pro Gly Leu Gln Phe Leu Ser Asn Glu Gln Phe  
 35 40 45

Asn Gln Leu Phe Thr Met His Gly Thr Val Met Leu Leu Leu Tyr Gly  
 50 55 60

Thr Pro Ile Val Trp Gly Phe Ala Asn Tyr Val Leu Pro Leu Gln Ile  
 65 70 75 80

Gly Ala Pro Asp Val Ala Phe Pro Arg Leu Asn Ala Phe Gly Phe Trp  
 85 90 95

Ile Thr Thr Val Gly Gly Val Ala Met Leu Thr Gly Phe Leu Thr Pro  
 100 105 110

Gly Gly Ala Ala Asp Phe Gly Trp Thr Met Tyr Ser Pro Leu Ser Asp  
 115 120 125

Ala Ile His Ser Pro Gly Leu Gly Ser Asp Met Trp Ile Val Gly Val  
 130 135 140

Gly Ala Thr Gly Ile Gly Ser Val Ala Ser Ala Ile Asn Met Leu Thr  
 145 150 155 160

002290" 04220960



Thr Ile Leu Cys Leu Arg Ala Pro Gly Met Thr Met Phe Arg Met Pro  
 165 170 175  
 Ile Phe Thr Trp Asn Ile Phe Val Val Ser Val Leu Ala Leu Ile  
 180 185 190  
 Phe Pro Leu Leu Leu Ala Ala Ala Leu Gly Val Leu Tyr Asp Arg Lys  
 195 200 205  
 Leu Gly Gly His Leu Tyr Asp Pro Ala Asn Gly Gly Ser Leu Leu Trp  
 210 215 220  
 Gln His Leu Phe Trp Phe Phe Gly His Pro Glu Val Tyr Val Leu Ala  
 225 230 235 240  
 Leu Pro Phe Phe Gly Ile Val Ser Glu Ile Ile Pro Val Phe Ser Arg  
 245 250 255  
 Lys Pro Met Phe Gly Tyr Val Gly Leu Ile Phe Ala Thr Leu Ser Ile  
 260 265 270  
 Gly Ala Leu Ser Met Ala Val Trp Ala His His Met Phe Val Thr Gly  
 275 280 285  
 Ala Val Leu Leu Pro Phe Phe Ser Phe Met Thr Phe Leu Ile Ser Val  
 290 295 300  
 Pro Thr Gly Val Lys Phe Phe Asn Trp Val Gly Thr Met Trp Lys Gly  
 305 310 315 320  
 His Ile Thr Trp Glu Thr Pro Met Ile Trp Ser Val Gly Phe Met Ala  
 325 330 335  
 Thr Phe Leu Phe Gly Gly Leu Thr Gly Ile Met Leu Ala Ser Pro Pro  
 340 345 350  
 Leu Asp Phe His Leu Ala Asp Ser Tyr Phe Leu Ile Ala His Phe His  
 355 360 365  
 Tyr Thr Leu Phe Gly Thr Val Val Phe Ala Ser Cys Ala Gly Val Tyr  
 370 375 380  
 Phe Trp Phe Pro Lys Met Thr Gly Arg Met Met Asp Glu Arg Leu Gly  
 385 390 395 400  
 Lys Ile His Phe Trp Leu Thr Phe Val Gly Phe His Gly Thr Phe Leu  
 405 410 415  
 Ile Gln His Trp Val Gly Asn Met Gly Met Pro Arg Arg Tyr Ala Asp  
 420 425 430  
 Tyr Leu Asp Ser Asp Gly Phe Thr Ile Tyr Asn Gln Ile Ser Thr Val  
 435 440 445  
 Phe Tyr Phe Leu Leu Gly Leu Ser Val Ile Pro Phe Ile Trp Asn Val  
 450 455 460  
 Phe Lys Ser Trp Arg Tyr Gly Glu Leu Val Thr Val Asp Asp Pro Trp  
 465 470 475 480

00E290" 04220960



```
<210> 655
<211> 385
<212> DNA
<213> Corynebacterium glutamicum
```

<400> 655																
acctatgacc	gctgtggcgc		ctagggtcga		cgggcacgtc		gcccctcaga		ggccccgagcc		60					
gacaggccat																
gcacgcaagg		gcagcaaagc		atggttaatg		atg		acc	acc	acc	gac	115				
						Met		Thr	Thr	Thr	Asp	5				
						1										
cac	aag	cag	ctg	ggc	att	atg	tac	atc	att	atg	tcc	ttc	agc	ttc	ttt	163
His	Lys	Gln	Leu	Gly	Ile	Met	Tyr	Ile	Ile	Met	Ser	Phe	Ser	Phe	Phe	
				10		15				20						
ttc																
ctc		ggt	ggc	ttg	atg	gcc	ctg	ctt	atc	cga	gcg	gag	ctt	ttc	acc	211
Phe	Leu	Gly	Gly	Leu	Met	Ala	Leu	Leu	Ile	Arg	Ala	Glu	Leu	Phe	Thr	
				25		30				35						
cct																
ggt		ctg	cag	ttc	ctg	tct	aat	gag	cag	ttc	aac	cag	ctg	ttc	acc	259
Pro	Gly	Leu	Gln	Phe	Leu	Ser	Asn	Glu	Gln	Phe	Asn	Gln	Leu	Phe	Thr	
				40		45				50						
atg																
cac		gga	act	gtc	atg	ctg	ctg	ctg	tac	gga	act	cca	att	gtt	tgg	307
Met	His	Gly	Thr	Val	Met	Leu	Leu	Leu	Tyr	Gly	Thr	Pro	Ile	Val	Trp	
		55		60				65								
ggt																
ttt		gct	aac	tac	gtc	ctg	cca	ctt	cca	acc	acc	ang	caa	gcc	ttc	355
Gly	Phe	Ala	Asn	Tyr	Val	Leu	Pro	Leu	Pro	Thr	Thr	Xaa	Gln	Ala	Phe	
		70		75				80				85				
tct																
aaa		acc	cgg	gtg	aac	tct	ccc	agg	gag							385
Ser	Lys	Thr	Arg	Val	Asn	Ser	Pro	Arg	Glu							
				90		95										

<210>	656
<211>	95
<212>	PRT

[illegible]



&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 656

Met Thr Thr Thr Asp His Lys Gln Leu Gly Ile Met Tyr Ile Ile Met  
1 5 10 15

Ser Phe Ser Phe Phe Phe Leu Gly Gly Leu Met Ala Leu Leu Ile Arg  
20 25 30

Ala Glu Leu Phe Thr Pro Gly Leu Gln Phe Leu Ser Asn Glu Gln Phe  
35 40 45

Asn Gln Leu Phe Thr Met His Gly Thr Val Met Leu Leu Leu Tyr Gly  
50 55 60

Thr Pro Ile Val Trp Gly Phe Ala Asn Tyr Val Leu Pro Leu Pro Thr  
65 70 75 80

Thr Xaa Gln Ala Phe Ser Lys Thr Arg Val Asn Ser Pro Arg Glu  
85 90 95

&lt;210&gt; 657

&lt;211&gt; 972

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(949)

&lt;223&gt; FRXA02480

&lt;400&gt; 657

tacgttctgg cgctgccgtt cttcggcatt gtttctgaga tcattcctgt gttctcccgt 60

aagccaatgt tcgggttacg tcggcctgat cttcgcaacc ttg tcc att ggt gca 115  
Leu Ser Ile Gly Ala  
1 5

ctg tcc atg gct gtg tgg gct cac cac atg ttc gtt act ggc gca gtt 163  
Leu Ser Met Ala Val Trp Ala His His Met Phe Val Thr Gly Ala Val  
10 15 20

ttg ctt ccg ttc ttc tcc ttc atg acg ttc ctg att tcg gtt cct acc 211  
Leu Leu Pro Phe Phe Ser Phe Met Thr Phe Leu Ile Ser Val Pro Thr  
25 30 35

ggc gtt aag ttc ttc aac tgg gtt gga acc atg tgg aag ggt cac atc 259  
Gly Val Lys Phe Phe Asn Trp Val Gly Thr Met Trp Lys Gly His Ile  
40 45 50

act tgg gaa acc cca atg atc tgg tct gtt ggc ttc atg gct acc ttc 307  
Thr Trp Glu Thr Pro Met Ile Trp Ser Val Gly Phe Met Ala Thr Phe  
55 60 65

ctc ttc ggt ggt ctg acc ggc att atg ctg gcg tcc cca cca ctg gac 355  
Leu Phe Gly Gly Leu Thr Gly Ile Met Leu Ala Ser Pro Pro Leu Asp  
70 75 80 85

ttc cac ttg gct gac tcc tac ttc ctg atc gcg cac ttc cac tac acc 403  
Phe His Leu Ala Asp Ser Tyr Phe Leu Ile Ala His Phe His Tyr Thr

09602740-062300



				90				95				100							
ctc	ttc	ggt	acc	gtg	gtg	ttc	gca	tcg	tgt	gca	ggc	ggt	tac	ttc	tgg	451			
Leu	Phe	Gly	Thr	Val	Val	Phe	Ala	Ser	Cys	Ala	Gly	Val	Tyr	Phe	Trp				
105								110				115							
ttc	ccg	aag	atg	act	ggc	cgc	atg	atg	gac	gag	cgt	ctt	ggc	aag	atc	499			
Phe	Pro	Lys	Met	Thr	Gly	Arg	Met	Met	Asp	Glu	Arg	Leu	Gly	Lys	Ile				
120								125				130							
cac	ttc	tgg	ttg	acc	ttc	gtc	ggt	ttc	cac	gga	acc	ttc	ctc	atc	cag	547			
His	Phe	Trp	Leu	Thr	Phe	Val	Gly	Phe	His	Gly	Thr	Phe	Leu	Ile	Gln				
135								140				145							
cac	tgg	gtg	ggc	aac	atg	ggt	atg	cca	cgt	cgt	tac	gct	gac	tac	ctg	595			
His	Trp	Val	Gly	Asn	Met	Gly	Met	Pro	Arg	Arg	Tyr	Ala	Asp	Tyr	Leu				
150								155				160				165			
gat	tct	gat	ggt	ttc	acc	atc	tac	aac	cag	atc	tcc	acc	gtg	ttc	tac	643			
Asp	Ser	Asp	Gly	Phe	Thr	Ile	Tyr	Asn	Gln	Ile	Ser	Thr	Val	Phe	Tyr				
				170								175				180			
ttc	ctg	ctt	ggc	ctg	tct	gtc	att	cca	ttc	atc	tgg	aac	gtc	ttc	aag	691			
Phe	Leu	Leu	Gly	Leu	Ser	Val	Ile	Pro	Phe	Ile	Trp	Asn	Val	Phe	Lys				
185								190				195							
tcc	tgg	cgc	tac	ggt	gag	ctc	gtt	acc	gtt	gat	gat	cct	tgg	ggt	tac	739			
Ser	Trp	Arg	Tyr	Gly	Glu	Leu	Val	Thr	Val	Asp	Asp	Pro	Trp	Gly	Tyr				
200								205				210							
ggc	aac	tcc	ctg	gag	tgg	gca	acc	tcc	tgc	cct	cct	cct	cgc	cac	aac	787			
Gly	Asn	Ser	Leu	Glu	Trp	Ala	Thr	Ser	Cys	Pro	Pro	Pro	Arg	His	Asn				
215								220				225							
ttc	gca	tcc	ttg	cct	cgt	atc	cgc	tcc	gag	cgc	cct	gcg	ttc	gag	ctg	835			
Phe	Ala	Ser	Leu	Pro	Arg	Ile	Arg	Ser	Glu	Arg	Pro	Ala	Phe	Glu	Leu				
230								235				240				245			
cac	tac	ccg	cac	atg	att	gaa	cgc	atg	cgc	gca	gag	gca	cac	act	gga	883			
His	Tyr	Pro	His	Met	Ile	Glu	Arg	Met	Arg	Ala	Glu	Ala	His	Thr	Gly				
				250								255				260			
cat	cac	gat	gat	att	aat	gct	cca	gaa	ttg	ggt	acc	gcc	cca	gcc	ctt	931			
His	His	Asp	Asp	Ile	Asn	Ala	Pro	Glu	Leu	Gly	Thr	Ala	Pro	Ala	Leu				
				265								270				275			
gca	tct	gac	tcc	agc	cgc	taaaaagcgtc tgattttaagt cgg										972			
Ala	Ser	Asp	Ser	Ser	Arg														
280																			

```
<210> 658
<211> 283
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 658  
 Leu Ser Ile Gly Ala Leu Ser Met Ala Val Trp Ala His His Met Phe  
           1                          5                          10                          15  
 Val Thr Gly Ala Val Leu Leu Pro Phe Phe Ser Phe Met Thr Phe Leu

[illegible]



0960240-05300

0960240-05300

0960240-05300



<400> 659

tgcctaactac gtcctgccac ttcagatcgg tgcgcctgac gtagcttttcc cacgttgaaa																60
tgcttttcggc ttctgaatca ccaccgtcgg tgggtgtcgcg atg ctg acc ggc ttc																115
Met Leu Thr Gly Phe																5
cta acc ccg ggt ggt gct gcc gac ttg ggt gga cca tgt act ccc cac																163
Leu Thr Pro Gly Gly Ala Ala Asp Leu Gly Gly Pro Cys Thr Pro His																20
tgt ctg acg caa ttc act ccc cag gcc ttg gtt cta aca tgt gga ttg																211
Cys Leu Thr Gln Phe Thr Pro Gln Ala Leu Val Leu Thr Cys Gly Leu																35
tcg ggt gtc ggt gca act ggt att ggc tcc gtt gct tcc gca att aac																259
Ser Gly Val Gly Ala Thr Gly Ile Gly Ser Val Ala Ser Ala Ile Asn																40
atg ctc acc acc atc ctc tgc ctc cgc gca cct ggt atg acc atg ttc																307
Met Leu Thr Thr Ile Leu Cys Leu Arg Ala Pro Gly Met Thr Met Phe																55
cgt atg cct att ttc acc tgg aat atc ttc gtt gtt tcc gtt ctt gct																355
Arg Met Pro Ile Phe Thr Trp Asn Ile Phe Val Val Ser Val Leu Ala																70
ctg ctg atc ttc cca ctg ctg ctc gct gct gca ctg ggt gtt ctg tat																403
Leu Leu Ile Phe Pro Leu Leu Leu Ala Ala Ala Leu Gly Val Leu Tyr																90
gac cgc aag ctt ggt gga cac ctg tac gat cca gct aac ggc ggc tcc																451
Asp Arg Lys Leu Gly Gly His Leu Tyr Asp Pro Ala Asn Gly Gly Ser																105
ctc ctg tgg cag cac ctg ttc tgg ttc ttc gga cac cct gag gtt tac																499
Leu Leu Trp Gln His Leu Phe Trp Phe Phe Gly His Pro Glu Val Tyr																120
gtt ctg gcg ctg ccg ttc ttc ggc att gtt tct gag atc att cct gtg																547
Val Leu Ala Leu Pro Phe Phe Gly Ile Val Ser Glu Ile Ile Pro Val																135
ttc tcc cgt aag cca atg ttc ggg tta cgt cgg cct gat ctt cgc aac																595
Phe Ser Arg Lys Pro Met Phe Gly Leu Arg Arg Pro Asp Leu Arg Asn																150
ctt gtc cat tgg tgc act gtc cat ggc tgt gtg ggc tca cca cat gtt																643
Leu Val His Trp Cys Thr Val His Gly Cys Val Gly Ser Pro His Val																170
cgt tac tgg cgc agt ttt gct tcc gtt ctt ctc ctt cat gac gtt cct																691
Arg Tyr Trp Arg Ser Phe Ala Ser Val Leu Leu Leu His Asp Val Pro																185
gat ttc ggt tcc tac cgg cgt taagtctctc aactggggttg gaa																735
Asp Phe Gly Ser Tyr Arg Arg																200

<210> 660

036024b



&lt;211&gt; 204

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 660

```

Met Leu Thr Gly Phe Leu Thr Pro Gly Gly Ala Ala Asp Leu Gly Gly
 1             5             10             15

Pro Cys Thr Pro His Cys Leu Thr Gln Phe Thr Pro Gln Ala Leu Val
          20             25             30

Leu Thr Cys Gly Leu Ser Gly Val Gly Ala Thr Gly Ile Gly Ser Val
          35             40             45

Ala Ser Ala Ile Asn Met Leu Thr Thr Ile Leu Cys Leu Arg Ala Pro
 50             55             60

Gly Met Thr Met Phe Arg Met Pro Ile Phe Thr Trp Asn Ile Phe Val
 65             70             75             80

Val Ser Val Leu Ala Leu Leu Ile Phe Pro Leu Leu Leu Ala Ala Ala
          85             90             95

Leu Gly Val Leu Tyr Asp Arg Lys Leu Gly Gly His Leu Tyr Asp Pro
          100             105             110

Ala Asn Gly Gly Ser Leu Leu Trp Gln His Leu Phe Trp Phe Phe Gly
 115             120             125

His Pro Glu Val Tyr Val Leu Ala Leu Pro Phe Phe Gly Ile Val Ser
 130             135             140

Glu Ile Ile Pro Val Phe Ser Arg Lys Pro Met Phe Gly Leu Arg Arg
 145             150             155             160

Pro Asp Leu Arg Asn Leu Val His Trp Cys Thr Val His Gly Cys Val
          165             170             175

Gly Ser Pro His Val Arg Tyr Trp Arg Ser Phe Ala Ser Val Leu Leu
          180             185             190

Leu His Asp Val Pro Asp Phe Gly Ser Tyr Arg Arg
 195             200

```

&lt;210&gt; 661

&lt;211&gt; 1200

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1177)

&lt;223&gt; RXA02140

&lt;400&gt; 661

aacacaagat atggaatcgg ctggcaaata ggctattctg cgaagataga aatgaccgta 60

```

aggtctctgg tttttgtgtg gacaggaagg cagaacacac gtg gaa cag caa aat 115
                               Val Glu Gln Gln Asn
                               1             5

```

002230.062740.062300







```
<210> 662
<211> 359
<212> PRT
<213> Corynebacterium glutamicum
```

Val	Glu	Gln	Gln	Asn	Lys	Arg	Gly	Leu	Lys	Arg	Lys	Ala	Leu	Leu	Gly
1				5					10					15	

Gly Val Leu Gly Leu Gly Gly Leu Ala Met Ala Gly Cys Glu Val Ala  
20 25 30

Pro Pro Gly Gly Val Leu Gly Asp Phe Leu Arg Met Gly Trp Pro Asp  
35 40 45

Gly Ile Thr Pro Glu Ala Val Ala Met Gly Asn Phe Trp Ser Trp Val  
50 55 60

Trp Val Ala Ala Trp Ile Ile Gly Ile Ile Met Trp Gly Leu Phe Leu  
65 70 75 80

Thr Ala Ile Phe Ala Trp Gly Ala Lys Arg Ala Glu Lys Arg Gly Glu  
85 90 95

Gly Glu Phe Pro Lys Gln Leu Gln Tyr Asn Val Pro Leu Glu Leu Val  
100 105 110

Leu Thr Ile Val Pro Ile Ile Ile Val Met Val Leu Phe Phe Phe Thr

**SECRET**



	115					120					125				
Val	Gln 130	Thr	Gln	Asp	Lys	Val 135	Thr	Ala	Leu	Asp	Lys 140	Asn	Pro	Glu	Val
Thr 145	Val	Asp	Val	Thr	Ala 150	Tyr	Gln	Trp	Asn	Trp 155	Lys	Phe	Gly	Tyr	Ser 160
Glu	Ile	Asp	Gly	Ser 165	Leu	Ala	Pro	Gly	Gly 170	Gln	Asp	Tyr	Gln	Gly 175	Ser
Asp	Pro	Glu	Arg 180	Gln	Ala	Ala	Ala	Glu 185	Ala	Ser	Lys	Lys	Asp 190	Pro	Ser
Gly	Asp	Asn 195	Pro	Ile	His	Gly	Asn 200	Ser	Lys	Ser	Asp	Val 205	Ser	Tyr	Leu
Glu	Phe 210	Asn	Arg	Ile	Glu	Thr 215	Leu	Gly	Thr	Thr	Asp 220	Glu	Ile	Pro	Val
Met 225	Val	Leu	Pro	Val	Asn 230	Thr	Pro	Ile	Glu	Phe 235	Asn	Leu	Ala	Ser	Ala 240
Asp	Val	Ala	His	Ser 245	Phe	Trp	Val	Pro	Glu 250	Phe	Leu	Phe	Lys	Arg 255	Asp
Ala	Tyr	Ala	His 260	Pro	Glu	Ala	Asn	Lys 265	Ser	Gln	Arg	Val	Phe 270	Gln	Ile
Glu	Glu 275	Ile	Thr	Glu	Glu	Gly	Ala 280	Phe	Val	Gly	Arg	Cys 285	Ala	Glu	Met
Cys 290	Gly	Thr	Tyr	His	Ala	Met 295	Met	Asn	Phe	Glu	Leu 300	Arg	Val	Val	Asp
Arg 305	Asp	Ser	Phe	Ala	Glu 310	Tyr	Ile	Ser	Phe	Arg 315	Asp	Ser	Asn	Pro	Asp 320
Ala	Thr	Asn	Ala	Gln 325	Ala	Leu	Glu	His	Ile 330	Gly	Gln	Ala	Pro	Tyr 335	Ala
Thr	Ser	Thr	Ser 340	Pro	Phe	Val	Ser	Asp 345	Arg	Thr	Ala	Thr	Arg 350	Asp	Gly
Glu	Asn 355	Thr	Gln	Ser	Asn	Ala									

<210> 663

<211> 774

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) .. (751)

<223> RXA02142

<400> 663

acgaaaagtt cccggaaggt cgattgaaaa gtttgcgaat tgggggaaaa ttcgcatcaa 60



aagccgagtt caaactttca attgaaacgg ggggcttgaa gtg act ttg gcc aac 115  
Val Thr Leu Ala Asn  
1 5

caa aca gcc ata cta gat agc gtg acg agc gca gtt gga aat aca ggt 163  
Gln Thr Ala Ile Leu Asp Ser Val Thr Ser Ala Val Gly Asn Thr Gly  
10 15 20

atg gca gca cca caa cgt gtt gcg gca ctg aac cgt ccg aat atg gtc 211  
Met Ala Ala Pro Gln Arg Val Ala Ala Leu Asn Arg Pro Asn Met Val  
25 30 35

agt gtc ggc acc att gtg ttc ctg tct cag gaa tta atg ttc ttc gcc 259  
Ser Val Gly Thr Ile Val Phe Leu Ser Gln Glu Leu Met Phe Phe Ala  
40 45 50

ggg cta ttc gcg atg tac ttc gtg tcc cgt gcg aac gga ctg gca aat 307  
Gly Leu Phe Ala Met Tyr Phe Val Ser Arg Ala Asn Gly Leu Ala Asn  
55 60 65

gga tca tgg gga gag cag aca gat cac ctc aac gtg ccc tac gca ctg 355  
Gly Ser Trp Gly Glu Gln Thr Asp His Leu Asn Val Pro Tyr Ala Leu  
70 75 80 85

ttg att acg gtc att ctg gtg tct tcc tca gtg act tgc cag ttc gga 403  
Leu Ile Thr Val Ile Leu Val Ser Ser Ser Val Thr Cys Gln Phe Gly  
90 95 100

gtt ttt gcg gct gaa agg ggt gac gtt tac ggc ctc cgc aag tgg ttc 451  
Val Phe Ala Ala Glu Arg Gly Asp Val Tyr Gly Leu Arg Lys Trp Phe  
105 110 115

ttg gtc acg att atc ctc gga tca atc ttc gtg atc gga cag ggc tac 499  
Leu Val Thr Ile Ile Leu Gly Ser Ile Phe Val Ile Gly Gln Gly Tyr  
120 125 130

gag tac atc act ctc gta ggt cac gga ctt aca atc cag agc agt gtc 547  
Glu Tyr Ile Thr Leu Val Gly His Gly Leu Thr Ile Gln Ser Ser Val  
135 140 145

tac gga tcg gca ttc ttt att aca acc ggt ttc cac gca ctg cac gtg 595  
Tyr Gly Ser Ala Phe Phe Ile Thr Thr Gly Phe His Ala Leu His Val  
150 155 160 165

atc gcg ggt gtt atg gcc ttc gtt gtg gtt ctt atg aga atc cat aag 643  
Ile Ala Gly Val Met Ala Phe Val Val Val Leu Met Arg Ile His Lys  
170 175 180

tcg aag ttc act ccg gca cag gca acc gca gca atg gtt gtg tct tat 691  
Ser Lys Phe Thr Pro Ala Gln Ala Thr Ala Ala Met Val Val Ser Tyr  
185 190 195

tac tgg cac ttc gtt gac gtg gtc tgg atc ggc ctc ttc atc act att 739  
Tyr Trp His Phe Val Asp Val Val Trp Ile Gly Leu Phe Ile Thr Ile  
200 205 210

tac ttc att cag taggcagtaa ggaatcctca acg 774  
Tyr Phe Ile Gln  
215

09602740-062300



```
<210> 664
<211> 217
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 664															
Val	Thr	Leu	Ala	Asn	Gln	Thr	Ala	Ile	Leu	Asp	Ser	Val	Thr	Ser	Ala
1				5					10					15	
Val	Gly	Asn	Thr	Gly	Met	Ala	Ala	Pro	Gln	Arg	Val	Ala	Ala	Leu	Asn
			20					25					30		
Arg	Pro	Asn	Met	Val	Ser	Val	Gly	Thr	Ile	Val	Phe	Leu	Ser	Gln	Glu
		35					40					45			
Leu	Met	Phe	Phe	Ala	Gly	Leu	Phe	Ala	Met	Tyr	Phe	Val	Ser	Arg	Ala
	50					55					60				
Asn	Gly	Leu	Ala	Asn	Gly	Ser	Trp	Gly	Glu	Gln	Thr	Asp	His	Leu	Asn
65					70					75					80
Val	Pro	Tyr	Ala	Leu	Leu	Ile	Thr	Val	Ile	Leu	Val	Ser	Ser	Ser	Val
				85					90					95	
Thr	Cys	Gln	Phe	Gly	Val	Phe	Ala	Ala	Glu	Arg	Gly	Asp	Val	Tyr	Gly
			100					105					110		
Leu	Arg	Lys	Trp	Phe	Leu	Val	Thr	Ile	Ile	Leu	Gly	Ser	Ile	Phe	Val
		115					120					125			
Ile	Gly	Gln	Gly	Tyr	Glu	Tyr	Ile	Thr	Leu	Val	Gly	His	Gly	Leu	Thr
	130					135					140				
Ile	Gln	Ser	Ser	Val	Tyr	Gly	Ser	Ala	Phe	Phe	Ile	Thr	Thr	Gly	Phe
145					150					155					160
His	Ala	Leu	His	Val	Ile	Ala	Gly	Val	Met	Ala	Phe	Val	Val	Val	Leu
				165					170					175	
Met	Arg	Ile	His	Lys	Ser	Lys	Phe	Thr	Pro	Ala	Gln	Ala	Thr	Ala	Ala
			180					185					190		
Met	Val	Val	Ser	Tyr	Tyr	Trp	His	Phe	Val	Asp	Val	Val	Trp	Ile	Gly
		195					200					205			
Leu	Phe	Ile	Thr	Ile	Tyr	Phe	Ile	Gln							
	210					215									

```
<210> 665
<211> 1347
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(1324)  
<223> RXA02144
```

<400> 665  
actcactcgg tagcttgggc ccagtggctg agggctctgtt catgtgggta ttccggcatct 60

**SECRET**



tggtcctcgt	ggccgcgcgct	atgtggattg	gatcacgttc	atg	agt	aac	aac	aac	115							
				Met	Ser	Asn	Asn	Asn								
				1				5								
gac	aaa	cag	tac	aca	acc	caa	gaa	ctc	aac	gcg	atg	agc	aat	gag	gat	163
Asp	Lys	Gln	Tyr	Thr	Thr	Gln	Glu	Leu	Asn	Ala	Met	Ser	Asn	Glu	Asp	
				10					15					20		
ctt	gca	cga	ctt	ggg	aca	gag	ctg	gac	gac	gtt	acc	att	gca	tac	cgc	211
Leu	Ala	Arg	Leu	Gly	Thr	Glu	Leu	Asp	Asp	Val	Thr	Ile	Ala	Tyr	Arg	
			25					30					35			
aag	gaa	cgt	ttc	cca	atc	gct	aat	gac	cca	gct	gag	aag	cgc	gct	gca	259
Lys	Glu	Arg	Phe	Pro	Ile	Ala	Asn	Asp	Pro	Ala	Glu	Lys	Arg	Ala	Ala	
		40					45					50				
cgt	gca	gtt	act	ttc	tgg	cta	gtc	ctc	ggc	atc	att	ggg	gga	ctt	ggg	307
Arg	Ala	Val	Thr	Phe	Trp	Leu	Val	Leu	Gly	Ile	Ile	Gly	Gly	Leu	Gly	
	55					60					65					
ttc	ctg	gct	acc	tac	att	ttc	tgg	cct	tgg	gag	tac	aag	gca	cac	gga	355
Phe	Leu	Ala	Thr	Tyr	Ile	Phe	Trp	Pro	Trp	Glu	Tyr	Lys	Ala	His	Gly	
	70				75					80					85	
gat	gaa	ggg	ctc	ctg	gcg	tac	acc	ttg	tac	acc	cca	atg	ctg	ggg	att	403
Asp	Glu	Gly	Leu	Leu	Ala	Tyr	Thr	Leu	Tyr	Thr	Pro	Met	Leu	Gly	Ile	
				90					95					100		
act	tcc	ggg	ctt	tgc	atc	ctg	tcc	ctg	gga	ttt	gca	gtt	gtc	ctt	tat	451
Thr	Ser	Gly	Leu	Cys	Ile	Leu	Ser	Leu	Gly	Phe	Ala	Val	Val	Leu	Tyr	
			105					110					115			
gtc	aag	aag	ttc	att	cca	gag	gaa	atc	gca	gta	cag	cgt	cgc	cac	gac	499
Val	Lys	Lys	Phe	Ile	Pro	Glu	Glu	Ile	Ala	Val	Gln	Arg	Arg	His	Asp	
		120					125					130				
ggg	cct	tct	gaa	gaa	gtt	gac	cgc	cgc	acc	atc	gtt	gca	ctt	ctc	aat	547
Gly	Pro	Ser	Glu	Glu	Val	Asp	Arg	Arg	Thr	Ile	Val	Ala	Leu	Leu	Asn	
	135					140					145					
gac	tct	tgg	cag	acc	tct	act	ctt	ggg	cgt	cgc	aag	ctg	atc	atg	gga	595
Asp	Ser	Trp	Gln	Thr	Ser	Thr	Leu	Gly	Arg	Arg	Lys	Leu	Ile	Met	Gly	
					155				160						165	
ctt	gca	ggg	ggc	gga	gca	gta	ctg	gcc	ggc	ctg	acc	atc	atc	gct	cca	643
Leu	Ala	Gly	Gly	Gly	Ala	Val	Leu	Ala	Gly	Leu	Thr	Ile	Ile	Ala	Pro	
				170					175					180		
atg	ggc	ggg	atg	atc	aag	aac	cct	tgg	aat	cct	aag	gaa	ggc	cca	atg	691
Met	Gly	Gly	Met	Ile	Lys	Asn	Pro	Trp	Asn	Pro	Lys	Glu	Gly	Pro	Met	
			185				190						195			
gac	gtt	cag	ggg	gac	ggc	acc	ctg	tgg	act	tcc	ggg	tgg	act	ctc	gtt	739
Asp	Val	Gln	Gly	Asp	Gly	Thr	Leu	Trp	Thr	Ser	Gly					



[illegible]

```
<210> 666
<211> 408
<212> PRT
<213> Corynebacterium glutamicum
```

```

<400> 666
Met Ser Asn Asn Asn Asp Lys Gln Tyr Thr Thr Gln Glu Leu Asn Ala
  1                               5                               10                               15
Met Ser Asn Glu Asp Leu Ala Arg Leu Gly Thr Glu Leu Asp Asp Val
                20                25                30

```







<400> 667																																	
aacgcaaggt		gcacactcac		cgcaggggata		tttaaataat		aaggactcac		aacttaaata		60																					
tatgagtgat		ttgaaaatgc		aacgttctg		aggagaaccc		ttg		gac		acg		atc		aag		115															
										Leu		Asp		Thr		Ile		Lys															
										1								5															
gcc		tat		att		gcg		cta		acg		aag		ccc		agg		gtt		att		gaa		ctc		ctc		ctt		gtc		163	
Ala		Tyr		Ile		Ala		Leu		Thr		Lys		Pro		Arg		Val		Ile		Glu		Leu		Leu		Leu		Val			
								10										15										20					
gcc		aca		atc		ccc		aca		atg		ctt		cag		gct		gaa		cgc		ggg		gag		aac		aac		att		211	
Ala		Thr		Ile		Pro		Thr		Met		Leu		Gln		Ala		Glu		Arg		Gly		Glu		Asn		Asn		Ile			
						25										30												35					
gtg		ctc		atc		ttg		ctg		act		gtg		ttc		ggg		ggc		tgg		atg		ggg		gcg		gcc		gcc		259	
Val		Leu		Ile		Leu		Leu		Thr		Val		Phe		Gly		Gly		Trp		Met		Gly		Ala		Ala		Ala			
						40								45										50									
gcc		aac		acc		ttc		aac		atg		gtg		gca		gac		tcc		gat		att		gat		cag		cgc		atg		307	
Ala		Asn		Thr		Phe		Asn		Met		Val		Ala		Asp		Ser		Asp		Ile		Asp		Gln		Arg		Met			
		55										60										65											
gga		cgc		act		agg		gct		cgc		cct		ttg		gtg		cgc		cac		acc		gtg		agt		aat		cgc		355	
Gly		Arg		Thr		Arg		Ala		Arg		Pro		Leu		Val		Arg		His		Thr		Val		Ser		Asn		Arg			
		70						75										80												85			
gac		gcc		tcc		att		ttt		gcg		tgg		gtc		ctg		aca		gtg		gcc		agc		ttc		ttg		tgg		403	
Asp		Ala		Ser		Ile		Phe		Ala		Trp		Val		Leu		Thr		Val		Ala		Ser		Phe		Leu		Trp			
								90										95										100					
ctg		tgg		ctg		ctg		tgc		gat		tcg		atg		ctc		gcc		ggc		atc		ttc		gtg		ttg		atc		451	
Leu		Trp		Leu		Leu		Cys		Asp		Ser		Met		Leu		Ala		Gly		Ile		Phe		Val		Leu		Ile			
						105										110										115							
acg		att		ttc		ttc		tac		att		ttt		gtc		tac		acc		aag		tgg		ctg		aag		cgc		cgc		499	
Thr		Ile		Phe		Phe		Tyr		Ile		Phe		Val		Tyr		Thr		Lys		Trp		Leu		Lys		Arg		Arg			
				120										125																			

**SECRET**







[illegible]

<210> 669

<211> 1161

<212> DNA

<213> Corynebacterium glutamicum

<220>



<223> RXA02743

atatccttaa aagttcccqg gagtttcagt gqcaaatacc accacttcca taccgqqaac 60

gct ccc tca aat aat cca gtt gag ttg aag ccc att act ttc tgg gca 163  
Ala Pro Ser Asn Asn Pro Val Glu Leu Lys Pro Ile Thr Phe Trp Ala  
10 15 20

cag gga ggc atc acc gtt acg ggc tct atc gtc cgt gtc aca ggc tcc 259  
Gln Gly Gly Ile Thr Val Thr Gly Ser Ile Val Arg Val Thr Gly Ser  
40 45 50

cca gtc gca ggc gca gca cca tgg atc cac cag gca gtg gaa ttt ggt 355  
Pro Val Ala Gly Ala Ala Pro Trp Ile His Gln Ala Val Glu Phe Gly  
70 75 80 85

att gca gtt ctt ggc gca aaa cgc cgc cgc gag atc ctg gtc cat tcc 451  
Ile Ala Val Leu Gly Ala Lys Arg Arg Arg Glu Ile Leu Val His Ser  
105 110 115

acc gtg ctg gtt gat ttg cac tgg tac gcc gtt gct ttg cac ttc ctg 547  
Thr Val Leu Val Asp Leu His Trp Tyr Ala Val Ala Leu His Phe Leu  
135 140 145

ggc gag ccc gat gac ggc gag att acc acc aca ttc ccc acg tgg atc 643  
Gly Glu Pro Asp Asp Gly Glu Ile Thr Thr Thr Phe Pro Thr Trp Ile  
170 175 180

acc ggc acc atg acc acc ggc gct ggc gtt cac tct ggc gat gca tca 739  
Thr Gly Thr Met Thr Thr Gly Ala Gly Val His Ser Gly Asp Ala Ser

**SECRET**



```

<400> 670
Val Ser Thr Ser Asp Ala Pro Ser Asn Asn Pro Val Glu Leu Lys Pro
  1          5          10          15

Ile Thr Phe Trp Ala Pro Thr Ile Lys Val Gln Arg Ile Leu Ala Leu
      20          25          30

Leu Leu Leu Ile Phe Gln Gly Gly Ile Thr Val Thr Gly Ser Ile Val
    35          40          45

Arg Val Thr Gly Ser Gly Leu Gly Cys Asp Thr Trp Pro Leu Cys His
  50          55          60

Glu Gly Ser Leu Val Pro Val Ala Gly Ala Ala Pro Trp Ile His Gln
  65          70          75          80

Ala Val Glu Phe Gly Asn Arg Met Leu Thr Phe Val Leu Ala Ala Ala

```

# THE BIBLE



```
<220>  
<221> CDS  
<222> (101)..(421)  
<223> RXA01227
```



<400> 671

ggataatcga aaatatgtgc cccttggtga agggtcgggg agctaataagg atgacagtga																60
acctatttttc cacgtcttta tccgtagtat tggagatccg      atg acc tac aca atc																115
																Met Thr Tyr Thr Ile.
																1                      5
gcc cag gcc tgc gtt gat gtc ctg gat cga gcc tgc gtc gag gaa tgt	163															
Ala Gln Pro Cys Val Asp Val Leu Asp Arg Ala Cys Val Glu Glu Cys																
								10        15        20								
ccc gtg gac tgc atc tac gag ggc aaa cgg atg ctc tac atc cac ccc	211															
Pro Val Asp Cys Ile Tyr Glu Gly Lys Arg Met Leu Tyr Ile His Pro																
								25        30        35								
gat gag tgc gtc gac tgc ggt gcc tgc gag ccc gtc tgc ccg gtt gaa	259															
Asp Glu Cys Val Asp Cys Gly Ala Cys Glu Pro Val Cys Pro Val Glu																
								40        45        50								
gcc atc ttc tac gaa gat gat gtt ccc cac gaa tgg tgg gac tac acc	307															
Ala Ile Phe Tyr Glu Asp Asp Val Pro His Glu Trp Trp Asp Tyr Thr																
								55        60        65								
ggc gct aac gcc gcc ttt ttc gac gac ctc ggt tcg cca ggc ggt gcc	355															
Gly Ala Asn Ala Ala Phe Phe Asp Asp Leu Gly Ser Pro Gly Gly Ala																
70                      75                80                85																
gcc agc ctg ggt ccg cag gac ttc gac gcc cag ctc gtc gcg gtg ctg	403															
Ala Ser Leu Gly Pro Gln Asp Phe Asp Ala Gln Leu Val Ala Val Leu																
								90        95        100								
ccg cca cag aac cag aac taggacctga tatcgGCCCT aaa	444															
Pro Pro Gln Asn Gln Asn																
								105								

<210> 672

<211> 107

<212> PRT

<213> Corynebacterium glutamicum

<400> 672

Met	Thr	Tyr	Thr	Ile	Ala	Gln	Pro	Cys	Val	Asp	Val	Leu	Asp	Arg	Ala
1				5					10					15	
Cys	Val	Glu	Glu	Cys	Pro	Val	Asp	Cys	Ile	Tyr	Glu	Gly	Lys	Arg	Met
			20					25					30		
Leu	Tyr	Ile	His	Pro	Asp	Glu	Cys	Val	Asp	Cys	Gly	Ala	Cys	Glu	Pro
		35					40					45			
Val	Cys	Pro	Val	Glu	Ala	Ile	Phe	Tyr	Glu	Asp	Asp	Val	Pro	His	Glu
	50					55					60				
Trp	Trp	Asp	Tyr	Thr	Gly	Ala	Asn	Ala	Ala	Phe	Phe	Asp	Asp	Leu	Gly
65					70					75					80
Ser	Pro	Gly	Gly	Ala	Ala	Ser	Leu	Gly	Pro	Gln	Asp	Phe	Asp	Ala	Gln
				85					90					95	
Leu	Val	Ala	Val	Leu	Pro	Pro	Gln	Asn	Gln	Asn					

**THE UNIVERSITY OF CHICAGO**



105

```
<220>  
<221> CDS  
<222> (101)..(415)  
<223> BXA01865
```

<400> 673															
ggtggaattt ggcctgcggt caaggggaag tagcataata agcctaaagc tttcccatat															60
ttattagcct cttagagttc tcaggagaaa acgaaatccc															115
Met Thr Tyr Thr Ile															5
1															
gca cag ccc tgc gtt gac gtc ttg gat cgt gcc tgc gtt gaa gaa tgc															163
Ala Gln Pro Cys Val Asp Val Leu Asp Arg Ala Cys Val Glu Glu Cys															20
10 15															
cca gta gat tgc atc tac gaa ggt aag cgc atg ctg tac atc cac ccg															211
Pro Val Asp Cys Ile Tyr Glu Gly Lys Arg Met Leu Tyr Ile His Pro															35
25 30															
gat gag tgc gtt gac tgt ggt gca tgt gag cct gct tgc cca gtt gag															259
Asp Glu Cys Val Asp Cys Gly Ala Cys Glu Pro Ala Cys Pro Val Glu															50
40 45															
gca atc ttc tac gag gac gat gtc cca gac gaa tgg ctt gac tac aac															307
Ala Ile Phe Tyr Glu Asp Asp Val Pro Asp Glu Trp Leu Asp Tyr Asn															65
55 60															
gat gcc aac gct gca ttc ttc gat gat ctg ggc tcc cca ggt ggt gcg															355
Asp Ala Asn Ala Ala Phe Phe Asp Asp Leu Gly Ser Pro Gly Gly Ala															85
70 75 80															
gct aag ctt gga cca caa gat ttt gat cac cca atg atc gct gcg ctg															403
Ala Lys Leu Gly Pro Gln Asp Phe Asp His Pro Met Ile Ala Ala Leu															100
90 95 100															
ccg cct cag gca taatctaacg catgacctct cgc															438
Pro Pro Gln Ala															105

<400> 674  
Met Thr Tyr Thr Ile Ala Gln Pro Cys Val Asp Val Leu Asp Arg Ala  
1 5 10 15  
Cys Val Glu Glu Cys Pro Val Asp Cys Ile Tyr Glu Gly Lys Arg Met  
20 25 30

	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2
--	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	---



Leu Tyr Ile His Pro Asp Glu Cys Val Asp Cys Gly Ala Cys Glu Pro  
                   35                  40                  45  
 Ala Cys Pro Val Glu Ala Ile Phe Tyr Glu Asp Asp Val Pro Asp Glu  
           50                  55                  60  
 Trp Leu Asp Tyr Asn Asp Ala Asn Ala Ala Phe Phe Asp Asp Leu Gly  
   65                  70                  75                  80  
 Ser Pro Gly Gly Ala Ala Lys Leu Gly Pro Gln Asp Phe Asp His Pro  
                   85                  90                  95  
 Met Ile Ala Ala Leu Pro Pro Gln Ala  
           100                  105

&lt;210&gt; 675

&lt;211&gt; 441

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(418)

&lt;223&gt; RXA00680

&lt;400&gt; 675

ttcttgcattc cccagaagcc gaatacatca ctgggcaaac actcatcggtt gatggtggcc 60  
 gacagttcat ctaagtacta aaagttctaa ggagaagatc atg tct act att cat 115  
   Met Ser Thr Ile His  
   1                  5  
 ttc att gat cat gct ggc aaa acc cgc acc atc gag gcg act gtt ggt 163  
 Phe Ile Asp His Ala Gly Lys Thr Arg Thr Ile Glu Ala Thr Val Gly  
                   10                  15                  20  
 gat tca gta atg gag acc gca gtc cga aac gga gtg cct gga att gtt 211  
 Asp Ser Val Met Glu Thr Ala Val Arg Asn Gly Val Pro Gly Ile Val  
                   25                  30                  35  
 gct gaa tgc ggc ggt tcc tta tcg tgt gca acc tgc cat gtg ttt gtt 259  
 Ala Glu Cys Gly Gly Ser Leu Ser Cys Ala Thr Cys His Val Phe Val  
                   40                  45                  50  
 gac cct gca cag tat gat gcg ctt ccc cca atg gag gag atg gaa gat 307  
 Asp Pro Ala Gln Tyr Asp Ala Leu Pro Pro Met Glu Glu Met Glu Asp  
           55                  60                  65  
 gaa atg ctg tgg ggt gct gcc gtg gac cgt gag gat tgc tcc cgt ttg 355  
 Glu Met Leu Trp Gly Ala Ala Val Asp Arg Glu Asp Cys Ser Arg Leu  
   70                  75                  80                  85  
 tct tgc caa atc aag gtc acc gaa ggc atg gat ctt tcg ttg acc acg 403  
 Ser Cys Gln Ile Lys Val Thr Glu Gly Met Asp Leu Ser Leu Thr Thr  
                   90                  95                  100  
 cca gaa acg caa gtg tgaggttgaa tcatgaatac ttc 441  
 Pro Glu Thr Gln Val  
           105

09602740-062300



```
<210> 676
<211> 106
<212> PRT
<213> Corynebacterium glutamicum
```

```

<400> 676
Met Ser Thr Ile His Phe Ile Asp His Ala Gly Lys Thr Arg Thr Ile
  1              5              10              15

Glu Ala Thr Val Gly Asp Ser Val Met Glu Thr Ala Val Arg Asn Gly
      20              25              30

Val Pro Gly Ile Val Ala Glu Cys Gly Gly Ser Leu Ser Cys Ala Thr
      35              40              45

Cys His Val Phe Val Asp Pro Ala Gln Tyr Asp Ala Leu Pro Pro Met
      50              55              60

Glu Glu Met Glu Asp Glu Met Leu Trp Gly Ala Ala Val Asp Arg Glu
  65              70              75              80

Asp Cys Ser Arg Leu Ser Cys Gln Ile Lys Val Thr Glu Gly Met Asp
      85              90              95

Leu Ser Leu Thr Thr Pro Glu Thr Gln Val
      100              105

```

```
<210> 677
<211> 1389
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(1366)
<223> RXA00679
```

<400> 677																	
ggaccgtgag gattgctccc gtttgtcttg ccaaatacaag gtcaccgaag gcatggatct																60	
ttcgttgacc acgccagaaa cgcaagtgtg aggttgaatc																	
												atg	aat	act	tca	gct	115
												Met	Asn	Thr	Ser	Ala	
												1				5	
gaa act gga atc ttg atc atc ggt gca aac caa tcg ggt gtg cag ctg																163	
Glu	Thr	Gly	Ile	Leu	Ile	Ile	Gly	Ala	Asn	Gln	Ser	Gly	Val	Gln	Leu		
				10		15								20			
gcg att tcc ctg cgg gcc acg ggt ttc acc gaa tcg atc acg ctt cta																211	
Ala	Ile	Ser	Leu	Arg	Ala	Thr	Gly	Phe	Thr	Glu	Ser	Ile	Thr	Leu	Leu		
				25		30								35			
ggc gag gag gat cac cgc ccc tac cag cgt ccc gcc ttg tcc aag gag																259	
Gly	Glu	Glu	Asp	His	Arg	Pro	Tyr	Gln	Arg	Pro	Ala	Leu	Ser	Lys	Glu		
				40		45								50			
ttc ctc cag gac aag atc gac aaa gag cgt ctg att ttc cgt tcc aat																307	
Phe	Leu	Gln	Asp	Lys	Ile	Asp	Lys	Glu	Arg	Leu	Ile	Phe	Arg	Ser	Asn		
55				60				65									

[illegible]



gag	tat	tgg	gaa	gaa	aat	aat	att	cgc	ctg	gtc	aag	ggc	gtg	cgc	atc	355
Glu	Tyr	Trp	Glu	Glu	Asn	Asn	Ile	Arg	Leu	Val	Lys	Gly	Val	Arg	Ile	
70					75					80					85	
gaa	cgc	att	gaa	aag	aac	gac	gac	gga	tca	ggg	gtc	gcc	tac	ggc	gcc	403
Glu	Arg	Ile	Glu	Lys	Asn	Asp	Asp	Gly	Ser	Gly	Val	Ala	Tyr	Gly	Ala	
				90				95						100		
gga	caa	gaa	ttc	gct	ttt	cga	cgt	ctc	gct	cta	gcg	gtt	ggg	gcc	cgc	451
Gly	Gln	Glu	Phe	Ala	Phe	Arg	Arg	Leu	Ala	Leu	Ala	Val	Gly	Ala	Arg	
			105					110					115			
cct	cgc	cac	ctc	gac	ctc	ccg	ggc	gcc	acc	ttg	gag	ggg	gtc	acc	tac	499
Pro	Arg	His	Leu	Asp	Leu	Pro	Gly	Ala	Thr	Leu	Glu	Gly	Val	Thr	Tyr	
		120					125					130				
ctg	cgc	aac	gcg	gac	gac	gcc	ttg	gcg	ctc	aaa	gcg	atg	att	ggg	tct	547
Leu	Arg	Asn	Ala	Asp	Asp	Ala	Leu	Ala	Leu	Lys	Ala	Met	Ile	Gly	Ser	
	135					140					145					
gtc	acc	gat	gcc	gtt	gta	gtc	ggg	ggg	ggg	ttc	atc	gga	ttg	gaa	gct	595
Val	Thr	Asp	Ala	Val	Val	Val	Gly	Gly	Gly	Phe	Ile	Gly	Leu	Glu	Ala	
150					155					160					165	
gcg	tgt	tcg	ctt	cat	gac	ctc	ggc	aaa	aat	gtc	acc	gtc	ctg	gaa	tat	643
Ala	Cys	Ser	Leu	His	Asp	Leu	Gly	Lys	Asn	Val	Thr	Val	Leu	Glu	Tyr	
				170				175						180		
ggg	ccg	cgt	ctg	att	ggc	cga	gcg	gtg	ggg	gaa	gaa	acc	gca	gca	ttc	691
Gly	Pro	Arg	Leu	Ile	Gly	Arg	Ala	Val	Gly	Glu	Glu	Thr	Ala	Ala	Phe	
			185					190					195			
ttc	ctc	gaa	caa	cac	cgt	tcc	cgt	ggc	gta	aat	atc	gtg	ctt	gat	gcc	739
Phe	Leu	Glu	Gln	His	Arg	Ser	Arg	Gly	Val	Asn	Ile	Val	Leu	Asp	Ala	
		200					205					210				
cgc	atg	aaa	cag	ttt	gtg	ggc	aag	gat	gga	aag	ctc	agc	ggc	att	gag	787
Arg	Met	Lys	Gln	Phe	Val	Gly	Lys	Asp	Gly	Lys	Leu	Ser	Gly	Ile	Glu	
	215					220					225					
cta	gaa	gat	ggc	aca	gta	att	cct	gcc	caa	cta	gtc	att	gtg	ggc	atc	835
Leu	Glu	Asp	Gly	Thr	Val	Ile	Pro	Ala	Gln	Leu	Val	Ile	Val	Gly	Ile	
230					235					240					245	
ggg	gtc	att	ccg	aac	aca	gaa	ctt	gcc	gct	gtt	ctg	ggc	tta	gac	atc	883
Gly	Val	Ile	Pro	Asn	Thr	Glu	Leu	Ala	Ala	Val	Leu	Gly	Leu	Asp	Ile	
				250				255						260		
aac	aac	ggc	atc	gtg	gtg	gat	aaa	cat	gcc	gtc	gcg	tca	gat	ggc	acc	931
Asn	Asn	Gly	Ile	Val	Val	Asp	Lys	His	Ala	Val	Ala	Ser	Asp	Gly	Thr	
			265					270					275			
acc	att	gcg	att	ggc	gat	gtc	gcc	aac	att	ccc	aat	cca	atc	cct	ggg	979
Thr	Ile	Ala	Ile	Gly	Asp	Val	Ala	Asn	Ile	Pro	Asn	Pro	Ile	Pro	Gly	
		280					285					290				
tcc	ccc	gct	gat	gaa	cgc	atc	cga	cta	gaa	agc	gtc	aat	aac	gcc	atc	1027
Ser	Pro	Ala	Asp	Glu	Arg	Ile	Arg	Leu	Glu	Ser	Val	Asn	Asn	Ala	Ile	
	295					300					305					

09602740-062300







<210> 679

THE UNIVERSITY OF CHICAGO



```
<211> 1074
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(1051)
<223> RXA00224
```

<400> 679																																
gtgatgtcat		tgggtgcacg		gggtgctgctg		aaaagattgc		tgagtacctc		gcttcagaga		60																				
acctcatcta		gccactatct		tcacaaagga		gaacatttta		atg		tct		att		tct		tat		115														
										Met		Ser		Ile		Ser Tyr		5														
										1																						
gtg		ctg		gtt		gag		cag		cta		gat		ggc		cgc		cca		gaa		cca		gtt		acc		ctt		gaa		163
Val		Leu		Val		Glu		Gln		Leu		Asp		Gly		Arg		Pro		Glu		Pro		Val		Thr		Leu		Glu		
						10										15										20						
ttg		atc		act		gct		gct		cgc		gca		ctc		ggg		gac		gtc		gtt		gcc		gtt		gtc		gtt		211
Leu		Ile		Thr		Ala		Ala		Arg		Ala		Leu		Gly		Asp		Val		Val		Ala		Val		Val		Val		
						25										30										35						
ggc		gag		cca		ggg		gcc		ggc		gta		aac		ctt		gct		gct		gag		ctc		ggc		aat		tgg		259
Gly		Glu		Pro		Gly		Ala		Gly		Val		Asn		Leu		Ala		Ala		Glu		Leu		Gly		Asn		Trp		
				40										45										50								
ggg		gca		gca		cag		gtt		gtt		tcc		gct		gaa		atc		tct		ggc		gct		tcc		aac		cgt		307
Gly		Ala		Ala		Gln		Val		Val		Ser		Ala		Glu		Ile		Ser		Gly		Ala		Ser		Asn		Arg		
				55								60										65										
ttg		atc		ttg		cct		gct		gtt		gat		gcg		ctg		cac		att		ttg		gct		gcg		aac		aac		355
Leu		Ile		Leu		Pro		Ala		Val		Asp		Ala		Leu		His		Ile		Leu		Ala		Ala		Asn		Asn		
				70						75								80										85				
cca		ggg		cca		att		gtt		atc		gct		gca		act		gca		agc		ggg		aat		gag		atc		gct		403
Pro		Gly		Pro		Ile		Val		Ile		Ala		Ala		Thr		Ala		Ser		Gly		Asn		Glu		Ile		Ala		
						90								95												100						
ggg		cgt		ttg		gct		gcc		cgt		ttg		gct		tct		ggg		gtg		ctc		acc		gat		gtc		gtc		451
Gly		Arg		Leu		Ala		Ala		Arg		Leu		Ala		Ser		Gly		Val		Leu		Thr		Asp		Val		Val		
				105										110										115								
gga		atc		aat		gcc		gac		cgc		acc		gca		cag		cag		tcc		att		ttc		ggc		gac		acc		499
Gly		Ile		Asn		Ala		Asp		Arg		Thr		Ala		Gln		Gln		Ser		Ile		Phe		Gly		Asp		Thr		
				120								125								130										</		

**00000000000000000000**















atc tagccactat cttcacaaag gag  
Ile

909

&lt;210&gt; 682

&lt;211&gt; 262

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 682

Met Ser Thr Ile Val Val Leu Val Lys Asn Val Pro Asp Thr Trp Ser  
1 5 10 15

Lys Arg Thr Leu Glu Ala Asp Phe Thr Leu Asp Arg Glu Gly Val Asp  
20 25 30

Arg Val Leu Asp Glu Ile Asn Glu Phe Ala Leu Glu Gln Ala Leu Arg  
35 40 45

Leu Arg Glu Ser Asn Pro Asp Ala Gly Tyr Arg Val Val Ala Leu Ser  
50 55 60

Ala Gly Pro Ala Gly Gly Glu Glu Ala Leu Arg Lys Ala Leu Ser Met  
65 70 75 80

Gly Ala Asp Glu Ala Ile Gln Leu Ser Asp Asp Ala Leu Ala Gly Ser  
85 90 95

Asp Leu Leu Gly Thr Ala Trp Ala Leu Asn Asn Ala Ile Asn Thr Ile  
100 105 110

Ala Gly Val Ala Leu Ile Val Thr Gly Ser Ala Ser Ser Asp Gly Ser  
115 120 125

Met Gly Ala Leu Pro Gly Val Leu Ala Glu Tyr Arg Gln Val Pro Ala  
130 135 140

Leu Thr Asn Leu Ser Ala Leu Lys Val Glu Gly Ala Ser Ile Thr Ala  
145 150 155 160

Thr Arg Ile Asp Asn His Gly Thr Tyr Glu Leu Gln Ala Ala Leu Pro  
165 170 175

Ala Val Val Ser Ile Ser Asp Lys Ala Asp Lys Pro Arg Phe Pro Asn  
180 185 190

Phe Lys Gly Ile Met Ala Ala Lys Lys Ala Glu Ile Lys Lys Leu Ser  
195 200 205

Leu Ala Glu Ile Gly Val Ala Pro Glu Gln Val Gly Leu Ser His Ala  
210 215 220

Ala Thr Ala Val Thr Ala Ala Ala Asp Arg Pro Glu Arg Ser Gln Gly  
225 230 235 240

Asp Val Ile Gly Ala Ser Gly Ala Ala Glu Lys Ile Ala Glu Tyr Leu  
245 250 255

Ala Ser Glu Asn Leu Ile

09602740-062300



```
<210> 683
<211> 2378
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (82) .. (2355)  
<223> RXN00606
```

[illegible]



[illegible]



**00000000000000000000**



actgacagtc qcg 2378

<213> Corynebacterium glutamicum

His Ala Leu Phe Lys Ser Ser Leu Phe Met Leu Ile Gly Val Ile Asp  
130 135 140

**09-06-2018**



**096270**



465                      470                      475                      480  
 Thr Val Leu Val Ala Val Leu Ala Ala Phe Ala Ala Phe Met Ala Val  
                                  485                                   490                                   495  
 Trp Gly Leu Leu Gly Arg His Glu Arg Ser Glu Leu Ala Met Trp Tyr  
                                  500                                   505                                   510  
 Leu Asn Gln Gly Pro Glu Ile Thr Ser Gly Ala Asn Val Val Asn Thr  
                                  515                                   520                                   525  
 Ile Leu Val Glu Phe Arg Ala Leu Asp Thr Leu Gly Glu Leu Ser Val  
                                  530                                   535                                   540  
 Leu Gly Met Ala Ala Val Val Ile Gly Ala Met Val Ala Ser Met Pro  
 545                                   550                                   555                                   560  
 Arg His Pro Phe Ala Lys Gly Thr His Pro Arg Pro Phe Gly Gln Ser  
                                  565                                   570                                   575  
 Gln Leu Asn Ser Ile Pro Leu Arg Met Leu Leu Lys Val Leu Val Pro  
                                  580                                   585                                   590  
 Ala Leu Cys Phe Leu Ser Phe Met Val Phe Met Arg Gly His Asn Asp  
                                  595                                   600                                   605  
 Pro Gly Gly Gly Phe Ile Ala Ala Leu Ile Ala Gly Gly Ala Leu Met  
                                  610                                   615                                   620  
 Leu Leu Tyr Leu Ser Lys Ala Lys Asp Gly Arg Ile Phe Arg Pro Asn  
 625                                   630                                   635                                   640  
 Val Pro Phe Ile Leu Thr Gly Ala Gly Ile Leu Met Ala Val Phe Ser  
                                  645                                   650                                   655  
 Gly Val Leu Gly Leu Thr His Gly Ser Phe Leu Tyr Ala Ile His Phe  
                                  660                                   665                                   670  
 Asn Phe Val Gly Gln His Trp Thr Thr Ser Met Ile Phe Asp Leu Gly  
                                  675                                   680                                   685  
 Val Tyr Leu Ala Val Leu Gly Met Val Ser Met Ala Ile Asn Gly Leu  
                                  690                                   695                                   700  
 Gly Gly Tyr Leu Arg Pro Gly Thr Asp Asn Ala Asp Leu Asp Tyr Ala  
 705                                   710                                   715                                   720  
 Arg Arg Ser Gly Pro Leu Pro Ala Thr Pro Thr Val Glu Pro Glu Pro  
                                  725                                   730                                   735  
 Glu Gly Asp Glu Asp Trp Pro Glu Pro Ile Asn Pro Ala Gly Asp Asn  
                                  740                                   745                                   750  
 Lys Glu Glu Ala Asn Arg  
                                  755

&lt;210&gt; 685

&lt;211&gt; 1872

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

002290" 04220960



&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1849)

&lt;223&gt; FRXA00606

&lt;400&gt; 685

```

atggataacc agactggcac gcgcgatatt cgtcgcctcg gtttcttggt caagaaaaat 60

gccgttcacg tttgtgtctg tattaatagg tgcgttgctg atg gca tcg gtt ccg 115
                Met Ala Ser Val Pro
                1                    5

ccg ttg ctc ggc ttc gtg tcc aaa gaa ggc atg atc aca gcg ttc atg 163
Pro Leu Leu Gly Phe Val Ser Lys Glu Gly Met Ile Thr Ala Phe Met
                10                    15                    20

gac gcc ccc atc ggc aac tcc tat gtt gta tta ctg ctg gtc ggc gca 211
Asp Ala Pro Ile Gly Asn Ser Tyr Val Val Leu Leu Leu Val Gly Ala
                25                    30                    35

gca atc ggc gcg gtc cta acc ttc aca tac tcc gcg aaa ctc gtg ctc 259
Ala Ile Gly Ala Val Leu Thr Phe Thr Tyr Ser Ala Lys Leu Val Leu
                40                    45                    50

ggc gca ttc gtc gac ggc cca cgc gac atg tca cac gtc aag gaa gcc 307
Gly Ala Phe Val Asp Gly Pro Arg Asp Met Ser His Val Lys Glu Ala
                55                    60                    65

ccc gtc tcc ctc tgg ctt ccg gcc gcc ctg cct gga ctt atg tct ctg 355
Pro Val Ser Leu Trp Leu Pro Ala Ala Leu Pro Gly Leu Met Ser Leu
                70                    75                    80                    85

cca cta gtc cta gta ctt tcg ctt ttc gac gcc ccc gtc tcc gcc gca 403
Pro Leu Val Leu Val Leu Ser Leu Phe Asp Ala Pro Val Ser Ala Ala
                90                    95                    100

gcc acc tcc gcc gcg ggg gaa gcg gcg cac atg cac ctg gca ttg tgg 451
Ala Thr Ser Ala Ala Gly Glu Ala Ala His Met His Leu Ala Leu Trp
                105                    110                    115

cac ggc atc aac acc cca ctg ttg att tcc ttg ggt gtg ctg gtg gcc 499
His Gly Ile Asn Thr Pro Leu Leu Ile Ser Leu Gly Val Leu Val Ala
                120                    125                    130

gga atc ctt ggt gtg ctg ttc cgc aaa gag ctg tgg aaa atc gcc gag 547
Gly Ile Leu Gly Val Leu Phe Arg Lys Glu Leu Trp Lys Ile Ala Glu
                135                    140                    145

acc agc cct ttc ccc atc gcc aca ggc aac gac atc cta tcg atg ctg 595
Thr Ser Pro Phe Pro Ile Ala Thr Gly Asn Asp Ile Leu Ser Met Leu
                150                    155                    160                    165

gtt tac cga gcc aac ttg ctg ggt aaa ttc ttc ggt cgc atg gct gat 643
Val Tyr Arg Ala Asn Leu Leu Gly Lys Phe Phe Gly Arg Met Ala Asp
                170                    175                    180

tcg atg agc cca cgc agg cac ttg gtc agc ctc atc gtg ctg ctc tgg 691
Ser Met Ser Pro Arg Arg His Leu Val Ser Leu Ile Val Leu Leu Trp
                185                    190                    195

```

09602740-06290-0420960



[illegible]



```

<400> 686
Met  Ala  Ser  Val  Pro  Pro  Leu  Leu  Gly  Phe  Val  Ser  Lys  Glu  Gly  Met
   1              5              10              15

Ile  Thr  Ala  Phe  Met  Asp  Ala  Pro  Ile  Gly  Asn  Ser  Tyr  Val  Val  Leu
          20              25              30

Leu  Leu  Val  Gly  Ala  Ala  Ile  Gly  Ala  Val  Leu  Thr  Phe  Thr  Tyr  Ser
          35              40              45

Ala  Lys  Leu  Val  Leu  Gly  Ala  Phe  Val  Asp  Gly  Pro  Arg  Asp  Met  Ser
   50              55              60

His  Val  Lys  Glu  Ala  Pro  Val  Ser  Leu  Trp  Leu  Pro  Ala  Ala  Leu  Pro
   65              70              75              80

```

[illegible]







DEPT. OF THE ARMY  
WASHINGTON, D. C. 20315



cct ttc gcg ggt att ttt gct ggc atc tgg ttg ttt gca cac acc gct	259
Pro Phe Ala Gly Ile Phe Ala Gly Ile Trp Leu Phe Ala His Thr Ala	
40 45 50	
gaa cac ggc ccg att gct cac aac gtg ggc ctt tat gtc ggt ggc gtg	307
Glu His Gly Pro Ile Ala His Asn Val Gly Leu Tyr Val Gly Gly Val	
55 60 65	
gca atc ccc ttt gct gcc gat acg ttc agc gcc atc atg ttg atc acc	355
Ala Ile Pro Phe Ala Ala Asp Thr Phe Ser Ala Ile Met Leu Ile Thr	
70 75 80 85	
acc tcg atc gtt gcg gtg gct gcc aac tgg ttt gcc acc atc gtc ggt	403
Thr Ser Ile Val Ala Val Ala Ala Asn Trp Phe Ala Thr Ile Val Gly	
90 95 100	
gaa acc cgc gcg cgt ttc tat cca gcg ctc aca ttg atg ctg atc acg	451
Glu Thr Arg Ala Arg Phe Tyr Pro Ala Leu Thr Leu Met Leu Ile Thr	
105 110 115	
ggc gtc aac ggt gct ctg ctg act gcc gat ctg ttc aac ttc ttt gtg	499
Gly Val Asn Gly Ala Leu Leu Thr Ala Asp Leu Phe Asn Phe Phe Val	
120 125 130	
ttc atc gaa gtg atg ctg ctg cct tcc tat ggt ttg atc gcc atg acc	547
Phe Ile Glu Val Met Leu Leu Pro Ser Tyr Gly Leu Ile Ala Met Thr	
135 140 145	
gga acg tgg gcg cgc cta gcc tct gga cga atc ttc gta cta gtc aat	595
Gly Thr Trp Ala Arg Leu Ala Ser Gly Arg Ile Phe Val Leu Val Asn	
150 155 160 165	
ctc tct gcc tcc aca ttg ctg gtt gca ggt gtg gga atc gtc tac ggt	643
Leu Ser Ala Ser Thr Leu Leu Val Ala Gly Val Gly Ile Val Tyr Gly	
170 175 180	
gtc ata ggc tca gtc aac atc gca gct ctg caa gat gtc gta gag ggc	691
Val Ile Gly Ser Val Asn Ile Ala Ala Leu Gln Asp Val Val Glu Gly	
185 190 195	
aac ccc ctg gtt gcc agc gca atg ggc atc gtg gtt att gcc atc gcg	739
Asn Pro Leu Val Ala Ser Ala Met Gly Ile Val Val Ile Ala Ile Ala	
200 205 210	
gtt aaa gcc ggt gta ttc cca gtg cac aca tgg ctg cca cgc acc tat	787
Val Lys Ala Gly Val Phe Pro Val His Thr Trp Leu Pro Arg Thr Tyr	
215 220 225	
cct ggt aca tca gca gct gtg atg ggg ttg ttc tcc ggt ttg cac acc	835
Pro Gly Thr Ser Ala Ala Val Met Gly Leu Phe Ser Gly Leu His Thr	
230 235 240 245	
aaa gtc gcg gta tac atg ctc tat cgc att tgg gtc cac att ttt aac	883
Lys Val Ala Val Tyr Met Leu Tyr Arg Ile Trp Val His Ile Phe Asn	
250 255 260	
atg gat ccc acg tgg aat tgg ctg att gtc gca ttc atg gtg ata tcc	931
Met Asp Pro Thr Trp Asn Trp Leu Ile Val Ala Phe Met Val Ile Ser	
265 270 275	
atg ctg gtc ggt ggc ttc gct gga ctt gct gaa aac tcc atc cgt cgc	979

09602740-062300



**DECLASSIFICATION AUTHORITY**



<400> 688															
Met 1	Ala	Met	Asp	Val 5	Leu	Leu	Pro	Ile	Phe 10	Val	Ala	Val	Pro	Leu 15	Ala
Ala	Ser	Ala	Ile 20	Ala	Val	Leu	Leu	Pro 25	Trp	Arg	Leu	Ile	Arg 30	Asp	Ile
Leu	His	Ile 35	Ile	Val	Pro	Phe	Ala 40	Gly	Ile	Phe	Ala	Gly 45	Ile	Trp	Leu
Phe	Ala 50	His	Thr	Ala	Glu	His 55	Gly	Pro	Ile	Ala	His 60	Asn	Val	Gly	Leu
Tyr 65	Val	Gly	Gly	Val	Ala 70	Ile	Pro	Phe	Ala	Ala 75	Asp	Thr	Phe	Ser	Ala 80
Ile	Met	Leu	Ile	Thr 85	Thr	Ser	Ile	Val	Ala 90	Val	Ala	Ala	Asn	Trp 95	Phe
Ala	Thr	Ile	Val 100	Gly	Glu	Thr	Arg	Ala 105	Arg	Phe	Tyr	Pro	Ala 110	Leu	Thr
Leu	Met	Leu 115	Ile	Thr	Gly	Val	Asn 120	Gly	Ala	Leu	Leu	Thr 125	Ala	Asp	Leu
Phe	Asn 130	Phe	Phe	Val	Phe	Ile 135	Glu	Val	Met	Leu	Leu 140	Pro	Ser	Tyr	Gly
Leu 145	Ile	Ala	Met	Thr	Gly 150	Thr	Trp	Ala	Arg	Leu 155	Ala	Ser	Gly	Arg	Ile 160
Phe	Val	Leu	Val	Asn 165	Leu	Ser	Ala	Ser	Thr 170	Leu	Leu	Val	Ala	Gly 175	Val
Gly	Ile	Val	Tyr 180	Gly	Val	Ile	Gly	Ser 185	Val	Asn	Ile	Ala	Ala 190	Leu	Gln
Asp	Val	Val 195	Glu	Gly	Asn	Pro	Leu 200	Val	Ala	Ser	Ala	Met 205	Gly	Ile	Val
Val 210	Ile	Ala	Ile	Ala	Val	Lys 215	Ala	Gly	Val	Phe	Pro 220	Val	His	Thr	Trp
Leu 225	Pro	Arg	Thr	Tyr	Pro 230	Gly	Thr	Ser	Ala	Ala 235	Val	Met	Gly	Leu	Phe 240
Ser	Gly	Leu	His	Thr 245	Lys	Val	Ala	Val	Tyr 250	Met	Leu	Tyr	Arg	Ile 255	Trp
Val	His	Ile	Phe 260	Asn	Met	Asp	Pro	Thr 265	Trp	Asn	Trp	Leu	Ile 270	Val	Ala
Phe	Met	Val 275	Ile	Ser	Met	Leu	Val 280	Gly	Gly	Phe	Ala	Gly 285	Leu	Ala	Glu



Asn Ser Ile Arg Arg Val Leu Ala Tyr Gln Met Val Asn Gly Met Pro  
 290 295 300  
 Phe Ile Leu Ile Met Met Ala Phe Thr Ser Asp Asp Pro Gln Arg Ala  
 305 310 315 320  
 Leu Ala Ala Gly Leu Leu Tyr Thr Leu His His Met Ile Thr Ile Ala  
 325 330 335  
 Ala Leu Val Leu Thr Ser Gly Ala Ile Glu Glu Thr Tyr Gly Thr Gly  
 340 345 350  
 Met Leu Ser Lys Leu Ser Gly Leu Ala Arg Arg Glu Pro Val Val Ala  
 355 360 365  
 Ala Val Phe Ala Ala Gly Ala Phe Ser Val Val Gly Phe Pro Pro Phe  
 370 375 380  
 Ser Gly Met Trp Gly Lys Ala Leu Ile Leu Leu Glu Ile Ala Arg Val  
 385 390 395 400  
 Gly Asn Ile Ala Ala Trp Ile Ala Ile Ala Ala Ile Ile Ile Ala Ser  
 405 410 415  
 Leu Gly Ala Leu Leu Ser Met Ile Arg Val Trp Arg Glu Val Phe Trp  
 420 425 430  
 Gly Gly Ala Met His Gln Arg Gly Val Ser Pro Gln Leu Arg Ile Ser  
 435 440 445  
 Pro Ala Lys Ile Ala Pro Ala Leu Ser Leu Ile Ile Leu Ser Val Gly  
 450 455 460  
 Met Phe Ile Phe Ala Gly Pro Leu Ile Asp Ala Thr Leu Thr Ala Thr  
 465 470 475 480  
 Asp Gly Leu Leu Asn Thr Asp Ala Tyr Gln Gln Ala Val Leu Gly Glu  
 485 490 495  
 Asn Ala Ile Gly Val Pro Ser Pro Ser Tyr Gln Gly Gly Asn  
 500 505 510

&lt;210&gt; 689

&lt;211&gt; 865

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(865)

&lt;223&gt; FRXA00608

&lt;400&gt; 689

cgacgacacc cgttccatcg aaccagatga cgatcaatcg cctttgacta ctagegctcg 60

ttcagtcacc aaccacacag atcaggagga taaagcttaa atg gcc atg gat gtt 115

Met Ala Met Asp Val

1

5

ctc ctt cct att ttc gtt gca gtt ccc ctt gct gcc tct gcc att gcg 163

09602740-062300



Leu	Leu	Pro	Ile	Phe	Val	Ala	Val	Pro	Leu	Ala	Ala	Ser	Ala	Ile	Ala		
				10					15					20			
gtg	ctt	ctg	ccg	tgg	cgt	ctc	atc	cgc	gat	att	ttg	cac	atc	atc	gtg	211	
Val	Leu	Leu	Pro	Trp	Arg	Leu	Ile	Arg	Asp	Ile	Leu	His	Ile	Ile	Val		
			25					30					35				
cct	ttc	gcg	ggg	att	ttt	gct	ggc	atc	tgg	ttg	ttt	gca	cac	acc	gct	259	
Pro	Phe	Ala	Gly	Ile	Phe	Ala	Gly	Ile	Trp	Leu	Phe	Ala	His	Thr	Ala		
		40					45					50					
gaa	cac	ggc	ccg	att	gct	cac	aac	gtg	ggc	ctt	tat	gtc	ggg	ggc	gtg	307	
Glu	His	Gly	Pro	Ile	Ala	His	Asn	Val	Gly	Leu	Tyr	Val	Gly	Gly	Val		
	55					60					65						
gca	atc	ccc	ttt	gct	gcc	gat	acg	ttc	agc	gcc	atc	atg	ttg	atc	acc	355	
Ala	Ile	Pro	Phe	Ala	Ala	Asp	Thr	Phe	Ser	Ala	Ile	Met	Leu	Ile	Thr		
70					75				80						85		
acc	tcg	atc	gtt	gcg	gtg	gct	gcc	aac	tgg	ttt	gcc	acc	atc	gtc	ggg	403	
Thr	Ser	Ile	Val	Ala	Val	Ala	Ala	Asn	Trp	Phe	Ala	Thr	Ile	Val	Gly		
				90					95					100			
gaa	acc	cgc	gcg	cgt	ttc	tat	cca	gcg	ctc	aca	ttg	atg	ctg	atc	acg	451	
Glu	Thr	Arg	Ala	Arg	Phe	Tyr	Pro	Ala	Leu	Thr	Leu	Met	Leu	Ile	Thr		
			105					110					115				
ggc	gtc	aac	ggg	gct	ctg	ctg	act	gcc	gat	ctg	ttc	aac	ttc	ttt	gtg	499	
Gly	Val	Asn	Gly	Ala	Leu	Leu	Thr	Ala	Asp	Leu	Phe	Asn	Phe	Phe	Val		
		120					125					130					
ttc	atc	gaa	gtg	atg	ctg	ctg	cct	tcc	tat	ggg	ttg	atc	gcc	atg	acc	547	
Phe	Ile	Glu	Val	Met	Leu	Leu	Pro	Ser	Tyr	Gly	Leu	Ile	Ala	Met	Thr		
	135					140					145						
gga	acg	tgg	gcg	cgc	cta	gcc	tct	gga	cga	atc	ttc	gta	cta	gtc	aat	595	
Gly	Thr	Trp	Ala	Arg	Leu	Ala	Ser	Gly	Arg	Ile	Phe	Val	Leu	Val	Asn		
150					155					160					165		
ctc	tct	gcc	tcc	aca	ttg	ctg	gtt	gca	ggg	gtg	gga	atc	gtc	tac	ggg	643	
Leu	Ser	Ala	Ser	Thr	Leu	Leu	Val	Ala	Gly	Val	Gly	Ile	Val	Tyr	Gly		
				170					175					180			
gtc	ata	ggc	tca	gtc	aac	atc	gca	gct	ctg	caa	gat	gtc	gta	gag	ggc	691	
Val	Ile	Gly	Ser	Val	Asn	Ile	Ala	Ala	Leu	Gln	Asp	Val	Val	Glu	Gly		
			185					190					195				
aac	ccc	ctg	gtt	gcc	agc	gca	atg	ggc	atc	gtg	gtt	att	gcc	atc	gcg	739	
Asn	Pro	Leu	Val	Ala	Ser	Ala	Met	Gly	Ile	Val	Val	Ile	Ala	Ile	Ala		
		200					205					210					
gtt	aaa	gcc	ggg	gta	ttc	cca	gtg	cac	aca	tgg	ctg	cca	cgc	acc	tat	787	
Val	Lys	Ala	Gly	Val	Phe	Pro	Val	His	Thr	Trp	Leu	Pro	Arg	Thr	Tyr		
	215					220					225						
cct	ggg	aca	tca	gca	gct	gtg	atg	ggg	ttg	ttc	tcc	ggg	ttg	cac	acc	835	
Pro	Gly	Thr	Ser	Ala	Ala	Val	Met	Gly	Leu	Phe	Ser	Gly	Leu	His	Thr		
230					235					240					245		
aaa	gtc	gcg	gta	tac	atg	ctc	tat	cgc	att							865	
Lys	Val	Ala	Val	Tyr	Met	Leu	Tyr	Arg	Ile								

002290"04220960



255

<400> 690

Ser Gly Leu His Thr Lys Val Ala Val Tyr Met Leu Tyr Arg Ile  
245 250 255

<210> 691  
<211> 2118  
<212> DNA

[illegible]



<220>

<221> CDS

<222> (1) .. (2118)

<223> RXA00913

<400> 691

[illegible]



[illegible]



**00000000000000000000000000000000**



2118

<400> 692															
Ile 1	Ile	Ser	Val	Val 5	Gly	Ile	Gly	Thr	Arg 10	Glu	Ala	Leu	Leu	Ala 15	Gly
Leu	Ala	Leu	Thr 20	Val	Ala	His	Ser	Leu 25	Phe	Lys	Ala	Thr	Leu 30	Phe	Met
Thr	Val	Gly 35	Ala	Ile	Asp	His	Thr 40	Thr	Gly	Thr	Arg	Asp 45	Ile	Arg	Lys
Leu	Ser 50	Gly	Leu	Trp	Arg	Lys 55	Gln	Pro	Ile	Leu	Phe 60	Ala	Val	Ala	Ala
Val 65	Ser	Ala	Ala	Ser	Met 70	Ala	Gly	Ile	Pro	Pro 75	Leu	Phe	Gly	Phe	Ile 80
Ala	Lys	Glu	Thr	Ala 85	Leu	Asp	Thr	Val	Leu 90	Asn	Glu	Gln	Met	Leu 95	His
Gly	Met	Pro	Gly 100	Arg	Leu	Met	Leu	Ala 105	Gly	Ile	Val	Leu	Gly 110	Ser	Ile
Phe	Thr	Met 115	Ala	Tyr	Ser	Cys	Tyr 120	Phe	Leu	Tyr	Glu 125	Ala	Phe	Ala	Thr
Lys 130	His	Ser	Lys	Phe	Pro	Glu 135	Ala	Asn	Gly	Val	Ser 140	Pro	Ala	Val	Glu
Ala 145	Met	His	Pro	Val	Lys 150	Phe	Lys	Leu	Trp	Ile 155	Ala	Pro	Val	Ile	Leu 160
Ala	Ile	Leu	Thr 165	Val	Val	Phe	Gly	Val	Phe 170	Pro	Lys	Pro	Val	Ser 175	Glu
Ala	Ile	Val	Thr 180	His	Leu	Asp	Asn	Val 185	Thr	Pro	Ser	Leu	Asp 190	Asp	Val
His	Thr	Lys 195	Leu	Ala	Leu	Trp	His 200	Gly	Leu	Asn	Leu 205	Pro	Leu	Leu	Leu
Ser 210	Val	Val	Ile	Ile	Ile	Ser 215	Gly	Phe	Ile	Ile	Phe 220	Trp	Glu	Arg	Asp
Thr 225	Val	Glu	Arg	Leu	Arg 230	Pro	Asn	Thr	Ala	Ala 235	Phe	Gly	Ser	Ala	Asp 240
Thr	Ala	Tyr	Asp 245	Ala	Ile	Leu	Asp	Ala	Leu 250	Arg	Val	Leu	Ser	His 255	Arg
Leu	Thr	Ala	Ser	Thr	Gln	Arg	Gly	Ser	Leu	Thr	Leu	Asn	Val	Gly	Val



260					265					270					
Ile	Phe	Phe	Val	Leu	Thr	Ile	Val	Pro	Leu	Ile	Ala	Leu	Ile	Thr	Gly
		275					280					285			
Glu	Gln	Ser	Asp	Val	Arg	Met	Glu	Leu	Trp	Asp	Ser	Pro	Ile	Gln	Gly
	290					295					300				
Phe	Ile	Ala	Ala	Ile	Ile	Ile	Val	Val	Ala	Ile	Val	Ala	Thr	Thr	Met
305					310					315					320
Asp	Asn	Arg	Leu	Ser	Ala	Leu	Ile	Leu	Val	Gly	Val	Thr	Gly	Tyr	Gly
			325						330					335	
Ile	Ala	Val	Ile	Phe	Ala	Leu	His	Gly	Ala	Pro	Asp	Leu	Ala	Leu	Thr
			340					345					350		
Gln	Val	Leu	Val	Glu	Thr	Ile	Val	Met	Val	Val	Phe	Met	Leu	Val	Leu
		355					360					365			
Arg	Lys	Met	Pro	Thr	Glu	Val	Ala	Trp	Lys	Ala	Glu	Pro	Lys	Gln	Ser
	370					375					380				
Arg	Val	Arg	Ala	Trp	Leu	Ala	Gly	Ala	Thr	Gly	Leu	Ser	Val	Val	Ile
385					390					395					400
Val	Thr	Ile	Phe	Ala	Met	Asn	Ala	Arg	Thr	Thr	Glu	Pro	Ile	Ser	Val
			405						410					415	
Tyr	Met	Gln	Asp	Leu	Ala	Tyr	Glu	Ile	Gly	His	Gly	Ala	Asn	Thr	Val
			420					425					430		
Asn	Val	Leu	Leu	Val	Asp	Leu	Arg	Gly	Phe	Asp	Thr	Phe	Gly	Glu	Ile
		435					440					445			
Ser	Val	Leu	Val	Ile	Ala	Ala	Thr	Gly	Ile	Ala	Ser	Leu	Val	Tyr	Arg
	450					455					460				
Asn	Arg	Ser	Phe	Arg	Lys	Asp	Ser	Arg	Arg	Pro	Thr	Leu	Ala	Thr	Thr
465					470					475					480
Gly	Arg	Arg	Trp	Leu	Ala	Ala	Ala	Val	Asp	Thr	Glu	Arg	Ala	Gln	Asn
				485					490					495	
Arg	Ser	Leu	Met	Val	Asp	Val	Ala	Thr	Arg	Ile	Leu	Phe	Pro	Ala	Met
			500					505					510		
Ile	Met	Leu	Ser	Val	Tyr	Phe	Phe	Phe	Ala	Gly	His	Asn	Ala	Pro	Gly
		515					520					525			
Gly	Gly	Phe	Ala	Gly	Gly	Leu	Val	Ala	Ser	Leu	Ala	Phe	Ala	Leu	Arg
	530					535					540				
Tyr	Leu	Ala	Gly	Gly	Arg	Glu	Glu	Leu	Glu	Glu	Ala	Leu	Pro	Ile	Asp
545					550					555					560
Ala	Gly	Arg	Ile	Leu	Gly	Thr	Gly	Leu	Phe	Val	Ser	Ala	Thr	Ala	Val
				565					570					575	
Leu	Trp	Pro	Met	Val	Leu	Leu	Gly	Glu	Pro	Pro	Leu	Thr	Ser	His	Ile
			580					585					590		

09602740-062300



Trp Asp Leu Thr Leu Pro Leu Ile Gly Glu Ile His Ile Ala Ser Ala  
 595 600 605  
 Leu Leu Phe Asp Leu Gly Val Tyr Leu Ile Val Ile Gly Leu Thr Met  
 610 615 620  
 His Ile Leu Asn Ser Leu Gly Gly Gln Leu Asp Arg Asp Glu Glu Met  
 625 630 635 640  
 Arg Lys Gln Arg Ala Arg Asp Arg Ala Arg Arg Leu Ala Arg Asn Gln  
 645 650 655  
 Arg Arg Glu Ala Ala Thr Val Gly Ala Arg Arg Ser Asn Glu Lys Ser  
 660 665 670  
 Thr Arg Gln Met Pro Thr Ile Arg Pro Pro Gly Ala Asp Thr Glu Ser  
 675 680 685  
 Val Glu Gln Asn Gly Glu Asn Gln Thr Ser Ile Ser Thr Lys Arg Leu  
 690 695 700  
 Lys Gln  
 705

<210> 693  
 <211> 955  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(955)  
 <223> RXA00909

<400> 693  
 tcgatgtgtg ttgctaactg ggggtggcac gcacgttggc gttgttgttt ggtgtggctc 60  
 cagagtaatc cacaacgcgc aaaggggaac tggagaacac gtg ctc att ctt ttt 115  
 Val Leu Ile Leu Phe  
 1 5  
 ctc gcg ctc act gca gcc gca gta gtc gcc ccc atc ctg atc cga act 163  
 Leu Ala Leu Thr Ala Ala Ala Val Val Ala Pro Ile Leu Ile Arg Thr  
 10 15 20  
 ctc ggt cga cca gct ttt ggt ctg ctg gcg ctt gta cct ggc att ggt 211  
 Leu Gly Arg Pro Ala Phe Gly Leu Leu Ala Leu Val Pro Gly Ile Gly  
 25 30 35  
 ttt ttc tgg gtg ctt tcg gag ttc atc aaa ggc act ttc aag gat gga 259  
 Phe Phe Trp Val Leu Ser Glu Phe Ile Lys Gly Thr Phe Lys Asp Gly  
 40 45 50  
 ggt gaa ctc ctc ctc cac tat gcc tgg atg cct tcg gct cac ctc aat 307  
 Gly Glu Leu Leu Leu His Tyr Ala Trp Met Pro Ser Ala His Leu Asn  
 55 60 65  
 atc gat ttc cgt atg gat tcc ctc gcg gcg ctg ttc tca ctc atc gtc 355  
 Ile Asp Phe Arg Met Asp Ser Leu Ala Ala Leu Phe Ser Leu Ile Val

09602740-062300



```
<210> 694
<211> 285
<212> PRT
<213> Corynebacterium glutamicum
<400> 694
```

<400> 694



Val Leu Ile Leu Phe Leu Ala Leu Thr Ala Ala Ala Val Val Ala Pro  
 1 5 10 15  
 Ile Leu Ile Arg Thr Leu Gly Arg Pro Ala Phe Gly Leu Leu Ala Leu  
 20 25 30  
 Val Pro Gly Ile Gly Phe Phe Trp Val Leu Ser Glu Phe Ile Lys Gly  
 35 40 45  
 Thr Phe Lys Asp Gly Gly Glu Leu Leu Leu His Tyr Ala Trp Met Pro  
 50 55 60  
 Ser Ala His Leu Asn Ile Asp Phe Arg Met Asp Ser Leu Ala Ala Leu  
 65 70 75 80  
 Phe Ser Leu Ile Val Leu Gly Val Gly Ala Leu Val Leu Leu Tyr Cys  
 85 90 95  
 Trp Gly Tyr Phe Asp Ser Asn Ala Gly Arg Leu Ser Ala Phe Gly Ala  
 100 105 110  
 Glu Leu Val Ala Phe Ala Met Ala Met Phe Gly Leu Val Ile Ser Asp  
 115 120 125  
 Asn Ile Leu Leu Met Tyr Val Phe Trp Glu Ile Thr Ser Val Leu Ser  
 130 135 140  
 Phe Leu Leu Val Gly Tyr Tyr Gly Glu Arg Ala Ser Ser Arg Arg Ser  
 145 150 155 160  
 Ala Gly Gln Ala Leu Met Val Thr Thr Leu Gly Gly Leu Ala Met Leu  
 165 170 175  
 Val Gly Ile Ile Leu Met Gly Thr Gln Thr Gly Val Trp Arg Phe Ser  
 180 185 190  
 Glu Ile Pro Ala Tyr Ser Ser Ser Trp Ala Asp Val Pro Tyr Ile Ser  
 195 200 205  
 Ala Ala Ala Ala Leu Ile Leu Ala Gly Ala Leu Ser Lys Ser Ala Ile  
 210 215 220  
 Ala Pro Thr His Phe Trp Leu Pro Gly Ala Met Ala Ala Pro Thr Pro  
 225 230 235 240  
 Val Ser Ala Tyr Leu His Ser Ala Ala Met Val Lys Ala Gly Ile Tyr  
 245 250 255  
 Leu Val Ala Arg Leu Ser Pro Asp Leu Asn Val Val Gly Ser Trp Tyr  
 260 265 270  
 Leu Ile Ile Ile Pro Leu Gly Met Leu Thr Met Leu Met  
 275 280 285

&lt;210&gt; 695

&lt;211&gt; 927

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

09602740-062300



<400> 695

**SECRET**



200	205	210	
ttc tgc ctc acc aca tcc atg ggt tgg gat ctc ggc cgc gcc ttc ttc			787
Phe Cys Leu Thr Thr Ser Met Gly Trp Asp Leu Gly Arg Ala Phe Phe			
215	220	225	
acc tca gtg cta tta ctg ctc aca gcc aaa ccc gtt tta ggt gct tta			835
Thr Ser Val Leu Leu Leu Thr Ala Lys Pro Val Leu Gly Ala Leu			
230	235	240	245
cga cgc gcc agc cgc cgc gcc gct ttc ggc gtc gag cgt gac ttc ggg			883
Arg Arg Ala Ser Arg Arg Ala Ala Phe Gly Val Glu Arg Asp Phe Gly			
250	255	260	
gag gcc ggg gtg cct cgg gtc taaagatttt gttggcttgc ttc			927
Glu Ala Gly Val Pro Arg Val			
265			

&lt;210&gt; 696

&lt;211&gt; 268

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 696

Met Ile Asn Ala Ile Thr Leu Lys Pro Lys`Thr Phe Leu Thr Leu Ser			
1	5	10	15
Phe Leu Ala Val Leu Ser Ile Val Ile Phe Phe Trp Pro Leu Ile Val			
20	25	30	
Asn Pro Glu Ser Phe Leu Ser Asp Lys Ala Gln Ala Pro Leu Tyr Ile			
35	40	45	
Ala Ile Val Ile Pro Leu Val Leu Ala Ala Val Ile Ala Glu Ile Ser			
50	55	60	
Glu Asn Gly Phe Asp Val Lys Ala Val Ala Met Leu Gly Val Leu Thr			
65	70	75	80
Ala Met Val Ala Val Val Arg Pro Phe Gly Ala Gly Ala Ala Gly Phe			
85	90	95	
Glu Ala Val Phe Phe Val Leu Ile Leu Gly Gly Arg Ala Phe Gly Pro			
100	105	110	
Gly Phe Gly Phe Ile Leu Gly Asn Thr Gly Leu Phe Ala Ser Ala Leu			
115	120	125	
Leu Thr Ala Gly Ile Gly Pro Trp Leu Pro Tyr Gln Met Leu Ala Ala			
130	135	140	
Ala Trp Val Ser Phe Gly Ala Gly Leu Leu Pro Gln Val Arg Gly Lys			
145	150	155	160
Lys Glu Met Leu Ile Ile Val Leu Tyr Ala Ile Val Ser Ser Leu Gly			
165	170	175	
Tyr Gly Thr Met Met Asn Met Ser Phe Trp Pro Tyr Ala Ile Gly Val			
180	185	190	

09602740-062300



```
<210> 697
<211> 1587
<212> DNA
<213> Corynebacterium glutamicum
```

<400> 697																
agacccaaga gtaaaatccc aggatttgct tatacttgcg ctcatggata atcaacttcg																60
tcccacttttg cattatcaag ctcaaaaccc gcaccggcga																115
Val 1																Gly 5
gcg aca ggc tac att ggc ggc agg ttg att act gag tta ctt gct gcc																163
Ala Thr Gly Tyr Ile Gly Gly Arg Leu Ile Thr Glu Leu Leu Ala Ala																20
10 15																
ggt ttc caa gtt cgg gcc acc tcg agg aaa aaa aca agt ctt cag cgc																211
Gly Phe Gln Val Arg Ala Thr Ser Arg Lys Lys Thr Ser Leu Gln Arg																35
25 30																
ttt gac tgg tac gag gac gtc gag gca gtg gaa gcg gat ctg act gac																259
Phe Asp Trp Tyr Glu Asp Val Glu Ala Val Glu Ala Asp Leu Thr Asp																50
40 45																
gcg act gag tta gat acg tta ttt aag gat gta gac gtt gtt tac tat																307
Ala Thr Glu Leu Asp Thr Leu Phe Lys Asp Val Asp Val Val Tyr Tyr																65
55 60																
cta gtg cat tcc atg gga ggt aag aat gtt gat ttt gaa gag caa gag																355
Leu Val His Ser Met Gly Gly Lys Asn Val Asp Phe Glu Glu Gln Glu																85
70 75 80																
caa cgc act gct gaa aat gta att caa gct gct gat caa gcc ggg ata																403
Gln Arg Thr Ala Glu Asn Val Ile Gln Ala Ala Asp Gln Ala Gly Ile																100
90 95																
aaa cag att gtc tac ctt tcc ggc tta cac ccg cgt aat cga aaa ata																451
Lys Gln Ile Val Tyr Leu Ser Gly Leu His Pro Arg Asn Arg Lys Ile																115
105 110																

**SECRET**



gaa Glu	gaa Glu	cta Leu 120	tct Ser	aag Lys	cac His	atg Met	cgc Arg 125	tca Ser	cgg Arg	gaa Glu	aag Lys	gtc Val 130	gcc Ala	cag Gln	att Ile	499
ttg Leu	ctg Leu 135	gca Ala	ggc Gly	cag Gln	aca Thr	cca Pro 140	gct Ala	tta Leu	att Ile	tta Leu	agg Arg 145	gct Ala	gcc Ala	aca Thr	att Ile	547
att Ile 150	ggg Gly	tcc Ser	ggc Gly	tct Ser	gca Ala 155	tca Ser	ttt Phe	gaa Glu	ata Ile	atc Ile 160	cgt Arg	cat His	ctc Leu	acg Thr	gag Glu 165	595
cgt Arg	ttg Leu	cct Pro	aga Arg	atg Met 170	ata Ile	gcg Ala	cct Pro	cag Gln	tgg Trp 175	att Ile	act Thr	aat Asn	cag Gln	att Ile 180	gag Glu	643
cct Pro	tta Leu	gca Ala 185	ata Ile	cgg Arg	gat Asp	gtt Val	ttg Leu	cat His 190	tac Tyr	cta Leu	atc Ile	tcg Ser	gcg Ala 195	gct Ala	gat Asp	691
tta Leu	aag Lys 200	gat Asp	cca Pro	gtc Val	aac Asn	cgc Arg	tcc Ser 205	tgc Cys	gat Asp	att Ile	ggg Gly 210	tgt Cys	gga Gly	aag Lys	tcg Ser	739
tat Tyr 215	gaa Glu	ttt Phe	gcg Ala	gat Asp	cta Leu	ttg Leu 220	cgt Arg	atc Ile	tat Tyr	gcc Ala 225	gat Asp	gtt Val	cgg Arg	gga Gly	ctg Leu	787
aaa Lys 230	cgt Arg	cat His	gta Val	aat Asn	tcc Ser 235	gta Val	cct Pro	ctc Leu	aat Asn	ttg Leu 240	ccc Pro	atg Met	gac Asp	aag Lys	cta Leu 245	835
tcc Ser	ggg Gly	ctt Leu	tgg Trp	att Ile 250	agt Ser	cta Leu	gtg Val	aca Thr	cct Pro 255	gtt Val	cca Pro	ttt Phe	caa Gln	ttg Leu 260	tct Ser	883
ttc Phe	cct Pro	tta Leu	gct Ala 265	caa Gln	tca Ser	atg Met	gct Ala	gag Glu 270	gat Asp	gcc Ala	gtc Val	act Thr	gaa Glu 275	gag Glu	cac His	931
agc Ser	att Ile	aaa Lys 280	gat Asp	att Ile	att Ile	tca Ser	gat Asp 285	cca Pro	ccc Pro	gat Asp	ggg Gly 290	ttt Phe	att Ile	gag Glu	tat Tyr	979
cgg Arg	gaa Glu 295	gca Ala	gtg Val	gag Glu	ctg Leu	gca Ala 300	tta Leu	gct Ala	gca Ala	gaa Glu	ttt Phe 305	gat Asp	cgt Arg	gga Gly	gtt Val	1027
cca Pro 310	acg Thr	tca Ser	tgg Trp	gat Asp	cga Arg 315	agc Ser	tgg Trp	act Thr	gta Val	caa Gln 320	caa Gln	ccg Pro	tgg Trp	gct Ala	ggc Gly 325	1075
cag Gln	cct Pro	acc Thr	gat Asp	cca Pro 330	gag Glu	tgg Trp	gcg Ala	ggc Gly	aaa Lys 335	gct Ala	gta Val	tat Tyr	gaa Glu	gac Asp	gtc Val	1123
cgc Arg	aca Thr	gaa Glu 345	gat Asp	act Thr	gat Asp	ctc Leu	cga Arg	gca Ala 350	gcg Ala	cag Gln	gtc Val	tgg Trp	ccg Pro 355	atc Ile	att Ile	1171
gaa	ggg	ttg	ggg	ggc	gtg	aac	ggc	tgg	tat	tct	gca	cca	ctg	cta	tgg	1219



Glu Gly Leu Gly Gly Val Asn Gly Trp Tyr Ser Ala Pro Leu Leu Trp  
           360                          365                          370  
 cga ttg cgg ggt atc gct gac aga ctc atc ggc ggt cca ggt ttg ggc 1267  
 Arg Leu Arg Gly Ile Ala Asp Arg Leu Ile Gly Gly Pro Gly Leu Gly  
           375                          380                          385  
 gga cgg cgg gat ccc cgt cat ttg aaa ctt ggg gat cgc att gat tgg 1315  
 Gly Arg Arg Asp Pro Arg His Leu Lys Leu Gly Asp Arg Ile Asp Trp  
           390                          395                          400                          405  
 tgg cgg gtt act gag atc gat cca cca cat aga tta gtg ctc acc gca 1363  
 Trp Arg Val Thr Glu Ile Asp Pro Pro His Arg Leu Val Leu Thr Ala  
                           410                          415                          420  
 gag atg aaa gta gat ggt ggc gct tgg ctg atc ctg gaa gtt gcg gac 1411  
 Glu Met Lys Val Asp Gly Gly Ala Trp Leu Ile Leu Glu Val Ala Asp  
                           425                          430                          435  
 aag gaa aat ggc gga tgt act tat acc cag cgc gca ata ttt gag ccg 1459  
 Lys Glu Asn Gly Gly Cys Thr Tyr Thr Gln Arg Ala Ile Phe Glu Pro  
                           440                          445                          450  
 aag ggt ttg ccc ggt tat ctc tat tgg tgg gtt gtt tca ccg ttc cat 1507  
 Lys Gly Leu Pro Gly Tyr Leu Tyr Trp Trp Val Val Ser Pro Phe His  
           455                          460                          465  
 gcg att att ttt cct tat atg cgt tcg aat att tta aaa gct gcg cgt 1555  
 Ala Ile Ile Phe Pro Tyr Met Arg Ser Asn Ile Leu Lys Ala Ala Arg  
           470                          475                          480                          485  
 aaa ctc act taatcgacaga gtaggcgtct aaa 1587  
 Lys Leu Thr

&lt;210&gt; 698

&lt;211&gt; 488

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 698

Val Leu Val Thr Gly Ala Thr Gly Tyr Ile Gly Gly Arg Leu Ile Thr  
   1                          5                          10                          15  
 Glu Leu Leu Ala Ala Gly Phe Gln Val Arg Ala Thr Ser Arg Lys Lys  
           20                          25                          30  
 Thr Ser Leu Gln Arg Phe Asp Trp Tyr Glu Asp Val Glu Ala Val Glu  
           35                          40                          45  
 Ala Asp Leu Thr Asp Ala Thr Glu Leu Asp Thr Leu Phe Lys Asp Val  
           50                          55                          60  
 Asp Val Val Tyr Tyr Leu Val His Ser Met Gly Gly Lys Asn Val Asp  
           65                          70                          75                          80  
 Phe Glu Glu Gln Glu Gln Arg Thr Ala Glu Asn Val Ile Gln Ala Ala  
                           85                          90                          95  
 Asp Gln Ala Gly Ile Lys Gln Ile Val Tyr Leu Ser Gly Leu His Pro

002290"04730960



100					105					110					
Arg	Asn	Arg	Lys	Ile	Glu	Glu	Leu	Ser	Lys	His	Met	Arg	Ser	Arg	Glu
	115						120					125			
Lys	Val	Ala	Gln	Ile	Leu	Leu	Ala	Gly	Gln	Thr	Pro	Ala	Leu	Ile	Leu
	130					135					140				
Arg	Ala	Ala	Thr	Ile	Ile	Gly	Ser	Gly	Ser	Ala	Ser	Phe	Glu	Ile	Ile
145					150					155					160
Arg	His	Leu	Thr	Glu	Arg	Leu	Pro	Arg	Met	Ile	Ala	Pro	Gln	Trp	Ile
				165					170					175	
Thr	Asn	Gln	Ile	Glu	Pro	Leu	Ala	Ile	Arg	Asp	Val	Leu	His	Tyr	Leu
			180					185					190		
Ile	Ser	Ala	Ala	Asp	Leu	Lys	Asp	Pro	Val	Asn	Arg	Ser	Cys	Asp	Ile
		195					200					205			
Gly	Cys	Gly	Lys	Ser	Tyr	Glu	Phe	Ala	Asp	Leu	Leu	Arg	Ile	Tyr	Ala
	210					215					220				
Asp	Val	Arg	Gly	Leu	Lys	Arg	His	Val	Asn	Ser	Val	Pro	Leu	Asn	Leu
225					230					235					240
Pro	Met	Asp	Lys	Leu	Ser	Gly	Leu	Trp	Ile	Ser	Leu	Val	Thr	Pro	Val
				245					250					255	
Pro	Phe	Gln	Leu	Ser	Phe	Pro	Leu	Ala	Gln	Ser	Met	Ala	Glu	Asp	Ala
			260					265					270		
Val	Thr	Glu	Glu	His	Ser	Ile	Lys	Asp	Ile	Ile	Ser	Asp	Pro	Pro	Asp
		275					280					285			
Gly	Phe	Ile	Glu	Tyr	Arg	Glu	Ala	Val	Glu	Leu	Ala	Leu	Ala	Ala	Glu
	290					295					300				
Phe	Asp	Arg	Gly	Val	Pro	Thr	Ser	Trp	Asp	Arg	Ser	Trp	Thr	Val	Gln
305					310					315					320
Gln	Pro	Trp	Ala	Gly	Gln	Pro	Thr	Asp	Pro	Glu	Trp	Ala	Gly	Lys	Ala
				325					330					335	
Val	Tyr	Glu	Asp	Val	Arg	Thr	Glu	Asp	Thr	Asp	Leu	Arg	Ala	Ala	Gln
			340					345					350		
Val	Trp	Pro	Ile	Ile	Glu	Gly	Leu	Gly	Gly	Val	Asn	Gly	Trp	Tyr	Ser
		355					360					365			
Ala	Pro	Leu	Leu	Trp	Arg	Leu	Arg	Gly	Ile	Ala	Asp	Arg	Leu	Ile	Gly
	370					375					380				
Gly	Pro	Gly	Leu	Gly	Gly	Arg	Arg	Asp	Pro	Arg	His	Leu	Lys	Leu	Gly
385					390					395					400
Asp	Arg	Ile	Asp	Trp	Trp	Arg	Val	Thr	Glu	Ile	Asp	Pro	Pro	His	Arg
				405					410					415	
Leu	Val	Leu	Thr	Ala	Glu	Met	Lys	Val	Asp	Gly	Gly	Ala	Trp	Leu	Ile
			420					425					430		

09602740-062300



<400> 699																
agaccaaga gtaaaatccc aggatttgct tatacttgcg ctcatggata atcaacttcg																60
tcccacttttg cattatcaag ctcaaaaccc gcaccggcga																115
Val 1 Leu 1 Val 1 Thr 5 Gly 5																
gcg aca ggc tac att ggc ggc agg ttg att act gag tta ctt gct gcc																163
Ala Thr Gly Tyr Ile Gly Gly Arg Leu Ile Thr Glu Leu Leu Ala Ala																
10 15 20																
ggt ttc caa gtt cgg gcc acc tcg agg aaa aaa aca agt ctt cag cgc																211
Gly Phe Gln Val Arg Ala Thr Ser Arg Lys Lys Thr Ser Leu Gln Arg																
25 30 35																
ttt gac tgg tac gag gac gtc gag gca gtg gaa gcg gat ctg act gac																259
Phe Asp Trp Tyr Glu Asp Val Glu Ala Val Glu Ala Asp Leu Thr Asp																
40 45 50																
gcg act gag gta gat acg tta ttt aag gat gta gac gtt gtt tac tat																307
Ala Thr Glu Leu Asp Thr Leu Phe Lys Asp Val Asp Val Val Tyr Tyr																
55 60 65																
cta gtg cat tcc atg gga ggt aag aat gtt gat ttt gaa gag caa gag																355
Leu Val His Ser Met Gly Gly Lys Asn Val Asp Phe Glu Glu Gln Glu																
70 75 80 85																
caa cgc act gct gaa aat gta att caa gct gct gat caa gcc ggg ata																403
Gln Arg Thr Ala Glu Asn Val Ile Gln Ala Ala Asp Gln Ala Gly Ile																
90 95 100																
aaa cag att gtc tac ctt tcc ggc tta cac ccg cgt aat cga aaa ata																451
Lys Gln Ile Val Tyr Leu Ser Gly Leu His Pro Arg Asn Arg Lys Ile																
105 110 115																
gaa gaa cta tct aag cac atg cgc tca cgg gaa aag gtc gcc cag att																499
Glu Glu Leu Ser Lys His Met Arg Ser Arg Glu Lys Val Ala Gln Ile																



**06-07-2018**



[illegible]

```
<210> 700
<211> 488
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 700															
Val	Leu	Val	Thr	Gly	Ala	Thr	Gly	Tyr	Ile	Gly	Gly	Arg	Leu	Ile	Thr
1				5					10					15	
Glu	Leu	Leu	Ala	Ala	Gly	Phe	Gln	Val	Arg	Ala	Thr	Ser	Arg	Lys	Lys
			20					25					30		
Thr	Ser	Leu	Gln	Arg	Phe	Asp	Trp	Tyr	Glu	Asp	Val	Glu	Ala	Val	Glu
		35					40					45			
Ala	Asp	Leu	Thr	Asp	Ala	Thr	Glu	Leu	Asp	Thr	Leu	Phe	Lys	Asp	Val
	50					55					60				
Asp	Val	Val	Tyr	Tyr	Leu	Val	His	Ser	Met	Gly	Gly	Lys	Asn	Val	Asp
65					70					75					80
Phe	Glu	Glu	Gln	Glu	Gln	Arg	Thr	Ala	Glu	Asn	Val	Ile	Gln	Ala	Ala
				85					90					95	
Asp	Gln	Ala	Gly	Ile	Lys	Gln	Ile	Val	Tyr	Leu	Ser	Gly	Leu	His	Pro
			100					105					110		

**060970** **Z** **O** **C** **I** **S** **E** **R** **A** **T** **I** **O** **N** **S**







<400> 701															
attgctctca tcgggttcgat atagactgaa ttgtctaggt taatatccaa tatggaagaa 60															
aaactagaca gttaagtaga ctgaatggcc tactaggtgc atg act tca gca atc 115															
Met Thr Ser Ala Ile 1 5															
acc acc gca act gat ctt cgc tcc gta ctg cga aac gta cca acc cca 163															
Thr Thr Ala Thr Asp Leu Arg Ser Val Leu Arg Asn Val Pro Thr Pro 10 15 20															
att agc ttc att gca acc cac acc gat cag cct ctg ggc atg atc gtt 211															
Ile Ser Phe Ile Ala Thr His Thr Asp Gln Pro Leu Gly Met Ile Val 25 30 35															
ggt tca ttc gtc agc att agc gcc gaa cca cca ttg gta ggc atc ttc 259															
Gly Ser Phe Val Ser Ile Ser Ala Glu Pro Pro Leu Val Gly Ile Phe 40 45 50															
ttg cag aag agc tct tct tca tgg cca gct atc gag cag gca tta gtt 307															
Leu Gln Lys Ser Ser Ser Ser Trp Pro Ala Ile Glu Gln Ala Leu Val 55 60 65															
acc ggc caa gag cta ggc att tct atc ctc ggc ggg gca cac gca gac 355															
Thr Gly Gln Glu Leu Gly Ile Ser Ile Leu Gly Gly Ala His Ala Asp 70 75 80 85															
cat gtg cgt aag ctt tct ggc cca tcc gac cag cgc ttt gaa aac ctt 403															
His Val Arg Lys Leu Ser Gly Pro Ser Asp Gln Arg Phe Glu Asn Leu 90 95 100															
ggg tgg gca tcc acc gaa aac ggt gcg att cac ctt gaa ggc gct gat 451															
Gly Trp Ala Ser Thr Glu Asn Gly Ala Ile His Leu Glu Gly Ala Asp 105 110 115															
gca caa cta acc acg aaa ctt cat gat ctc cag gaa atc ggc gat cac 499															
Ala Gln Leu Thr Thr Lys Leu His Asp Leu Gln Glu Ile Gly Asp His 120 125 130															

[illegible]




agc tca gcg ctg gtg tac cac cgc tca cag gtg tcc tcg ctg 589  
 Ser Ser Ala Leu Val Tyr His Arg Ser Gln Val Ser Ser Leu  
 150 155 160

```
<210> 702
<211> 163
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 702															
Met 1	Thr	Ser	Ala	Ile 5	Thr	Thr	Ala	Thr	Asp 10	Leu	Arg	Ser	Val	Leu 15	Arg
Asn	Val	Pro	Thr 20	Pro	Ile	Ser	Phe	Ile 25	Ala	Thr	His	Thr	Asp 30	Gln	Pro
Leu	Gly	Met 35	Ile	Val	Gly	Ser	Phe 40	Val	Ser	Ile	Ser	Ala 45	Glu	Pro	Pro
Leu 50	Val	Gly	Ile	Phe	Leu	Gln 55	Lys	Ser	Ser	Ser	Ser 60	Trp	Pro	Ala	Ile
Glu 65	Gln	Ala	Leu	Val	Thr 70	Gly	Gln	Glu	Leu	Gly 75	Ile	Ser	Ile	Leu	Gly 80
Gly	Ala	His	Ala	Asp 85	His	Val	Arg	Lys	Leu 90	Ser	Gly	Pro	Ser	Asp 95	Gln
Arg	Phe	Glu	Asn 100	Leu	Gly	Trp	Ala	Ser 105	Thr	Glu	Asn	Gly	Ala 110	Ile	His
Leu	Glu	Gly 115	Ala	Asp	Ala	Gln 120	Leu	Thr	Thr	Lys	Leu 125	His	Asp	Leu	Gln
Glu 130	Ile	Gly	Asp	His	Phe	Phe 135	Ala	Val	Leu	Glu	Val 140	Ile	Asp	Ala	Ser
Ala 145	Asp	Gln	Asp	Phe	Ser 150	Ser	Ala	Leu	Val	Tyr 155	His	Arg	Ser	Gln	Val 160
Ser	Ser	Leu													

```
<210> 703
<211> 1134
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(1111)  
<223> RXA00288
```





ggcgtgctaa aaaagcacgt caaatacaga atcggcagat tacatcgctg agcagagaaa 60

agt gag caa atc tcc gac gtg gat ttt gtt ttc agc tcg tgg act act 787  
Ser Glu Gln Ile Ser Asp Val Asp Phe Val Phe Ser Ser Trp Thr Thr

[illegible]



Gln Val Val Asp Glu Arg Leu Val Gly His Ala Pro Gln Ser Leu Gly



115						120						125					
Ala	His	Asp	Ala	Ala	Ala	Leu	Pro	Leu	Val	Ala	Leu	Thr	Ala	Trp	Glu		
130						135						140					
Ser	Leu	Phe	Asp	Arg	Leu	Gly	Val	Thr	Gln	Ser	Thr	Thr	Gly	Thr	Leu		
145						150						155					
Leu	Val	Leu	Gly	Gly	Ser	Gly	Gly	Val	Pro	Ser	Ala	Leu	Ile	Gln	Leu		
				165						170							
Ala	Arg	Ala	Leu	Thr	Gly	Leu	Lys	Val	Val	Ala	Thr	Ala	Ser	Arg	Pro		
			180					185					190				
Glu	Ser	Gln	Glu	Trp	Val	Thr	Lys	Leu	Gly	Ala	His	Glu	Val	Ile	Asp		
		195						200				205					
His	Ser	Lys	Asp	Leu	Ser	Glu	Gln	Ile	Ser	Asp	Val	Asp	Phe	Val	Phe		
210						215						220					
Ser	Ser	Trp	Thr	Thr	Gly	Arg	Glu	Val	Glu	Leu	Ala	Thr	Leu	Met	Lys		
225						230						235					
Pro	Gln	Ser	His	Leu	Val	Leu	Ile	Asp	Asp	Pro	Val	Asp	Pro	Asn	Leu		
				245						250							
Gly	Ala	Phe	Lys	Gln	Lys	Ala	Ile	Ala	Leu	His	Trp	Glu	Phe	Met	Phe		
			260						265					270			
Thr	Arg	Ala	Met	Phe	Asn	Thr	Pro	Asp	Met	Gly	Glu	Gln	Gly	Lys	Ile		
			275						280				285				
Leu	Asn	Lys	Ile	Ala	Asp	Met	Val	Asp	Arg	Gly	Gln	Phe	Glu	Ser	Val		
290						295						300					
Thr	Ala	Thr	Val	Leu	Asp	Gly	Leu	Asn	Ala	Ala	Asn	Ile	Met	Glu	Gly		
305						310						315					
His	Arg	Leu	Val	Glu	Gln	Gly	Lys	Thr	Ser	Gly	Lys	Ile	Val	Val	Arg		
				325						330							
335																	

Val

```
<210> 705
<211> 1089
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(1066)  
<223> RXA02741
```

<400> 705  
actggtcacc tggtttggtc tgcactctga ctccctcaa aagggcacaa tttggtcaat 60

ttcccaacct tgtctttcag tcatggttag tgtgggaacc atg aag gca atc tta 115  
Met Lys Ala Ile Leu  
1 5



gtt tcc cgc acc ggc gga cca gag gtg ttg gag ttc acc gac act gac 163  
 Val Ser Arg Thr Gly Gly Pro Glu Val Leu Glu Phe Thr Asp Thr Asp  
 10 15 20

gcc cca aag ccc act gat gat cag gtt tta gtt gaa gtt gat atg gct 211  
 Ala Pro Lys Pro Thr Asp Asp Gln Val Leu Val Glu Val Asp Met Ala  
 25 30 35

ggc gtc aac ttt att gat act tac tat cgc cag ggt gaa tat cac gct 259  
 Gly Val Asn Phe Ile Asp Thr Tyr Tyr Arg Gln Gly Glu Tyr His Ala  
 40 45 50

cgc ctg ccg ttt atc cca ggt ttt gaa ggc act ggt cgg gtg ttg gag 307  
 Arg Leu Pro Phe Ile Pro Gly Phe Glu Gly Thr Gly Arg Val Leu Glu  
 55 60 65

gat ccg cag ggg ttg att gcg gcg ggt acc aag gtg gcg tgg tgt gat 355  
 Asp Pro Gln Gly Leu Ile Ala Ala Gly Thr Lys Val Ala Trp Cys Asp  
 70 75 80 85

gcc atg ggt tcg tat gct cag cag gtg tgt gtg ccg cgg gat cgc ttg 403  
 Ala Met Gly Ser Tyr Ala Gln Gln Val Cys Val Pro Arg Asp Arg Leu  
 90 95 100

gtg gcg gtt ccc gag ggc gtg agt tcg gaa gtg gct gcg tcg atg ttg 451  
 Val Ala Val Pro Glu Gly Val Ser Ser Glu Val Ala Ala Ser Met Leu  
 105 110 115

atg cag gga atc act gcg cat tat cta acc aat ggt gtg tat gag ctt 499  
 Met Gln Gly Ile Thr Ala His Tyr Leu Thr Asn Gly Val Tyr Glu Leu  
 120 125 130

gaa gag ggc gat tct tgc ctc atc act gct ggc gcg ggt ggt gtt gga 547  
 Glu Glu Gly Asp Ser Cys Leu Ile Thr Ala Gly Ala Gly Gly Val Gly  
 135 140 145

ttg ttg gct acg cag atg gcg gcg gcc aag gga gtg cgc gtg tac agc 595  
 Leu Leu Ala Thr Gln Met Ala Ala Ala Lys Gly Val Arg Val Tyr Ser  
 150 155 160 165

gtg gtg tcc acg gat gaa aaa gct gag ctt gct ttg gat gcc ggt gct 643  
 Val Val Ser Thr Asp Glu Lys Ala Glu Leu Ala Leu Asp Ala Gly Ala  
 170 175 180

tat gag gtg ttt cgt tat tcc gat aat ttg gcg gag cag gtt cgt cgg 691  
 Tyr Glu Val Phe Arg Tyr Ser Asp Asn Leu Ala Glu Gln Val Arg Arg  
 185 190 195

cac aac ggg ggt cgc gga gtt gat gtg gtg tat gac ggt gtc ggc cag 739  
 His Asn Gly Gly Arg Gly Val Asp Val Val Tyr Asp Gly Val Gly Gln  
 200 205 210

tcc acg ttc aat gag tcc tta gag gct gtt cgt ccg cgc ggc act gtg 787  
 Ser Thr Phe Asn Glu Ser Leu Glu Ala Val Arg Pro Arg Gly Thr Val  
 215 220 225

tgt ttg ttt ggt gcg gcg tcg ggt cct gtg gag cct ttt gat ccg cag 835  
 Cys Leu Phe Gly Ala Ala Ser Gly Pro Val Glu Pro Phe Asp Pro Gln  
 230 235 240 245

09602740-062300



ctg ttg aac act cac ggt tcg atc ttc ttg acc cgc cca agc att ggc 883  
 Leu Leu Asn Thr His Gly Ser Ile Phe Leu Thr Arg Pro Ser Ile Gly  
                   250                  255                  260

gcg tgg acg tct gag gag ggc gaa ttt gcc aag cgt gca cag gcg gtc 931  
 Ala Trp Thr Ser Glu Glu Gly Glu Phe Ala Lys Arg Ala Gln Ala Val  
                   265                  270                  275

acg cag gcc atc gtc gaa ggc acc ttg cgg gtt cgc gtt act ggc aca 979  
 Thr Gln Ala Ile Val Glu Gly Thr Leu Arg Val Arg Val Thr Gly Thr  
                   280                  285                  290

tat tcg ctt gcc gac gcc tac atc gcc cac cgc gac ctt cag gcg cgt 1027  
 Tyr Ser Leu Ala Asp Ala Tyr Ile Ala His Arg Asp Leu Gln Ala Arg  
                   295                  300                  305

agc acg agc ggt tct ttg gtc ttg gaa atc ccg aag gac taaacacgca 1076  
 Ser Thr Ser Gly Ser Leu Val Leu Glu Ile Pro Lys Asp  
 310                  315                  320

taaaaagatc ctg 1089

&lt;210&gt; 706

&lt;211&gt; 322

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 706

Met Lys Ala Ile Leu Val Ser Arg Thr Gly Gly Pro Glu Val Leu Glu  
 1                  5                  10                  15

Phe Thr Asp Thr Asp Ala Pro Lys Pro Thr Asp Asp Gln Val Leu Val  
                   20                  25                  30

Glu Val Asp Met Ala Gly Val Asn Phe Ile Asp Thr Tyr Tyr Arg Gln  
                   35                  40                  45

Gly Glu Tyr His Ala Arg Leu Pro Phe Ile Pro Gly Phe Glu Gly Thr  
                   50                  55                  60

Gly Arg Val Leu Glu Asp Pro Gln Gly Leu Ile Ala Ala Gly Thr Lys  
                   65                  70                  75                  80

Val Ala Trp Cys Asp Ala Met Gly Ser Tyr Ala Gln Gln Val Cys Val  
                   85                  90                  95

Pro Arg Asp Arg Leu Val Ala Val Pro Glu Gly Val Ser Ser Glu Val  
                   100                  105                  110

Ala Ala Ser Met Leu Met Gln Gly Ile Thr Ala His Tyr Leu Thr Asn  
                   115                  120                  125

Gly Val Tyr Glu Leu Glu Glu Gly Asp Ser Cys Leu Ile Thr Ala Gly  
                   130                  135                  140

Ala Gly Gly Val Gly Leu Leu Ala Thr Gln Met Ala Ala Ala Lys Gly  
                   145                  150                  155                  160

Val Arg Val Tyr Ser Val Val Ser Thr Asp Glu Lys Ala Glu Leu Ala  
                   165                  170                  175

09602740-052300







cgc agg tgg ttg gat aaa ccg gtt gat gat gac acc atc cgc acc att 307  
 Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp Thr Ile Arg Thr Ile  
 55 60 65

att tcc gcc gca caa tcg gct gga acc tct tcc aat aag cag gtc att 355  
 Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser Asn Lys Gln Val Ile  
 70 75 80 85

tct gtc atc gtg gtt aaa gat cct gag ctg agg aaa ggc ctc gcg ggg 403  
 Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg Lys Gly Leu Ala Gly  
 90 95 100

atc act cgc cag atg ttt ccg cac ctt gag cag gtt ccc gcg gtg ctg 451  
 Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln Val Pro Ala Val Leu  
 105 110 115

att tgg ttg att gat tat tcc cga atc agt gcg gtg gca gcc aga gaa 499  
 Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala Val Ala Ala Arg Glu  
 120 125 130

gat ctc cca aca ggg gct ctt gat tat ctc gat gag gcc gcg tgg ggg 547  
 Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp Glu Ala Ala Trp Gly  
 135 140 145

ttc ctc gac gcc gga atc gca gct caa aac gct gca att gct gcg gag 595  
 Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala Ala Ile Ala Ala Glu  
 150 155 160 165

tca ctt gga ttg gga acg ctc tat ttg ggt tcg gtg cgc aac gat gcg 643  
 Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser Val Arg Asn Asp Ala  
 170 175 180

gaa gcc gtg cac aaa ttg ctt ggc ctt cca cct gag atc gtg cct gtc 691  
 Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro Glu Ile Val Pro Val  
 185 190 195

gtg ggc ttg gaa atg ggg cat gcg gat ccg cct gaa cct gcc gga att 739  
 Val Gly Leu Glu Met Gly His Ala Asp Pro Pro Glu Pro Ala Gly Ile  
 200 205 210

aaa cct ccc ctg cca caa gaa gcc att gtt cac tgg gat acc tac acc 787  
 Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His Trp Asp Thr Tyr Thr  
 215 220 225

gag aaa aac ctc gaa ctt atc gat tcc tac gac cgc gcc ctc gac act 835  
 Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp Arg Ala Leu Asp Thr  
 230 235 240 245

tac tat tct cgc tac ggc cag cac cag ctc tgg tcg aag cag acg gcg 883  
 Tyr Tyr Ser Arg Tyr Gly Gln His Gln Leu Trp Ser Lys Gln Thr Ala  
 250 255 260

cat agg gcg gcg tcg aaa agc ttt tca aaa acc aac agg cag ttc ctt 931  
 His Arg Ala Ala Ser Lys Ser Phe Ser Lys Thr Asn Arg Gln Phe Leu  
 265 270 275

agg ggc gtg ttt gag cgc gcc ggg ttt ggg ctg aga taaaagcatg 977  
 Arg Gly Val Phe Glu Arg Ala Gly Phe Gly Leu Arg  
 280 285

attatggacg cct 990

09602740-062300



<400>	708														
Met 1	Gln	Gly	Asn	Ser 5	Leu	Asn	Leu	Ala	Asp 10	Asn	Ser	Glu	Arg	Lys 15	Lys
Pro	Met	Pro	Ser 20	Pro	Gly	Glu	Leu	Leu	Ala 25	Ala	Arg	Tyr	Gly 30	Gln	Pro
Ala	Thr	Trp 35	Thr	Pro	Pro	Gln	Trp 40	Asn	Glu	Thr	Leu	Asp 45	Val	Ile	His
Gln	His 50	Arg	Ser	Val	Arg	Arg 55	Trp	Leu	Asp	Lys	Pro 60	Val	Asp	Asp	Asp
Thr 65	Ile	Arg	Thr	Ile	Ile 70	Ser	Ala	Ala	Gln	Ser 75	Ala	Gly	Thr	Ser	Ser 80
Asn	Lys	Gln	Val	Ile 85	Ser	Val	Ile	Val	Val 90	Lys	Asp	Pro	Glu	Leu 95	Arg
Lys	Gly	Leu	Ala 100	Gly	Ile	Thr	Arg	Gln	Met 105	Phe	Pro	His	Leu 110	Glu	Gln
Val	Pro	Ala 115	Val	Leu	Ile	Trp	Leu	Ile	Asp	Tyr	Ser	Arg 125	Ile	Ser	Ala
Val 130	Ala	Ala	Arg	Glu	Asp	Leu 135	Pro	Thr	Gly	Ala	Leu 140	Asp	Tyr	Leu	Asp
Glu 145	Ala	Ala	Trp	Gly	Phe 150	Leu	Asp	Ala	Gly	Ile 155	Ala	Ala	Gln	Asn	Ala 160
Ala	Ile	Ala	Ala	Glu 165	Ser	Leu	Gly	Leu	Gly 170	Thr	Leu	Tyr	Leu	Gly 175	Ser
Val	Arg	Asn	Asp 180	Ala	Glu	Ala	Val	His 185	Lys	Leu	Leu	Gly	Leu 190	Pro	Pro
Glu	Ile	Val 195	Pro	Val	Val	Gly	Leu 200	Glu	Met	Gly	His	Ala 205	Asp	Pro	Pro
Glu 210	Pro	Ala	Gly	Ile	Lys	Pro 215	Pro	Leu	Pro	Gln	Glu 220	Ala	Ile	Val	His
Trp 225	Asp	Thr	Tyr	Thr	Glu 230	Lys	Asn	Leu	Glu	Leu 235	Ile	Asp	Ser	Tyr	Asp 240
Arg	Ala	Leu	Asp	Thr 245	Tyr	Tyr	Ser	Arg	Tyr 250	Gly	Gln	His	Gln	Leu 255	Trp
Ser	Lys	Gln	Thr 260	Ala	His	Arg	Ala	Ala 265	Ser	Lys	Ser	Phe	Ser 270	Lys	Thr
Asn	Arg	Gln 275	Phe	Leu	Arg	Gly	Val 280	Phe	Glu	Arg	Ala	Gly 285	Phe	Gly	Leu

[illegible]



```
<210> 709
<211> 922
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(922)
<223> FRXA02560
```

<400> 709																
ttgggggcaag ccagctaacg catttcttgt ggaaaccgca gacattgagg ccgcccacgc 60																
ggaacttcta agagcagtggt aatgaaataa tccggtgctg atg cag ggc aac tcg 115																
Met Gln Gly Asn Ser 5																
ctt aat ctg gca gac aac agc gag aga aag aag ccc atg ccg tca cca 163																
Leu Asn Leu Ala Asp Asn Ser Glu Arg Lys Lys Pro Met Pro Ser Pro 20																
gga gaa ctt tta gcc gcc cgc tac gga caa cct gca acc tgg acg cca 211																
Gly Glu Leu Leu Ala Ala Arg Tyr Gly Gln Pro Ala Thr Trp Thr Pro 35																
ccg cag tgg aat gag acg ctt gat gtc att cac cag cat cga tca gtt 259																
Pro Gln Trp Asn Glu Thr Leu Asp Val Ile His Gln His Arg Ser Val 50																
cgc agg tgg ttg gat aaa ccg gtt gat gat gac acc atc cgc acc att 307																
Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp Thr Ile Arg Thr Ile 65																
att tcc gcc gca caa tcg gct gga acc tct tcc aat aag cag gtc att 355																
Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser Asn Lys Gln Val Ile 85																
tct gtc atc gtg gtt aaa gat cct gag ctg agg aaa ggc ctc gcg ggg 403																
Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg Lys Gly Leu Ala Gly 100																
atc act cgc cag atg ttt ccg cac ctt gag cag gtt ccc gcg gtg ctg 451																
Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln Val Pro Ala Val Leu 115																
att tgg ttg att gat tat tcc cga atc agt gcg gtg gca gcc aga gaa 499																
Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala Val Ala Ala Arg Glu 130																
gat ctc cca aca ggg gct ctt gat tat ctc gat gag gcc gcg tgg ggg 547																
Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp Glu Ala Ala Trp Gly 145																
ttc ctc gac gcc gga atc gca gct caa aac gct gca att gct gcg gag 595																
Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala Ala Ile Ala Ala Glu 165																

**00000000000000000000000000000000**







[illegible]

```
<210> 711
<211> 870
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(847)
<223> RXA01311
```

<400> 711																
tcgtctccgc atgggaacca ggcgagaatg gaaccttcgt ctgccacgca gaaccactgt																60
tcttcgaatc tgtcccactg cagacaagga actacaagta atg aaa ctt aca ctt																115
Met Lys Leu Thr Leu																5
gag atc tgg cgt caa gca ggc cca act gcg gaa ggc aag ttc gaa acc																163
Glu Ile Trp Arg Gln Ala Gly Pro Thr Ala Glu Gly Lys Phe Glu Thr																20
10 15																
gtc cag gtt gac gac gcc gtc gcg cag atg tcc atc ctg gag ctg ctt																211
Val Gln Val Asp Asp Ala Val Ala Gln Met Ser Ile Leu Glu Leu Leu																35
25 30																
gac cac gta aac aac aag ttc atc gaa gaa ggc aaa gaa cca ttc gcg																259
Asp His Val Asn Asn Lys Phe Ile Glu Glu Gly Lys Glu Pro Phe Ala																50
40 45																
ttc gcc tct gac tgc cgc gaa ggc att tgt ggt acc tgt ggt ctc ctc																307
Phe Ala Ser Asp Cys Arg Glu Gly Ile Cys Gly Thr Cys Gly Leu Leu																

**RECEIVED**



```
<210> 712
<211> 249
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 712  
Met Lys Leu Thr Leu Glu Ile Trp Arg Gln Ala Gly Pro Thr Ala Glu  
1 5 10 15  
Gly Lys Phe Glu Thr Val Gln Val Asp Asp Ala Val Ala Gln Met Ser



			20					25					30			
Ile	Leu	Glu 35	Leu	Leu	Asp	His	Val 40	Asn	Asn	Lys	Phe	Ile 45	Glu	Glu	Gly	
Lys	Glu 50	Pro	Phe	Ala	Phe	Ala 55	Ser	Asp	Cys	Arg	Glu 60	Gly	Ile	Cys	Gly	
Thr 65	Cys	Gly	Leu	Leu	Val 70	Asn	Gly	Arg	Pro	His 75	Gly	Ala	Asp	Gln	Asn 80	
Lys	Pro	Ala	Cys	Ala 85	Gln	Arg	Leu	Val	Ser 90	Tyr	Lys	Glu	Gly	Asp 95	Thr	
Leu	Lys	Ile	Glu 100	Pro	Leu	Arg	Ser	Ala 105	Ala	Tyr	Pro	Val	Ile 110	Lys	Asp	
Met	Val	Val 115	Asp	Arg	Ser	Ala	Leu 120	Asp	Arg	Val	Met	Glu 125	Gln	Gly	Gly	
Tyr	Val 130	Thr	Ile	Asn	Ala	Gly 135	Thr	Ala	Pro	Asp	Ala 140	Asp	Thr	Leu	His	
Val 145	Asn	His	Glu	Thr	Ala 150	Glu	Leu	Ala	Leu	Asp 155	His	Ala	Ala	Cys	Ile 160	
Gly	Cys	Gly	Ala	Cys 165	Val	Ala	Ala	Cys	Pro 170	Asn	Gly	Ala	Ala	His 175	Leu	
Phe	Thr	Gly	Ala 180	Lys	Leu	Val	His	Leu 185	Ser	Leu	Leu	Pro	Leu 190	Gly	Lys	
Glu	Glu	Arg 195	Gly	Leu	Arg	Ala	Arg 200	Lys	Met	Val	Asp	Glu 205	Met	Glu	Thr	
Asn	Phe 210	Gly	His	Cys	Ser	Leu 215	Tyr	Gly	Glu	Cys	Ala 220	Asp	Val	Cys	Pro	
Ala 225	Gly	Ile	Pro	Leu	Thr 230	Ala	Val	Ala	Ala	Val 235	Thr	Lys	Glu	Arg	Ala 240	
Arg	Ala	Ala	Phe	Arg 245	Gly	Lys	Asp	Asp								

```
<210> 713
<211> 929
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (1)..(906)  
<223> RXN03014
```

```

<400> 713
tac gtt ggt ttc gaa gtg ctg ctg gtg gcg tca tac gtg ctg ctc acc 48
Tyr Val Gly Phe Glu Val Leu Leu Val Ala Ser Tyr Val Leu Leu Thr
      1                      5              10              15

ttg ggt gca tcg ccg gca cgt gta cgt tcc gcc gtg ggt tac gtg atg 96

```



**SECRET**



```
<210> 714
<211> 302
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 714															
Tyr 1	Val	Gly	Phe	Glu 5	Val	Leu	Leu	Val	Ala 10	Ser	Tyr	Val	Leu	Leu 15	Thr
Leu	Gly	Ala	Ser 20	Pro	Ala	Arg	Val	Arg 25	Ser	Gly	Val	Gly	Tyr 30	Val	Met
Val	Ser	Met 35	Ala	Ser	Ser	Met	Val 40	Phe	Leu	Phe	Gly	Leu 45	Ala	Met	Val
Tyr 50	Ala	Ser	Val	Gly	Thr	Leu 55	Asn	Met	Ala	His	Val 60	Gly	Leu	Arg	Met
Glu 65	Asp	Val	Pro	Ser	Gly 70	Thr	Arg	Ser	Ala	Ile 75	Phe	Ala	Val	Leu	Leu 80
Val	Ala	Phe	Gly	Ile 85	Lys	Ala	Ala	Val	Phe 90	Pro	Leu	Asp	Ser	Trp 95	Leu
Pro	Asp	Ser	Tyr 100	Pro	Thr	Ala	Pro	Ser 105	Leu	Val	Thr	Ala	Val 110	Phe	Ala
Gly	Leu	Leu 115	Thr	Lys	Val	Gly	Val 120	Tyr	Ser	Ile	Ile	Arg 125	Ala	Arg	Ser
Ile 130	Ile	Phe	Thr	Asp	Gly	Ser 135	Leu	Asp	Thr	Met	Leu 140	Met	Trp	Val	Ala
Leu 145	Ala	Thr	Met	Leu	Ile 150	Gly	Ile	Leu	Gly	Ala 155	Met	Ala	Gln	Asn	Asp 160
Ile	Lys	Arg	Leu 165	Leu	Ser	Phe	Thr	Leu 170	Val	Ser	His	Ile	Gly	Tyr 175	Met
Ile	Phe	Gly	Val 180	Ala	Leu	Gly	Ser	Ala 185	Gln	Gly	Leu	Ser	Gly	Ala	Ile
Phe	Tyr	Ala 195	Ile	His	His	Ile	Leu 200	Val	Gln	Thr	Ser	Leu 205	Phe	Leu	Val
Val	Gly 210	Leu	Val	Glu	Arg	Gln 215	Ala	Gly	Ser	Ser	Ser 220	Leu	Arg	Arg	Leu

[illegible]



Gly Ser Leu Ala Tyr Ile Ser Pro Leu Leu Ala Ile Leu Tyr Phe Ile  
 225 230 235 240

Pro Ala Ile Asn Leu Gly Gly Ile Pro Pro Phe Ser Gly Phe Leu Gly  
 245 250 255

Lys Ile Met Leu Ile Glu Ala Gly Ala Arg Arg Trp Gln Leu Ala Gly  
 260 265 270

Met Gly Pro Tyr Arg Arg Arg Arg Cys His Leu Thr Ala His Leu Val  
 275 280 285

His His Gly Ser Gly Leu Val Gln Gly Leu Leu Ala Arg Pro  
 290 295 300

&lt;210&gt; 715

&lt;211&gt; 1280

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1257)

&lt;223&gt; FRXA00910

&lt;400&gt; 715

tac gtt ggt ttc gaa gtg ctg ctg gtg gcg tca tac gtg ctg ctc acc	48
Tyr Val Gly Phe Glu Val Leu Leu Val Ala Ser Tyr Val Leu Leu Thr	
1 5 10 15	
ttg ggt gca tcg ccg gca cgt gta cgt tcc ggc gtg ggt tac gtg atg	96
Leu Gly Ala Ser Pro Ala Arg Val Arg Ser Gly Val Gly Tyr Val Met	
20 25 30	
gtg tcc atg gcg tca tcg atg gtg ttc ctg ttt gga ctc gca atg gtt	144
Val Ser Met Ala Ser Ser Met Val Phe Leu Phe Gly Leu Ala Met Val	
35 40 45	
tac gcc tca gtg ggc acg ttg aac atg gct cac gtt ggc cta cgc atg	192
Tyr Ala Ser Val Gly Thr Leu Asn Met Ala His Val Gly Leu Arg Met	
50 55 60	
gaa gat gtt ccg tct gga act cgc tcc gcg atc ttc gca gtg ttg ctc	240
Glu Asp Val Pro Ser Gly Thr Arg Ser Ala Ile Phe Ala Val Leu Leu	
65 70 75 80	
gtg gca ttc ggt att aaa gct gcc gtg ttc ccc cta gat tcc tgg ctg	288
Val Ala Phe Gly Ile Lys Ala Ala Val Phe Pro Leu Asp Ser Trp Leu	
85 90 95	
ccg gac tcc tac ccc acc gcg cca tcg ctg gtc acc gcg gtg ttc gca	336
Pro Asp Ser Tyr Pro Thr Ala Pro Ser Leu Val Thr Ala Val Phe Ala	
100 105 110	
ggt ctg ttg acc aag gtg ggt gtg tat tcc atc att cga gca cgc tcg	384
Gly Leu Leu Thr Lys Val Gly Val Tyr Ser Ile Ile Arg Ala Arg Ser	
115 120 125	
att att ttc acc gat gga tcc ctt gac acc atg ctg atg tgg gtg gca	432
Ile Ile Phe Thr Asp Gly Ser Leu Asp Thr Met Leu Met Trp Val Ala	

09602740 062300



130	135	140	
ctc gcc acc atg ctc att ggt att ttg ggc gcg atg gcg caa aac gat Leu Ala Thr Met Leu Ile Gly Ile Leu Gly Ala Met Ala Gln Asn Asp 145 150 155 160			480
atc aaa cgt ttg ttg tca ttt act ctg gtc agc cac atc ggc tac atg Ile Lys Arg Leu Leu Ser Phe Thr Leu Val Ser His Ile Gly Tyr Met 165 170 175			528
atc ttc ggc gta gcc ctt gga tct gca cag ggt ttg tct ggt gcg atc Ile Phe Gly Val Ala Leu Gly Ser Ala Gln Gly Leu Ser Gly Ala Ile 180 185 190			576
ttc tac gca atc cac cac att ctg gtt cag act tcc ctg ttc ctg gtg Phe Tyr Ala Ile His His Ile Leu Val Gln Thr Ser Leu Phe Leu Val 195 200 205			624
gtc ggt ctg gtg gaa cgc caa gcc gga tcc tcc tcg ctg cga cgc ctt Val Gly Leu Val Glu Arg Gln Ala Gly Ser Ser Ser Leu Arg Arg Leu 210 215 220			672
gga tcc ctg gca tat atc tcc cca ctt ctt gcg att ttg tac ttc atc Gly Ser Leu Ala Tyr Ile Ser Pro Leu Leu Ala Ile Leu Tyr Phe Ile 225 230 235 240			720
ccc gcc atc aac ctg ggt ggt atc cca ccg ttc tcc ggc ttc ctg ggc Pro Ala Ile Asn Leu Gly Gly Ile Pro Pro Phe Ser Gly Phe Leu Gly 245 250 255			768
aag atc atg ctc atc gaa gcc ggc gcc gaa gat ggc agt tgg ctg gca Lys Ile Met Leu Ile Glu Ala Gly Ala Glu Asp Gly Ser Trp Leu Ala 260 265 270			816
tgg gtc ctt atc gca ggc gcc gtt gtc acc tca ctg ctc acc ttg tac Trp Val Leu Ile Ala Gly Ala Val Val Thr Ser Leu Leu Thr Leu Tyr 275 280 285			864
acc atg gtt ctg gtc tgg tcc aag gcc ttc tgg cgc gac cgt aaa gac Thr Met Val Leu Val Trp Ser Lys Ala Phe Trp Arg Asp Arg Lys Asp 290 295 300			912
gcc ccc gat gga gca acc gca ctt gcg cga ccc gca cct ttg gta gat Ala Pro Asp Gly Ala Thr Ala Leu Ala Arg Pro Ala Pro Leu Val Asp 305 310 315 320			960
gtc caa gac gaa gtc gcc gtt aaa gac cgc aac gat gtc gga cgg atg Val Gln Asp Glu Val Ala Val Lys Asp Arg Asn Asp Val Gly Arg Met 325 330 335			1008
cct tgg ggc atg gtc ttc tcc act gct ctc ctg gtt tca gca tct ctt Pro Trp Gly Met Val Phe Ser Thr Ala Leu Leu Val Ser Ala Ser Leu 340 345 350			1056
gct gta tcc gtg ctc gca gga cca ctg tca tct att act gga cgc gcc Ala Val Ser Val Leu Ala Gly Pro Leu Ser Ser Ile Thr Gly Arg Ala 355 360 365			1104
gcc gaa tcc gca caa gat gtc aac atc tac cgc gcc gca gta ctc ggc Ala Glu Ser Ala Gln Asp Val Asn Ile Tyr Arg Ala Ala Val Leu Gly 370 375 380			1152

0062740-062300



ccc aac tac ctc gac cca tca cgc aca ctc gag atg gag cgt tac gac 1200  
 Pro Asn Tyr Leu Asp Pro Ser Arg Thr Leu Glu Met Glu Arg Tyr Asp  
 385 390 395 400

gcc aac cgc gat gac atc aac cac cgc gtc gac acc aac gga acg gag 1248  
 Ala Asn Arg Asp Asp Ile Asn His Arg Val Asp Thr Asn Gly Thr Glu  
 405 410 415

gac caa cca tgatcagtggtg attcaaacga cga 1280  
 Asp Gln Pro

<210> 716

<211> 419

<212> PRT

<213> Corynebacterium glutamicum

<400> 716

Tyr Val Gly Phe Glu Val Leu Leu Val Ala Ser Tyr Val Leu Leu Thr  
 1 5 10 15

Leu Gly Ala Ser Pro Ala Arg Val Arg Ser Gly Val Gly Tyr Val Met  
 20 25 30

Val Ser Met Ala Ser Ser Met Val Phe Leu Phe Gly Leu Ala Met Val  
 35 40 45

Tyr Ala Ser Val Gly Thr Leu Asn Met Ala His Val Gly Leu Arg Met  
 50 55 60

Glu Asp Val Pro Ser Gly Thr Arg Ser Ala Ile Phe Ala Val Leu Leu  
 65 70 75 80

Val Ala Phe Gly Ile Lys Ala Ala Val Phe Pro Leu Asp Ser Trp Leu  
 85 90 95

Pro Asp Ser Tyr Pro Thr Ala Pro Ser Leu Val Thr Ala Val Phe Ala  
 100 105 110

Gly Leu Leu Thr Lys Val Gly Val Tyr Ser Ile Ile Arg Ala Arg Ser  
 115 120 125

Ile Ile Phe Thr Asp Gly Ser Leu Asp Thr Met Leu Met Trp Val Ala  
 130 135 140

Leu Ala Thr Met Leu Ile Gly Ile Leu Gly Ala Met Ala Gln Asn Asp  
 145 150 155 160

Ile Lys Arg Leu Leu Ser Phe Thr Leu Val Ser His Ile Gly Tyr Met  
 165 170 175

Ile Phe Gly Val Ala Leu Gly Ser Ala Gln Gly Leu Ser Gly Ala Ile  
 180 185 190

Phe Tyr Ala Ile His His Ile Leu Val Gln Thr Ser Leu Phe Leu Val  
 195 200 205

Val Gly Leu Val Glu Arg Gln Ala Gly Ser Ser Ser Leu Arg Arg Leu  
 210 215 220

0062300 "04/27/99" 09502740



Gly Ser Leu Ala Tyr Ile Ser Pro Leu Leu Ala Ile Leu Tyr Phe Ile  
 225 230 235 240  
 Pro Ala Ile Asn Leu Gly Gly Ile Pro Pro Phe Ser Gly Phe Leu Gly  
 245 250 255  
 Lys Ile Met Leu Ile Glu Ala Gly Ala Glu Asp Gly Ser Trp Leu Ala  
 260 265 270  
 Trp Val Leu Ile Ala Gly Ala Val Val Thr Ser Leu Leu Thr Leu Tyr  
 275 280 285  
 Thr Met Val Leu Val Trp Ser Lys Ala Phe Trp Arg Asp Arg Lys Asp  
 290 295 300  
 Ala Pro Asp Gly Ala Thr Ala Leu Ala Arg Pro Ala Pro Leu Val Asp  
 305 310 315 320  
 Val Gln Asp Glu Val Ala Val Lys Asp Arg Asn Asp Val Gly Arg Met  
 325 330 335  
 Pro Trp Gly Met Val Phe Ser Thr Ala Leu Leu Val Ser Ala Ser Leu  
 340 345 350  
 Ala Val Ser Val Leu Ala Gly Pro Leu Ser Ser Ile Thr Gly Arg Ala  
 355 360 365  
 Ala Glu Ser Ala Gln Asp Val Asn Ile Tyr Arg Ala Ala Val Leu Gly  
 370 375 380  
 Pro Asn Tyr Leu Asp Pro Ser Arg Thr Leu Glu Met Glu Arg Tyr Asp  
 385 390 395 400  
 Ala Asn Arg Asp Asp Ile Asn His Arg Val Asp Thr Asn Gly Thr Glu  
 405 410 415  
 Asp Gln Pro

<210> 717  
 <211> 1051  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1051)  
 <223> RXN01895

<400> 717  
 cgcgtagacg tgctcaacac gacaacgctt aaacggctgc acgcgtaaca cggcagaccg 60

cacaagcttt aagatccacg atcaggagac ttgacaaat atg tca gtt aac cca 115  
 Met Ser Val Asn Pro  
 1 5

acc cgc ccc gaa ggc ggc cgt cac cac gtc gtc gtc atc ggt tct ggt 163  
 Thr Arg Pro Glu Gly Gly Arg His His Val Val Val Ile Gly Ser Gly  
 10 15 20

002290"0420950



ttt ggt ggc ctt ttt gct gcc aag aac ctg gcc aag gca gac gtc gat 211  
 Phe Gly Gly Leu Phe Ala Ala Lys Asn Leu Ala Lys Ala Asp Val Asp  
 25 30 35

gtc act ctg att gac cgc acc aac cac cac ctc ttc cag cca ctg ctg 259  
 Val Thr Leu Ile Asp Arg Thr Asn His His Leu Phe Gln Pro Leu Leu  
 40 45 50

tac caa gtg gca acc ggt atc ctc tcc tcc ggt gaa atc gca cct tcc 307  
 Tyr Gln Val Ala Thr Gly Ile Leu Ser Ser Gly Glu Ile Ala Pro Ser  
 55 60 65

act cga cag atc ctg ggc tcc cag gaa aac gtc aac gtc atc aag ggc 355  
 Thr Arg Gln Ile Leu Gly Ser Gln Glu Asn Val Asn Val Ile Lys Gly  
 70 75 80 85

gaa gtc acc gac atc aac gtc gag tcc cag act gtg acc gcc tcc ctg 403  
 Glu Val Thr Asp Ile Asn Val Glu Ser Gln Thr Val Thr Ala Ser Leu  
 90 95 100

ggc gag ttc acc cgc gtt ttt gag tac gat tcc ttg gtc gtt ggt gct 451  
 Gly Glu Phe Thr Arg Val Phe Glu Tyr Asp Ser Leu Val Val Gly Ala  
 105 110 115

ggc gca ggt cag tcc tac ttc ggc aat gat cac ttc gct gag ttc gca 499  
 Gly Ala Gly Gln Ser Tyr Phe Gly Asn Asp His Phe Ala Glu Phe Ala  
 120 125 130

cct ggc atg aag tcc atc gac gat gca ctg gag att cgt gca cgc atc 547  
 Pro Gly Met Lys Ser Ile Asp Asp Ala Leu Glu Ile Arg Ala Arg Ile  
 135 140 145

atc ggt gct ttc gag cgc gct gag atc tgc gag gat cca gct gag cgc 595  
 Ile Gly Ala Phe Glu Arg Ala Glu Ile Cys Glu Asp Pro Ala Glu Arg  
 150 155 160 165

gaa cgc ctg ctc acc ttc gtc gtt gtt ggc gct ggc cca acc ggt gtt 643  
 Glu Arg Leu Leu Thr Phe Val Val Val Gly Ala Gly Pro Thr Gly Val  
 170 175 180

gag ctt gct ggc cag ttg gct gag atg gct cac cgc acc ctt gct ggt 691  
 Glu Leu Ala Gly Gln Leu Ala Glu Met Ala His Arg Thr Leu Ala Gly  
 185 190 195

gag tac aag aac ttc aac acc aac tcc gca aag atc atc ctg ctt gat 739  
 Glu Tyr Lys Asn Phe Asn Thr Asn Ser Ala Lys Ile Ile Leu Leu Asp  
 200 205 210

ggt gct cca cag gtt ctt cct cca ttc ggt aag cgc cta ggc cgc aac 787  
 Gly Ala Pro Gln Val Leu Pro Pro Phe Gly Lys Arg Leu Gly Arg Asn  
 215 220 225

gca cag cgc acc ctg gaa aag atg ggt gtc aac gtt cgc ctg aac gct 835  
 Ala Gln Arg Thr Leu Glu Lys Met Gly Val Asn Val Arg Leu Asn Ala  
 230 235 240 245

atg gtc acc aac gtt gac gct acc tcg gtc acc tac aag acc aag gac 883  
 Met Val Thr Asn Val Asp Ala Thr Ser Val Thr Tyr Lys Thr Lys Asp  
 250 255 260

09602740-062300



```
<210> 718
<211> 317
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 718															
Met 1	Ser	Val	Asn	Pro 5	Thr	Arg	Pro	Glu	Gly 10	Gly	Arg	His	His	Val 15	Val
Val	Ile	Gly	Ser 20	Gly	Phe	Gly	Gly	Leu 25	Phe	Ala	Ala	Lys	Asn 30	Leu	Ala
Lys	Ala	Asp 35	Val	Asp	Val	Thr	Leu 40	Ile	Asp	Arg	Thr	Asn 45	His	His	Leu
Phe 50	Gln	Pro	Leu	Leu	Tyr	Gln 55	Val	Ala	Thr	Gly	Ile 60	Leu	Ser	Ser	Gly
Glu 65	Ile	Ala	Pro	Ser	Thr 70	Arg	Gln	Ile	Leu	Gly 75	Ser	Gln	Glu	Asn	Val 80
Asn	Val	Ile	Lys	Gly 85	Glu	Val	Thr	Asp	Ile 90	Asn	Val	Glu	Ser	Gln 95	Thr
Val	Thr	Ala	Ser 100	Leu	Gly	Glu	Phe	Thr 105	Arg	Val	Phe	Glu	Tyr 110	Asp	Ser
Leu	Val	Val 115	Gly	Ala	Gly	Ala	Gly 120	Gln	Ser	Tyr	Phe	Gly 125	Asn	Asp	His
Phe 130	Ala	Glu	Phe	Ala	Pro	Gly 135	Met	Lys	Ser	Ile	Asp 140	Asp	Ala	Leu	Glu
Ile 145	Arg	Ala	Arg	Ile	Ile 150	Gly	Ala	Phe	Glu	Arg 155	Ala	Glu	Ile	Cys	Glu 160
Asp	Pro	Ala	Glu	Arg 165	Glu	Arg	Leu	Leu	Thr 170	Phe	Val	Val	Val	Gly 175	Ala
Gly	Pro	Thr	Gly 180	Val	Glu	Leu	Ala	Gly 185	Gln	Leu	Ala	Glu	Met 190	Ala	His
Arg	Thr	Leu 195	Ala	Gly	Glu	Tyr	Lys 200	Asn	Phe	Asn	Thr	Asn 205	Ser	Ala	Lys

**0**      **1**      **2**      **3**      **4**      **5**      **6**      **7**



```
<210> 719
<211> 816
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (1)..(816)  
<223> FRXA01895
```

<400> 719																
cac	cac	ctc	ttc	cag	cca	ctg	ctg	tac	caa	gtg	gca	acc	ggt	atc	ctc	48
His	His	Leu	Phe	Gln	Pro	Leu	Leu	Tyr	Gln	Val	Ala	Thr	Gly	Ile	Leu	
1				5		10				15						
tcc	tcc	ggt	gaa	atc	gca	cct	tcc	act	cga	cag	atc	ctg	ggc	tcc	cag	96
Ser	Ser	Gly	Glu	Ile	Ala	Pro	Ser	Thr	Arg	Gln	Ile	Leu	Gly	Ser	Gln	
20				25				30								
gaa	aac	gtc	aac	gtc	atc	aag	ggc	gaa	gtc	acc	gac	atc	aac	gtc	gag	144
Glu	Asn	Val	Asn	Val	Ile	Lys	Gly	Glu	Val	Thr	Asp	Ile	Asn	Val	Glu	
35				40				45								
tcc	cag	act	gtg	acc	gcc	tcc	ctg	ggc	gag	ttc	acc	cgc	gtt	ttt	gag	192
Ser	Gln	Thr	Val	Thr	Ala	Ser	Leu	Gly	Glu	Phe	Thr	Arg	Val	Phe	Glu	
50				55				60								
tac	gat	tcc	ttg	gtc	gtt	ggt	gct	ggc	gca	ggt	cag	tcc	tac	ttc	ggc	240
Tyr	Asp	Ser	Leu	Val	Val	Gly	Ala	Gly	Ala	Gly	Gln	Ser	Tyr	Phe	Gly	
65				70				75				80				
aat	gat	cac	ttc	gct	gag	ttc	gca	cct	ggc	atg	aag	tcc	atc	gac	gat	288
Asn	Asp	His	Phe	Ala	Glu	Phe	Ala	Pro	Gly	Met	Lys	Ser	Ile	Asp	Asp	
85				90				95								
gca	ctg	gag	att	cgt	gca	cgc	atc	atc	ggt	gct	ttc	gag	cgc	gct	gag	336
Ala	Leu	Glu	Ile	Arg	Ala	Arg	Ile	Ile	Gly	Ala	Phe	Glu	Arg	Ala	Glu	
100				105				110								



09602740-062300

09602740-062300

09602740-062300



65						70						75						80
Asn	Asp	His	Phe	Ala	Glu	Phe	Ala	Pro	Gly	Met	Lys	Ser	Ile	Asp	Asp			
				85					90					95				
Ala	Leu	Glu	Ile	Arg	Ala	Arg	Ile	Ile	Gly	Ala	Phe	Glu	Arg	Ala	Glu			
			100					105					110					
Ile	Cys	Glu	Asp	Pro	Ala	Glu	Arg	Glu	Arg	Leu	Leu	Thr	Phe	Val	Val			
		115					120					125						
Val	Gly	Ala	Gly	Pro	Thr	Gly	Val	Glu	Leu	Ala	Gly	Gln	Leu	Ala	Glu			
	130					135					140							
Met	Ala	His	Arg	Thr	Leu	Ala	Gly	Glu	Tyr	Lys	Asn	Phe	Asn	Thr	Asn			
145					150					155					160			
Ser	Ala	Lys	Ile	Ile	Leu	Leu	Asp	Gly	Ala	Pro	Gln	Val	Leu	Pro	Pro			
			165					170						175				
Phe	Gly	Lys	Arg	Leu	Gly	Arg	Asn	Ala	Gln	Arg	Thr	Leu	Glu	Lys	Met			
			180					185					190					
Gly	Val	Asn	Val	Arg	Leu	Asn	Ala	Met	Val	Thr	Asn	Val	Asp	Ala	Thr			
		195					200					205						
Ser	Val	Thr	Tyr	Lys	Thr	Lys	Asp	Gly	Glu	Glu	His	Thr	Ile	Glu	Ser			
	210					215					220							
Phe	Cys	Lys	Ile	Trp	Ser	Ala	Gly	Val	Ala	Ala	Ser	Pro	Leu	Gly	Lys			
225					230				235						240			
Leu	Val	Ala	Glu	Gln	Thr	Gly	Val	Glu	Thr	Asp	Arg	Ala	Gly	Arg	Val			
			245					250					255					
Met	Val	Asn	Asp	Asp	Leu	Ser	Val	Gly	Asp	Gln	Lys	Asn	Val	Phe	Val			
			260					265					270					

<210> 721  
 <211> 2409  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(2386)  
 <223> RXA00703

<400> 721  
 ctgggagtc tcttgatttt aggtttttcca cataccccca tatagattga agaattcatt 60

tttcggcatg ggttcaattg ccgggtctag actgtgacct atg aca acc cct cca 115  
 Met Thr Thr Pro Pro  
 1 5

act gag att tcg aac gtg aat ccc acc gcg aat gaa ttt gat gat ccg 163  
 Thr Glu Ile Ser Asn Val Asn Pro Thr Ala Asn Glu Phe Asp Asp Pro

006290"0720960



[illegible]



ccc atg cca gag acc ggt ctg atg aaa ttc cgt gag ccc caa tca gtc 931  
 Pro Met Pro Glu Thr Gly Leu Met Lys Phe Arg Glu Pro Gln Ser Val  
 265 270 275

aag ggc gcg ttg agc att tca gac aaa ctt gct gat gaa tac ttg cag 979  
 Lys Gly Ala Leu Ser Ile Ser Asp Lys Leu Ala Asp Glu Tyr Leu Gln  
 280 285 290

atc cgt ctt gat gga gac cgc gca ttc ttc cag gcg ctc aac aag gaa 1027  
 Ile Arg Leu Asp Gly Asp Arg Ala Phe Phe Gln Ala Leu Asn Lys Glu  
 295 300 305

ctc atc cgt aga gat gcc cta gat cat gca ttc ttg gat aaa ttc tgt 1075  
 Leu Ile Arg Arg Asp Ala Leu Asp His Ala Phe Leu Asp Lys Phe Cys  
 310 315 320 325

tca ggt gtg gat gaa acc atc gag cac ctc aaa tca ctc gat gat gag 1123  
 Ser Gly Val Asp Glu Thr Ile Glu His Leu Lys Ser Leu Asp Asp Glu  
 330 335 340

gtt ctg ctc aag gga tgc ggt ctg acg gca gcg gag atc aac aag gcc 1171  
 Val Leu Leu Lys Gly Cys Gly Leu Thr Ala Ala Glu Ile Asn Lys Ala  
 345 350 355

gct gac atg gtg gaa aag tct gac acc gtg gtg gtg tca tgg act ctc 1219  
 Ala Asp Met Val Glu Lys Ser Asp Thr Val Val Val Ser Trp Thr Leu  
 360 365 370

ggg gtc acc cag cat aag aac gct gtg tac acc atc cgt gaa atg gtg 1267  
 Gly Val Thr Gln His Lys Asn Ala Val Tyr Thr Ile Arg Glu Met Val  
 375 380 385

aac ttc ctg ctg ctt act gga aat att ggt aag cct ggc gca ggc act 1315  
 Asn Phe Leu Leu Leu Thr Gly Asn Ile Gly Lys Pro Gly Ala Gly Thr  
 390 395 400 405

gcc ccg ctt cgt ggg cac tca aac gtc cag ggt gat cga acc atg ggt 1363  
 Ala Pro Leu Arg Gly His Ser Asn Val Gln Gly Asp Arg Thr Met Gly  
 410 415 420

att tgg gag aaa atg ccg gag gca ttc ctt gct gct ctt gaa aac gag 1411  
 Ile Trp Glu Lys Met Pro Glu Ala Phe Leu Ala Ala Leu Glu Asn Glu  
 425 430 435

ttt ggt ttc gat gtg ccc cgc aag cac ggc ttc gac acg gta aat tcc 1459  
 Phe Gly Phe Asp Val Pro Arg Lys His Gly Phe Asp Thr Val Asn Ser  
 440 445 450

ctg cga gcc atg cgc gaa ggc aag acc aag ttc ttt ctc tcc ctc ggt 1507  
 Leu Arg Ala Met Arg Glu Gly Lys Thr Lys Phe Phe Leu Ser Leu Gly  
 455 460 465

ggc aac ctt gtt cga gtg tcc tca gat acg tct gtt gtc gaa aag ggc 1555  
 Gly Asn Leu Val Arg Val Ser Ser Asp Thr Ser Val Val Glu Lys Gly  
 470 475 480 485

atg gaa tcc aat gag ctg acg gtg cat ctg tcg acc aag ccc aat ggt 1603  
 Met Glu Ser Asn Glu Leu Thr Val His Leu Ser Thr Lys Pro Asn Gly  
 490 495 500

09602740-062300







Ser Asn Thr Pro Val Ser Lys Ser Val Val Val Arg Leu Glu Ala Thr  
                   745                                  750                                  755

gga cgt act gct tct tagaaaaaca ccagggaatt ttc  
 Gly Arg Thr Ala Ser  
                   760

2409

&lt;210&gt; 722

&lt;211&gt; 762

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 722

Met Thr Thr Pro Pro Thr Glu Ile Ser Asn Val Asn Pro Thr Ala Asn  
   1                                  5                                  10                                  15

Glu Phe Asp Asp Pro Asp Val Gly Arg Arg Ile Thr Ser Ala Ala Gly  
                                   20                                  25                                  30

Val Pro Gly Val Leu His Ala Leu Gln His Ala Val Pro Asn Arg Ala  
                                   35                                  40                                  45

Leu Leu Pro Leu Leu Thr Met Asn Lys Pro Gly Gly Ile Asp Cys Pro  
   50                                  55                                  60

Gly Cys Ala Trp Pro Glu Pro Ser Thr Ala Asn Leu Gly Val Val Glu  
   65                                  70                                  75                                  80

Phe Cys Glu Asn Gly Ala Lys Ala Val Ala Glu Glu Thr Thr Pro Asp  
                                   85                                  90                                  95

Arg Ala Gly Lys Glu Phe Trp Ala Glu His Ser Ile Tyr Asp Leu Arg  
                                   100                                  105                                  110

Glu Lys Thr Asp His Trp Leu Gly Lys Arg Gly Arg Ile Thr Glu Pro  
                                   115                                  120                                  125

Met Phe Tyr Asp Arg Ser Ser Gly Asp Asp His Tyr Arg Pro Ile Ser  
   130                                  135                                  140

Trp Asp Arg Ala Phe Ala Ile Ile Ala Ser Lys Leu Arg Glu Ile Glu  
   145                                  150                                  155                                  160

Pro Asp Glu Ala Val Phe Tyr Thr Ser Gly Arg Ala Pro Asn Glu Pro  
                                   165                                  170                                  175

Ala Tyr Met Leu Gln Leu Leu Ala Arg Arg Leu Gly Thr Asn Asn Leu  
                                   180                                  185                                  190

Pro Asp Cys Gly Asn Met Cys His Glu Ser Thr Gly Thr Ala Leu Gly  
                                   195                                  200                                  205

Glu Thr Leu Gly Leu Gly Lys Gly Ser Val Val Met Glu Asp Phe Tyr  
   210                                  215                                  220

Asn Thr Asp Leu Leu Ile Ser Val Gly Gln Asn Pro Gly Thr Asn His  
   225                                  230                                  235                                  240

Pro Arg Ala Leu Thr Ala Phe Lys Glu Leu Lys Glu Asn Gly Gly Lys  
                                   245                                  250                                  255

0062390"0720960



Ile Leu Ala Leu Asn Pro Met Pro Glu Thr Gly Leu Met Lys Phe Arg  
 260 265 270  
 Glu Pro Gln Ser Val Lys Gly Ala Leu Ser Ile Ser Asp Lys Leu Ala  
 275 280 285  
 Asp Glu Tyr Leu Gln Ile Arg Leu Asp Gly Asp Arg Ala Phe Phe Gln  
 290 295 300  
 Ala Leu Asn Lys Glu Leu Ile Arg Arg Asp Ala Leu Asp His Ala Phe  
 305 310 315 320  
 Leu Asp Lys Phe Cys Ser Gly Val Asp Glu Thr Ile Glu His Leu Lys  
 325 330 335  
 Ser Leu Asp Asp Glu Val Leu Leu Lys Gly Cys Gly Leu Thr Ala Ala  
 340 345 350  
 Glu Ile Asn Lys Ala Ala Asp Met Val Glu Lys Ser Asp Thr Val Val  
 355 360 365  
 Val Ser Trp Thr Leu Gly Val Thr Gln His Lys Asn Ala Val Tyr Thr  
 370 375 380  
 Ile Arg Glu Met Val Asn Phe Leu Leu Leu Thr Gly Asn Ile Gly Lys  
 385 390 395 400  
 Pro Gly Ala Gly Thr Ala Pro Leu Arg Gly His Ser Asn Val Gln Gly  
 405 410 415  
 Asp Arg Thr Met Gly Ile Trp Glu Lys Met Pro Glu Ala Phe Leu Ala  
 420 425 430  
 Ala Leu Glu Asn Glu Phe Gly Phe Asp Val Pro Arg Lys His Gly Phe  
 435 440 445  
 Asp Thr Val Asn Ser Leu Arg Ala Met Arg Glu Gly Lys Thr Lys Phe  
 450 455 460  
 Phe Leu Ser Leu Gly Gly Asn Leu Val Arg Val Ser Ser Asp Thr Ser  
 465 470 475 480  
 Val Val Glu Lys Gly Met Glu Ser Asn Glu Leu Thr Val His Leu Ser  
 485 490 495  
 Thr Lys Pro Asn Gly Ser Gln Ala Trp Pro Gly Glu Gln Ser Leu Ile  
 500 505 510  
 Leu Pro Val Ile Ala Arg Thr Asp Lys Asp Val Gln Lys Ser Gly Val  
 515 520 525  
 Gln Arg Val Thr Val Glu Asp Ser Ala Gly Ala Val His Ala Ser Thr  
 530 535 540  
 Gly Lys Arg Thr Ala Asn Lys Asp Leu Asn Leu Lys Ser Glu Cys Asp  
 545 550 555 560  
 Ile Ile Gly Thr Ile Gly Lys Gln Thr Phe Gly Asp Ala Phe Trp Gln  
 565 570 575

002290" 0420960



Pro Met Ile Asp Asn Tyr Asp Val Val Arg Asp His Ile Glu Ala Thr  
580 585 590

Ile Pro Gly Phe His Asp Phe Asn Arg Arg Ile Asp Asn Pro Gly Gly  
595 600 605

Phe Leu Leu Pro Asn Gly Pro Arg Glu Arg Ile Phe Asn Thr Ser Asn  
610 615 620

Gly Lys Ala Gln Leu Thr Val Asn Glu Thr Asn Val Ile Glu Leu Pro  
625 630 635 640

Lys Asp Tyr Leu Leu Met Asn Thr Val Arg Ser His Asp Gln Tyr Asn  
645 650 655

Ser Thr Ile Tyr Gly Leu Asp Asp Arg Tyr Arg Gly Val Arg Asn Gly  
660 665 670

Arg Arg Val Val Phe Val Asn Pro Gln Asp Cys Lys Gln Arg Gly Leu  
675 680 685

Lys Asp Gly Asp Ile Val Asp Ile Val Ser Val Phe Asp Asp Gly Glu  
690 695 700

Arg Arg Ala Pro Asn Phe Arg Val Val Glu Tyr Asp Thr Ala Arg Asp  
705 710 715 720

Cys Val Thr Thr Tyr Phe Pro Glu Ala Asn Val Leu Val Pro Leu Asp  
725 730 735

Ser Val Ala Glu Lys Ser Asn Thr Pro Val Ser Lys Ser Val Val Val  
740 745 750

Arg Leu Glu Ala Thr Gly Arg Thr Ala Ser  
755 760

<210> 723  
<211> 1038  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(1015)  
<223> RXN00705

<400> 723  
gttctggaac aagcactgat gattgggccc agtccacgtt ggtaaatgct ctgcatcttc 60  
aagaaatcat cgctaaaaat taccgcggagg ctaaataaaa atg ggt cgg att acc 115  
Met Gly Arg Ile Thr  
1 5  
caa aac ttg cag gtc cca cgc gtt gtg tcc act gac gag caa gtt ttt 163  
Gln Asn Leu Gln Val Pro Arg Val Val Ser Thr Asp Glu Gln Val Phe  
10 15 20  
gtt aac act cgt ccg gat act gtt gcg gtg gag gag cct cta gaa att 211  
Val Asn Thr Arg Pro Asp Thr Val Ala Val Glu Glu Pro Leu Glu Ile  
25 30 35

09602740.062300







atc gag gcg gcg cag gat tca ggt att ttc ctt gct ggt ttt gtt cgg 979  
 Ile Glu Ala Ala Gln Asp Ser Gly Ile Phe Leu Ala Gly Phe Val Arg  
           280                          285                          290

ggc aac aag ttt aac cac tat gcg ggc gag ctc gga taatgccaga 1025  
 Gly Asn Lys Phe Asn His Tyr Ala Gly Glu Leu Gly  
           295                          300                          305

acaggtagaa cag 1038

<210> 724

<211> 305

<212> PRT

<213> Corynebacterium glutamicum

<400> 724

Met Gly Arg Ile Thr Gln Asn Leu Gln Val Pro Arg Val Val Ser Thr  
   1                          5                          10                          15

Asp Glu Gln Val Phe Val Asn Thr Arg Pro Asp Thr Val Ala Val Glu  
                           20                          25                          30

Glu Pro Leu Glu Ile Arg Val Asn Gly Thr Ala Leu Thr Thr Thr Met  
                           35                          40                          45

Arg Thr Pro Gly His Asp Ile Glu Leu Val His Gly Leu Leu Leu Ser  
                           50                          55                          60

Glu Gly Leu Ile Thr Asp Ala Ser Glu Val Phe Thr Ala Arg Tyr Cys  
   65                          70                          75                          80

Ala Gly Ala Val Gly Pro Asp Asn Gln Asn Thr Tyr Asn Val Leu Glu  
                           85                          90                          95

Leu Asp Val Ile Pro Lys Asp Asn Pro Ala Arg Asp Pro Val Gln Asn  
                           100                          105                          110

Pro Ser His Asn Pro Glu Gly Ser Gln His Glu Ala Leu His Ile Pro  
                           115                          120                          125

Thr Phe Gln Pro Val Arg Glu Leu Asn Leu Val Ala Ala Gln Arg Asn  
   130                          135                          140

Val Leu Thr Thr Ser Ala Cys Gly Val Cys Gly Thr Thr Ser Ile Glu  
  145                          150                          155                          160

Gln Leu Met Asn Lys Lys Gly Trp Pro Ile Thr Pro Ile Thr Pro Asp  
                           165                          170                          175

Pro Arg Met Ile Val Ser Leu Pro Asp Lys Leu Lys Ser Lys Gln Lys  
                           180                          185                          190

Ile Phe Asp Lys Thr Gly Gly Val His Ala Ala Gly Leu Ala Thr Leu  
                           195                          200                          205

Asp Gly Glu Met Leu Ile Ile Arg Glu Asp Val Gly Arg His Asn Ala  
   210                          215                          220

Ala Asp Lys Val Ile Gly Asn Met Leu Met Ala Gly Lys Leu Pro Leu  
  225                          230                          235                          240

00602740-062300



Glu Asn Thr Ile Leu Val Met Ser Ser Arg Ala Ser Phe Glu Leu Val  
 245 250 255

Gln Lys Ala Ala Met Ala Gly Ile Ser Gly Val Ile Ala Val Gly Ala  
 260 265 270

Ala Thr Ser Leu Ala Ile Glu Ala Ala Gln Asp Ser Gly Ile Phe Leu  
 275 280 285

Ala Gly Phe Val Arg Gly Asn Lys Phe Asn His Tyr Ala Gly Glu Leu  
 290 295 300

Gly  
 305

<210> 725  
 <211> 908  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(885)  
 <223> FRXA00705

<400> 725  
 cca cgc gtt gtg tcc act gac gag caa gtt ttt gtt aac act cgt ccg 48  
 Pro Arg Val Val Ser Thr Asp Glu Gln Val Phe Val Asn Thr Arg Pro  
 1 5 10 15

gat act gtt gcg gtg gag gag cct cta gaa att cgg gtt aat ggc act 96  
 Asp Thr Val Ala Val Glu Glu Pro Leu Glu Ile Arg Val Asn Gly Thr  
 20 25 30

gcg ctt acc acc act atg cgc acg ccc ggc cat gat att gag ttg gtg 144  
 Ala Leu Thr Thr Thr Met Arg Thr Pro Gly His Asp Ile Glu Leu Val  
 35 40 45

cat ggc ctc ctc ttg tca gaa ggt ctg atc acg gat gct tct gag gtt 192  
 His Gly Leu Leu Leu Ser Glu Gly Leu Ile Thr Asp Ala Ser Glu Val  
 50 55 60

ttt acc gcc cgc tat tgt gca gga gct gtt ggc cca gat aat caa aat 240  
 Phe Thr Ala Arg Tyr Cys Ala Gly Ala Val Gly Pro Asp Asn Gln Asn  
 65 70 75 80

acg tac aac gtc tta gaa ctt gat gtc atc ccc aaa gac aat ccg gcc 288  
 Thr Tyr Asn Val Leu Glu Leu Asp Val Ile Pro Lys Asp Asn Pro Ala  
 85 90 95

cgg gat ccc gtc cag aat ccc tcc cat aat ccc gaa ggc agc caa cac 336  
 Arg Asp Pro Val Gln Asn Pro Ser His Asn Pro Glu Gly Ser Gln His  
 100 105 110

gaa gca ctc cac atc cca act ttc caa ccg gta cgc gaa cta aac ctc 384  
 Glu Ala Leu His Ile Pro Thr Phe Gln Pro Val Arg Glu Leu Asn Leu  
 115 120 125

gtg gca gcc caa cgc aat gtg ctg act acg tct gct tgt ggt gtt tgt 432

09602740-062300



<211> 295

<212> PRT

<213> Corynebacterium glutamicum

<400> 726

Pro Arg Val Val Ser Thr Asp Glu Gln Val Phe Val Asn Thr Arg Pro  
1 5 10 15

Asp Thr Val Ala Val Glu Glu Pro Leu Glu Ile Arg Val Asn Gly Thr  
20 25 30

Ala Leu Thr Thr Thr Met Arg Thr Pro Gly His Asp Ile Glu Leu Val  
35 40 45

His Gly Leu Leu Leu Ser Glu Gly Leu Ile Thr Asp Ala Ser Glu Val  
50 55 60



Phe Thr Ala Arg Tyr Cys Ala Gly Ala Val Gly Pro Asp Asn Gln Asn  
 65 70 75 80  
 Thr Tyr Asn Val Leu Glu Leu Asp Val Ile Pro Lys Asp Asn Pro Ala  
 85 90 95  
 Arg Asp Pro Val Gln Asn Pro Ser His Asn Pro Glu Gly Ser Gln His  
 100 105 110  
 Glu Ala Leu His Ile Pro Thr Phe Gln Pro Val Arg Glu Leu Asn Leu  
 115 120 125  
 Val Ala Ala Gln Arg Asn Val Leu Thr Thr Ser Ala Cys Gly Val Cys  
 130 135 140  
 Gly Thr Thr Ser Ile Glu Gln Leu Met Asn Lys Lys Gly Trp Pro Ile  
 145 150 155 160  
 Thr Pro Ile Thr Pro Asp Pro Arg Met Ile Val Ser Leu Pro Asp Lys  
 165 170 175  
 Leu Lys Ser Lys Gln Lys Ile Phe Asp Lys Thr Gly Gly Val His Ala  
 180 185 190  
 Ala Gly Leu Ala Thr Leu Asp Gly Glu Met Leu Ile Ile Arg Glu Asp  
 195 200 205  
 Val Gly Arg His Asn Ala Ala Asp Lys Val Ile Gly Asn Met Leu Met  
 210 215 220  
 Ala Gly Lys Leu Pro Leu Glu Asn Thr Ile Leu Val Met Ser Ser Arg  
 225 230 235 240  
 Ala Ser Phe Glu Leu Val Gln Lys Ala Ala Met Ala Gly Ile Ser Gly  
 245 250 255  
 Val Ile Ala Val Gly Ala Ala Thr Ser Leu Ala Ile Glu Ala Ala Gln  
 260 265 270  
 Asp Ser Gly Ile Phe Leu Ala Gly Phe Val Arg Gly Asn Lys Phe Asn  
 275 280 285  
 His Tyr Ala Gly Glu Leu Gly  
 290 295

&lt;210&gt; 727

&lt;211&gt; 1134

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1111)

&lt;223&gt; RXN00388

&lt;400&gt; 727

gaagagtact tcgaccacga cgactaacac cgcaatttaa aggcttttca agcctgcccc 60

acatcgaagc agttttcaca aagaataagg ttggaaaatt atg ttg ccc gtc aac 115

002290"0420960



caa	acg	tat	gcg	cag	ttc	tca	gac	act	gcc	ttc	gta	tcg	gca	tac	atc	163
Gln	Thr	Tyr	Ala	Gln	Phe	Ser	Asp	Thr	Ala	Phe	Val	Ser	Ala	Tyr	Ile	
				10					15					20		
atc	tac	gtt	ctg	gca	ctc	atc	ctc	tcc	ctc	gtc	tac	tac	gta	aaa	caa	211
Ile	Tyr	Val	Leu	Ala	Leu	Ile	Leu	Ser	Leu	Val	Tyr	Tyr	Val	Lys	Gln	
				25					30					35		
caa	ggc	att	atc	gac	gcc	cgc	cgc	gag	caa	acc	cgc	gtc	agc	gaa	ctc	259
Gln	Gly	Ile	Ile	Asp	Ala	Arg	Arg	Glu	Gln	Thr	Arg	Val	Ser	Glu	Leu	
				40					45					50		
gtt	ggg	gca	ggc	ggc	agc	gct	gat	gtt	gat	act	gac	ctg	cct	gat	gac	307
Val	Gly	Ala	Gly	Gly	Ser	Ala	Asp	Val	Asp	Thr	Asp	Leu	Pro	Asp	Asp	
				55					60					65		
atc	gcc	gac	ggg	gtc	ctc	gcc	gac	gaa	gac	ctt	gca	aaa	cgc	gaa	gaa	355
Ile	Ala	Asp	Gly	Val	Leu	Ala	Asp	Glu	Asp	Leu	Ala	Lys	Arg	Glu	Glu	
				70					75					80		
acc	gca	cgc	aaa	cta	gcc	aac	atg	acc	caa	tct	ctc	atg	tgg	ctc	ggc	403
Thr	Ala	Arg	Lys	Leu	Ala	Asn	Met	Thr	Gln	Ser	Leu	Met	Trp	Leu	Gly	
				90					95					100		
gtc	atg	gtg	cac	ctc	gta	tcc	gtc	gtg	atg	cgc	gcg	ctg	tct	gcc	agc	451
Val	Met	Val	His	Leu	Val	Ser	Val	Val	Met	Arg	Ala	Leu	Ser	Ala	Ser	
				105					110					115		
cga	ttc	ccc	ttc	ggc	aac	ctg	tat	gaa	tac	atc	ctc	atg	gtc	acc	ctc	499
Arg	Phe	Pro	Phe	Gly	Asn	Leu	Tyr	Glu	Tyr	Ile	Leu	Met	Val	Thr	Leu	
				120					125					130		
ttc	gcc	atg	atc	gga	gcc	gta	ctc	atc	ctg	cag	cgc	cca	caa	ttc	cgc	547
Phe	Ala	Met	Ile	Gly	Ala	Val	Leu	Ile	Leu	Gln	Arg	Pro	Gln	Phe	Arg	
				135					140					145		
gtg	gta	tgg	cca	tgg	atc	ctc	acc	cca	atg	ctg	gca	ctg	ctc	ttc	tac	595
Val	Val	Trp	Pro	Trp	Ile	Leu	Thr	Pro	Met	Leu	Ala	Leu	Leu	Phe	Tyr	
				150					155					160		
ggg	ggc	acc	cag	ctg	tac	tcc	gac	gca	gca	cca	gtc	gtt	cca	gca	ctg	643
Gly	Gly	Thr	Gln	Leu	Tyr	Ser	Asp	Ala	Ala	Pro	Val	Val	Pro	Ala	Leu	
				170					175					180		
cag	tcc	ttc	tgg	ttc	ccg	atc	cac	gtt	tcc	tcc	gtc	tcc	atc	ggc	gca	691
Gln	Ser	Phe	Trp	Phe	Pro	Ile	His	Val	Ser	Ser	Val	Ser	Ile	Gly	Ala	
				185					190					195		
tcc	atc	ggg	atc	gtc	tcc	ggg	att	gca	tcc	ctg	ctg	tac	ata	ctg	cgc	739
Ser	Ile	Gly	Ile	Val	Ser	Gly	Ile	Ala	Ser	Leu	Leu	Tyr	Ile	Leu	Arg	
				200					205					210		
atg	tgg	caa	cca	aag	ggg	aaa	gaa	aag	ggc	ttc	ttc	ggc	gca	gta	gca	787
Met	Trp	Gln	Pro	Lys	Gly	Lys	Glu	Lys	Gly	Phe	Phe	Gly	Ala	Val	Ala	
				215					220					225		
aaa	cca	ctc	cca	tcc	gga	aaa	acc	ctg	gat	aac	ctg	gca	tac	aag	acc	835
Lys	Pro	Leu	Pro	Ser	Gly	Lys	Thr	Le								



<400> 728															
Met	Leu	Pro	Val	Asn	Gln	Thr	Tyr	Ala	Gln	Phe	Ser	Asp	Thr	Ala	Phe
1				5					10					15	
Val	Ser	Ala	Tyr	Ile	Ile	Tyr	Val	Leu	Ala	Leu	Ile	Leu	Ser	Leu	Val
			20					25					30		
Tyr	Tyr	Val	Lys	Gln	Gln	Gly	Ile	Ile	Asp	Ala	Arg	Arg	Glu	Gln	Thr
		35					40					45			
Arg	Val	Ser	Glu	Leu	Val	Gly	Ala	Gly	Gly	Ser	Ala	Asp	Val	Asp	Thr
	50					55					60				
Asp	Leu	Pro	Asp	Asp	Ile	Ala	Asp	Gly	Val	Leu	Ala	Asp	Glu	Asp	Leu
65					70					75					80
Ala	Lys	Arg	Glu	Glu	Thr	Ala	Arg	Lys	Leu	Ala	Asn	Met	Thr	Gln	Ser
				85					90					95	
Leu	Met	Trp	Leu	Gly	Val	Met	Val	His	Leu	Val	Ser	Val	Val	Met	Arg
			100					105					110		
Ala	Leu	Ser	Ala	Ser	Arg	Phe	Pro	Phe	Gly	Asn	Leu	Tyr	Glu	Tyr	Ile
		115					120					125			
Leu	Met	Val	Thr	Leu	Phe	Ala	Met	Ile	Gly	Ala	Val	Leu	Ile	Leu	Gln
	130					135					140				



Arg Pro Gln Phe Arg Val Val Trp Pro Trp Ile Leu Thr Pro Met Leu  
 145 150 155 160  
 Ala Leu Leu Phe Tyr Gly Gly Thr Gln Leu Tyr Ser Asp Ala Ala Pro  
 165 170 175  
 Val Val Pro Ala Leu Gln Ser Phe Trp Phe Pro Ile His Val Ser Ser  
 180 185 190  
 Val Ser Ile Gly Ala Ser Ile Gly Ile Val Ser Gly Ile Ala Ser Leu  
 195 200 205  
 Leu Tyr Ile Leu Arg Met Trp Gln Pro Lys Gly Lys Glu Lys Gly Phe  
 210 215 220  
 Phe Gly Ala Val Ala Lys Pro Leu Pro Ser Gly Lys Thr Leu Asp Asn  
 225 230 235 240  
 Leu Ala Tyr Lys Thr Ala Ile Trp Thr Val Pro Ile Phe Gly Leu Gly  
 245 250 255  
 Ile Ile Leu Gly Ala Ile Trp Ala Glu Ala Ala Trp Gly Arg Phe Trp  
 260 265 270  
 Gly Trp Asp Pro Lys Glu Thr Val Ser Phe Ile Thr Trp Val Leu Tyr  
 275 280 285  
 Ala Gly Tyr Leu His Ala Arg Ala Thr Ala Gly Trp Arg Asn Thr Asn  
 290 295 300  
 Ala Ala Trp Ile Asn Ile Leu Ala Leu Val Thr Met Ile Phe Asn Leu  
 305 310 315 320  
 Phe Phe Ile Asn Met Val Val Ser Gly Leu His Ser Tyr Ala Gly Leu  
 325 330 335  
 Asn

<210> 729  
 <211> 326  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(303)  
 <223> FRXA00388

<400> 729  
 acc ctg gat aac ctg gca tac aag acc gcg atc tgg act gtc cca atc 48  
 Thr Leu Asp Asn Leu Ala Tyr Lys Thr Ala Ile Trp Thr Val Pro Ile  
 1 5 10 15  
 ttc ggc ctg ggc atc atc ttg ggt gcc atc tgg gca gaa gca gcc tgg 96  
 Phe Gly Leu Gly Ile Ile Leu Gly Ala Ile Trp Ala Glu Ala Ala Trp  
 20 25 30  
 ggt cgt ttc tgg gga tgg gat cct aag gaa aca gtc tcc ttc atc acc 144

00602740-062300



```

Gly Arg Phe Trp Gly Trp Asp Pro Lys Glu Thr Val Ser Phe Ile Thr
      35                      40                      45

tgg gtt ctc tac gct ggt tac ctc cac gca cgt gca act gct ggt tgg 192
Trp Val Leu Tyr Ala Gly Tyr Leu His Ala Arg Ala Thr Ala Gly Trp
      50                      55                      60

cgc aac acc aac gct gca tgg atc aac atc ctg gcg ctg gtc acg atg 240
Arg Asn Thr Asn Ala Ala Trp Ile Asn Ile Leu Ala Leu Val Thr Met
      65                      70                      75                      80

att ttt aat ctg ttc ttc atc aac atg gtc gta tct ggt ctg cac tct 288
Ile Phe Asn Leu Phe Phe Ile Asn Met Val Val Ser Gly Leu His Ser
      85                      90                      95

tac gcc gga ctg aac taagcacttt tgggtggcgg ggt 326
Tyr Ala Gly Leu Asn
      100

```

```

<210> 730
<211> 101
<212> PRT
<213> Corynebacterium glutamicum

```

```

<400> 730
Thr Leu Asp Asn Leu Ala Tyr Lys Thr Ala Ile Trp Thr Val Pro Ile
  1                      5                      10                      15

Phe Gly Leu Gly Ile Ile Leu Gly Ala Ile Trp Ala Glu Ala Ala Trp
      20                      25                      30

Gly Arg Phe Trp Gly Trp Asp Pro Lys Glu Thr Val Ser Phe Ile Thr
      35                      40                      45

Trp Val Leu Tyr Ala Gly Tyr Leu His Ala Arg Ala Thr Ala Gly Trp
      50                      55                      60

Arg Asn Thr Asn Ala Ala Trp Ile Asn Ile Leu Ala Leu Val Thr Met
      65                      70                      75                      80

Ile Phe Asn Leu Phe Phe Ile Asn Met Val Val Ser Gly Leu His Ser
      85                      90                      95

Tyr Ala Gly Leu Asn
      100

```

```

<210> 731
<211> 610
<212> DNA
<213> Corynebacterium glutamicum

```

```

<220>
<221> CDS
<222> (101)..(610)
<223> FRXA00386

```

```

<400> 731
gaagagtact tcgaccacga cgactaacac cgcaatttaa aggccttttca agcctgcccc 60

```

09602740-062300



Figure 1 consists of 12 bar charts, labeled (a) through (l), each representing a different demographic or attitudinal variable. Each chart has two sets of bars: one set for the 'Sample' (represented by white bars) and one set for the 'Population' (represented by grey bars). The y-axis for all charts represents the percentage, ranging from 0 to 100. The x-axis lists the categories for each variable.

- (a) Age:** Categories are 18-24, 25-34, 35-44, 45-54, 55-64, 65-74, 75-84, 85-94. The sample shows a higher percentage in the 18-24 and 25-34 age groups compared to the population.
- (b) Sex:** Categories are Male, Female. The sample is slightly more male than the population.
- (c) Education:** Categories are Less than High School, High School, Some College, College, Postgraduate. The sample has a higher percentage of college and postgraduate graduates.
- (d) Employment:** Categories are Full-time, Part-time, Unemployed, Retired. The sample has a higher percentage of full-time workers and a lower percentage of unemployed individuals.
- (e) Income:** Categories are Less than \$10,000, \$10,000-\$19,999, \$20,000-\$29,999, \$30,000-\$39,999, \$40,000-\$49,999, \$50,000-\$59,999, \$60,000-\$69,999, \$70,000-\$79,999, \$80,000-\$89,999, \$90,000-\$99,999, \$100,000 or more. The sample has a higher percentage in the higher income brackets.
- (f) Religion:** Categories are Catholic, Protestant, Jewish, Muslim, Other. The sample is predominantly Catholic.
- (g) Political Party:** Categories are Democrat, Republican, Independent. The sample is predominantly Democrat.
- (h) Marital Status:** Categories are Single, Married, Divorced, Widowed. The sample has a higher percentage of married individuals.
- (i) Number of Children:** Categories are 0, 1, 2, 3, 4, 5 or more. The sample has a higher percentage of individuals with 0 or 1 child.
- (j) Number of Siblings:** Categories are 0, 1, 2, 3, 4, 5 or more. The sample has a higher percentage of individuals with 0 or 1 sibling.
- (k) Number of Siblings Living:** Categories are 0, 1, 2, 3, 4, 5 or more. The sample has a higher percentage of individuals with 0 or 1 living sibling.
- (l) Number of Siblings Deceased:** Categories are 0, 1, 2, 3, 4, 5 or more. The sample has a higher percentage of individuals with 0 or 1 deceased sibling.

<211> 170

<213> Corynebacterium glutamicum

Met Leu Pro Val Asn Gln Thr Tyr Ala Gln Phe Ser Asp Thr Ala Phe  
1 5 10 15

Val Ser Ala Tyr Ile Ile Tyr Val Leu Ala Leu Ile Leu Ser Leu Val  
20 25 30



```
<210> 733
<211> 1095
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1072)
<223> RXA00945
```

<400> 733																
tcacagtacc	acccacaagc	cacaaggagg	gtatggagggt	gggcgtctaa	agccaaattt	60										
ttcccgggtgt	ttgaggcgat	tgcaccgtac	actaatgtgc	atg	ctt	gaa	cgc	ctc	115							
				Met	Leu	Glu	Arg	Leu								
				1				5								
aaa	cgc	cta	gat	ccg	ctc	att	gtc	ctc	att	gtg	ctg	gct	gtc	att	gtg	163
Lys	Arg	Leu	Asp	Pro	Leu	Ile	Val	Leu	Ile	Val	Leu	Ala	Val	Ile	Val	
				10					15					20		
gcg	atc	atc	att	cca	gtt	cgc	ggg	gtt	gct	gcg	gat	tgg	ttt	gat	gtc	211
Ala	Ile	Ile	Ile	Pro	Val	Arg	Gly	Val	Ala	Ala	Asp	Trp	Phe	Asp	Val	
			25					30					35			
gcc	gtc	aag	att	gcc	att	gcg	ctg	ctg	ttt	ttt	ctt	tat	ggg	gcc	cgc	259
Ala	Val	Lys	Ile	Ala	Ile	Ala	Leu	Leu	Phe	Phe	Leu	Tyr	Gly	Ala	Arg	
		40					45					50				
cta	tcc	acc	caa	gag	gcg	ctg	aat	ggt	ctg	aag	cac	tgg	agg	ctt	cac	307
Leu	Ser	Thr	Gln	Glu	Ala	Leu	Asn	Gly	Leu	Lys	His	Trp	Arg	Leu	His	
	55					60					65					

[illegible]



[illegible]







260	265	270
Ala Thr Gly Leu Pro Met	Ala Ala Val Ile Phe Gly Gly	Ala Asn Ile
275	280	285
Gly Leu Leu Ile Leu Pro	Leu Met Ile Phe His	Gln Val Gln Leu Met
290	295	300
Ile Cys Ala Trp Leu Ala	Ala Arg Tyr Gly Arg	Asp Ala Gln Glu Gln
305	310	315
		320
Lys Ala Asn Ala		

<210> 735  
 <211> 1281  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1258)  
 <223> RXN02556

<400> 735  
 tgccatcata ttaaggccaa attgcttgga tcctgggatt tatttaatta gattaaatcc 60  
 gtagaaaatta gcccatgaag catggaaagg cgaaaacccc ttg atc gtt tcc acc 115  
 Leu Ile Val Ser Thr  
 1 5  
 cag ccc att act gat cgc agc gca ctc tcg gca gaa cac gca gag gtg 163  
 Gln Pro Ile Thr Asp Arg Ser Ala Leu Ser Ala Glu His Ala Glu Val  
 10 15 20  
 atc aaa gca acg ctt cct ctc gtg ggc ggc aag att aat gag atc acg 211  
 Ile Lys Ala Thr Leu Pro Leu Val Gly Gly Lys Ile Asn Glu Ile Thr  
 25 30 35  
 ccg gtt ttc tac aac aag atg ttt gcg gct cac cca gaa ttg atc gct 259  
 Pro Val Phe Tyr Asn Lys Met Phe Ala Ala His Pro Glu Leu Ile Ala  
 40 45 50  
 aac acc ttc aac cgt ggc aat cag aag caa ggc gat cag cag aag gcg 307  
 Asn Thr Phe Asn Arg Gly Asn Gln Lys Gln Gly Asp Gln Gln Lys Ala  
 55 60 65  
 ctg gcg gct tcg att gca acg ttt gcc acc atg ctc gtt act cct gat 355  
 Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met Leu Val Thr Pro Asp  
 70 75 80 85  
 gct cct gac cca gtt cag ctg ctg tcc cgc att ggc cac aag cac gtg 403  
 Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile Gly His Lys His Val  
 90 95 100  
 tcc ctc ggc att act gct gat cag tac gac att gtt cac gag cac ctg 451  
 Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile Val His Glu His Leu  
 105 110 115  
 ttc gcc gca atc gtt gag gtt ttg gga gcg gaa act gtc acc gca cct 499

09602740-062300



Phe	Ala	Ala	Ile	Val	Glu	Val	Leu	Gly	Ala	Glu	Thr	Val	Thr	Ala	Pro		
		120					125					130					
gtc	gct	gaa	gcc	tgg	gat	gct	gtc	tac	tgg	atc	atg	gca	aat	gtg	ctg	547	
Val	Ala	Glu	Ala	Trp	Asp	Ala	Val	Tyr	Trp	Ile	Met	Ala	Asn	Val	Leu		
		135				140					145						
atc	ggg	ttt	gag	aac	aac	ctt	tat	gct	tcc	aac	gat	ctg	gag	cct	ggc	595	
Ile	Gly	Phe	Glu	Asn	Asn	Leu	Tyr	Ala	Ser	Asn	Asp	Leu	Glu	Pro	Gly		
150					155					160					165		
gac	gtc	ttc	cgc	gaa	gtc	acc	gtg	acc	gcg	aag	aag	cag	ctc	agc	gca	643	
Asp	Val	Phe	Arg	Glu	Val	Thr	Val	Thr	Ala	Lys	Lys	Gln	Leu	Ser	Ala		
				170					175					180			
acc	gtc	tgg	gaa	tac	acc	ctg	gca	ggg	gag	ctg	gtt	gcc	cca	gag	cca	691	
Thr	Val	Trp	Glu	Tyr	Thr	Leu	Ala	Gly	Glu	Leu	Val	Ala	Pro	Glu	Pro		
			185					190					195				
ggg	cag	tac	acc	tcc	atc	gga	gta	gtg	ctt	gac	gac	ggc	gcc	cgc	cag	739	
Gly	Gln	Tyr	Thr	Ser	Ile	Gly	Val	Val	Leu	Asp	Asp	Gly	Ala	Arg	Gln		
		200					205					210					
ctg	cgc	cag	tac	agc	ttg	ctc	ggc	ggc	tcc	gac	acc	gag	tac	cgc	att	787	
Leu	Arg	Gln	Tyr	Ser	Leu	Leu	Gly	Gly	Ser	Asp	Thr	Glu	Tyr	Arg	Ile		
		215				220				225							
gcg	gtt	gag	gat	aac	ggc	gag	gtt	tct	gga	ttc	ctg	cgt	gat	cgc	gta	835	
Ala	Val	Glu	Asp	Asn	Gly	Glu	Val	Ser	Gly	Phe	Leu	Arg	Asp	Arg	Val		
230					235					240					245		
tcc	gtt	ggg	gac	aag	att	gaa	gcc	acc	atc	gcg	gcc	ggc	gac	ctg	gtt	883	
Ser	Val	Gly	Asp	Lys	Ile	Glu	Ala	Thr	Ile	Ala	Ala	Gly	Asp	Leu	Val		
				250					255					260			
ctt	aac	aag	gac	acc	aat	cca	gtt	gtg	ctg	att	tcc	cag	ggc	atc	ggc	931	
Leu	Asn	Lys	Asp	Thr	Asn	Pro	Val	Val	Leu	Ile	Ser	Gln	Gly	Ile	Gly		
			265					270					275				
tcc	acc	cca	atg	gtg	ggc	atg	ctc	gca	ggg	atg	aac	cct	gaa	cgt	gac	979	
Ser	Thr	Pro	Met	Val	Gly	Met	Leu	Ala	Gly	Met	Asn	Pro	Glu	Arg	Asp		
		280					285					290					
gtt	gtg	gtt	ttg	cat	gct	gac	cag	gcc	gag	tcc	acc	tac	gcg	cag	gtg	1027	
Val	Val	Val	Leu	His	Ala	Asp	Gln	Ala	Glu	Ser	Thr	Tyr	Ala	Gln	Val		
		295				300					305						
gag	gaa	gtg	cag	ggg	ctc	gtc	gaa	aag	ctc	cct	aag	gct	gcg	ttt	gaa	1075	
Glu	Glu	Val	Gln	Gly	Leu	Val	Glu	Lys	Leu	Pro	Lys	Ala	Ala	Phe	Glu		
310					315					320					325		
atc	ttc	tac	cgc	gac	aac	gac	cag	tgg	ctc	gag	gtc	gct	ggc	cgc	att	1123	
Ile	Phe	Tyr	Arg	Asp	Asn	Asp	Gln	Trp	Leu	Glu	Val	Ala	Gly	Arg	Ile		
				330					335					340			
cca	tca	ggg	gcg	tcc	gtg	tac	ctg	tgc	ggg	ggc	gtg	gaa	ttc	ttg	aag	1171	
Pro	Ser	Gly	Ala	Ser	Val	Tyr	Leu	Cys	Gly	Gly	Val	Glu	Phe	Leu	Lys		
			345					350					355				
aac	gtg	cgt	gag	cag	atc	gag	gcg	ctc	gat	gag	cag	cct	cgc	gac	gta	1219	
Asn	Val	Arg	Glu	Gln	Ile	Glu	Ala	Leu	Asp	Glu	Gln	Pro	Arg	Asp	Val		

09602740-062300



360						365					370				
aac	ttc	gag	ctc	ttc	gca	cca	aac	gac	tg	ctg	att	tcc	taagcccaca	1268	
Asn	Phe	Glu	Leu	Phe	Ala	Pro	Asn	Asp	Trp	Leu	Ile	Ser			
375						380					385				

ccccagaact tcc 1281

```
<210> 736
<211> 386
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 736  
Leu Ile Val Ser Thr Gln Pro Ile Thr Asp Arg Ser Ala Leu Ser Ala  
1 5 10 15

Glu His Ala Glu Val Ile Lys Ala Thr Leu Pro Leu Val Gly Gly Lys  
20 25 30

Ile Asn Glu Ile Thr Pro Val Phe Tyr Asn Lys Met Phe Ala Ala His  
35 40 45

Pro Glu Leu Ile Ala Asn Thr Phe Asn Arg Gly Asn Gln Lys Gln Gly  
50 55 60

Asp Gln Gln Lys Ala Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met  
65 70 75 80

Leu Val Thr Pro Asp Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile  
85 90 95

Gly His Lys His Val Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile  
100 105 110

Val His Glu His Leu Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu  
115 120 125

Thr Val Thr Ala Pro Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile  
130 135 140

Met Ala Asn Val Leu Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn  
145 150 155 160

Asp Leu Glu Pro Gly Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys  
165 170 175

Lys Gln Leu Ser Ala Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu  
180 185 190

Val Ala Pro Glu Pro Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp  
195 200 205

Asp Gly Ala Arg Gln Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp  
210 215 220

Thr Glu Tyr Arg Ile Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe  
225 230 235 240

Leu Arg Asp Arg Val Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala

0960240 06300



aac acc ttc aac ggt ggc aat cag aag caa ggc gat cag cag aag gcg 307  
Asn Thr Phe Asn Gly Gly Asn Gln Lys Gln Gly Asp Gln Gln Lys Ala

006240 = 062400



55	60	65	
ctg gcg gct tcg att gca acg ttt gcc acc atg ctc gtt act cct gat			355
Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met Leu Val Thr Pro Asp			
70	75	80	85
gct cct gac cca gtt cag ctg ctg tcc cgc att ggc cac aag cac gtg			403
Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile Gly His Lys His Val			
	90	95	100
tcc ctc ggc att act gct gat cag tac gac att gtt cac gag cac ctg			451
Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile Val His Glu His Leu			
	105	110	115
ttc gcc gca atc gtt gag gtt ttg gga gcg gaa act gtc acc gca cct			499
Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu Thr Val Thr Ala Pro			
	120	125	130
gtc gct gaa gcc tgg gat gct gtc tac tgg atc atg gca aat gtg ctg			547
Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile Met Ala Asn Val Leu			
	135	140	145
atc ggt ttt gag aac aac ctt tat gct tcc aac gat ctg gag cct ggc			595
Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn Asp Leu Glu Pro Gly			
	150	155	160
gac gtc ttc cgc gaa gtc acc gtg acc gcg aag aag cag ctc agc gca			643
Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys Lys Gln Leu Ser Ala			
	170	175	180
acc gtc tgg gaa tac acc ctg gca ggt gag ctg gtt gcc cca gag cca			691
Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu Val Ala Pro Glu Pro			
	185	190	195
ggt cag tac acc tcc atc gga gta gtg ctt gac gac ggc gcc cgc cag			739
Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp Asp Gly Ala Arg Gln			
	200	205	210
ctg cgc cag tac agc ttg ctc ggc ggc tcc gac acc gag tac cgc att			787
Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp Thr Glu Tyr Arg Ile			
	215	220	225
gcg gtt gag gat aac ggc gag gtt tct gga ttc ctg cgt gat cgc gta			835
Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe Leu Arg Asp Arg Val			
	230	235	240
tcc gtt ggt gac aag att gaa gcc acc atc gcg gcc ggc gac ctg gtt			883
Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala Ala Gly Asp Leu Val			
	250	255	260
ctt aac aag gac acc aat cca gtt gtg ctg att tcc cag ggc atc ggc			931
Leu Asn Lys Asp Thr Asn Pro Val Val Leu Ile Ser Gln Gly Ile Gly			
	265	270	275
tcc acc cca atg gtg ggc atg ctc gca ggt atg aac cct gaa cgt gac			979
Ser Thr Pro Met Val Gly Met Leu Ala Gly Met Asn Pro Glu Arg Asp			
	280	285	290
gtt gtg gtt ttg cat gct gac cag gcc gag tcc acc tac gcg cag gtg			1027
Val Val Val Leu His Ala Asp Gln Ala Glu Ser Thr Tyr Ala Gln Val			
	295	300	305

09602740 062300



gag gaa gtg cag ggg ctc gtc gaa aag ctc cct aag gct gcg ttt gaa 1075  
 Glu Glu Val Gln Gly Leu Val Glu Lys Leu Pro Lys Ala Ala Phe Glu  
 310 315 320 325

atc ttc tac cgc gac aac gac cag tgg ctc gag gtc gct ggc cgc att 1123  
 Ile Phe Tyr Arg Asp Asn Asp Gln Trp Leu Glu Val Ala Gly Arg Ile  
 330 335 340

cca tca ggt gcg tcc gtg tac ctg tgc ggt ggc gtg gaa ttc ttg aag 1171  
 Pro Ser Gly Ala Ser Val Tyr Leu Cys Gly Gly Val Glu Phe Leu Lys  
 345 350 355

aac gtg cgt gag cag atc gag gcg ctc gat gag cag cct cgc gac gta 1219  
 Asn Val Arg Glu Gln Ile Glu Ala Leu Asp Glu Gln Pro Arg Asp Val  
 360 365 370

aac ttc gag ctc ttc gca cca aac gac tgg ctg att tcc taagcccaca 1268  
 Asn Phe Glu Leu Phe Ala Pro Asn Asp Trp Leu Ile Ser  
 375 380 385

ccccagaact tcc 1281

<210> 738

<211> 386

<212> PRT

<213> Corynebacterium glutamicum

<400> 738

Leu Ile Val Ser Thr Gln Pro Ile Thr Asp Arg Ser Ala Leu Ser Ala  
 1 5 10 15

Glu His Ala Glu Val Ile Lys Ala Thr Leu Pro Leu Val Gly Gly Lys  
 20 25 30

Ile Asn Glu Ile Thr Pro Val Phe Tyr Asn Lys Met Phe Ala Ala His  
 35 40 45

Pro Glu Leu Ile Ala Asn Thr Phe Asn Gly Gly Asn Gln Lys Gln Gly  
 50 55 60

Asp Gln Gln Lys Ala Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met  
 65 70 75 80

Leu Val Thr Pro Asp Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile  
 85 90 95

Gly His Lys His Val Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile  
 100 105 110

Val His Glu His Leu Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu  
 115 120 125

Thr Val Thr Ala Pro Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile  
 130 135 140

Met Ala Asn Val Leu Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn  
 145 150 155 160

Asp Leu Glu Pro Gly Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys

002290-0720960



ttgacatatc atctaaattt ccaagagagg acaccacaca gtg gct aac acg tca 115  
Val Ala Asn Thr Ser  
1 5



tcc gat tgg gca ggc gcc cca caa aat gca tca gca gac ggc gag ttc 163  
 Ser Asp Trp Ala Gly Ala Pro Gln Asn Ala Ser Ala Asp Gly Glu Phe  
                   10                  15                  20

gtt cgc gat acc aac tac atc gat gac cgc atc gtc gca gac gtt cca 211  
 Val Arg Asp Thr Asn Tyr Ile Asp Arg Ile Val Ala Asp Val Pro  
                   25                  30                  35

gcg gga tcc gaa cca att gct cag gaa gat ggc act ttc cat tgg cct 259  
 Ala Gly Ser Glu Pro Ile Ala Gln Glu Asp Gly Thr Phe His Trp Pro  
                   40                  45                  50

gtc gag gct ggt cgc tac cgt tta gtc gct gcc cgc gca tgt cca tgg 307  
 Val Glu Ala Gly Arg Tyr Arg Leu Val Ala Ala Arg Ala Cys Pro Trp  
                   55                  60                  65

gca cac cgc act gtt atc acc cgt cgt ctt ctc ggc ctg gag aac gtg 355  
 Ala His Arg Thr Val Ile Thr Arg Arg Leu Leu Gly Leu Glu Asn Val  
                   70                  75                  80                  85

atc tcg ctt ggt ctg acc ggc ccg act cac gac gtt cgt tcc tgg act 403  
 Ile Ser Leu Gly Leu Thr Gly Pro Thr His Asp Val Arg Ser Trp Thr  
                   90                  95                  100

ttc gat tta gat cca aac cat ctt gat ccc gtg ctg cag att cct cgt 451  
 Phe Asp Leu Asp Pro Asn His Leu Asp Pro Val Leu Gln Ile Pro Arg  
                   105                  110                  115

cta cag gac gcg tat ttc aac cgc ttc ccc gat tac ccg cgc ggc att 499  
 Leu Gln Asp Ala Tyr Phe Asn Arg Phe Pro Asp Tyr Pro Arg Gly Ile  
                   120                  125                  130

act gtc cca gcg ctc gtg gag gaa tcg tct aag aag gtc gtc acc aac 547  
 Thr Val Pro Ala Leu Val Glu Glu Ser Ser Lys Lys Val Val Thr Asn  
                   135                  140                  145

gat tac cct tcc atc acc atc gat ttc aat ctt gag tgg aag cag ttc 595  
 Asp Tyr Pro Ser Ile Thr Ile Asp Phe Asn Leu Glu Trp Lys Gln Phe  
                   150                  155                  160                  165

cac cgt gag ggt gcg cct aac ctc tac ccc gcg gag ctg cgc gag gag 643  
 His Arg Glu Gly Ala Pro Asn Leu Tyr Pro Ala Glu Leu Arg Glu Glu  
                   170                  175                  180

atg gcg ccg gtg atg aag cgc atc ttc act gag gtc aac aac ggc gta 691  
 Met Ala Pro Val Met Lys Arg Ile Phe Thr Glu Val Asn Asn Gly Val  
                   185                  190                  195

tac agg acc ggc ttt gcc ggt agc cag gaa gcg cac aac gag gcg tac 739  
 Tyr Arg Thr Gly Phe Ala Gly Ser Gln Glu Ala His Asn Glu Ala Tyr  
                   200                  205                  210

aag cgg ctt tgg gtt gcg ttg gac tgg cta gaa gat cgc tta tcg acg 787  
 Lys Arg Leu Trp Val Ala Leu Asp Trp Leu Glu Asp Arg Leu Ser Thr  
                   215                  220                  225

cga cgt tac ctc atg ggg gat cac atc acc gag gcg gat atc cgc ctc 835  
 Arg Arg Tyr Leu Met Gly Asp His Ile Thr Glu Ala Asp Ile Arg Leu  
                   230                  235                  240                  245

002290" 0422960



```
<210> 740
<211> 359
<212> PRT
<213> Corynebacterium glutamicum
```

Val Ala Asn Thr Ser Ser Asp Trp Ala Gly Ala Pro Gln Asn Ala Ser  
1 5 10 15

Ala Asp Gly Glu Phe Val Arg Asp Thr Asn Tyr Ile Asp Asp Arg Ile  
20 25 30

Val Ala Asp Val Pro Ala Gly Ser Glu Pro Ile Ala Gln Glu Asp Gly  
35 40 45

Thr Phe His Trp Pro Val Glu Ala Gly Arg Tyr Arg Leu Val Ala Ala  
50 55 60

Arg Ala Cys Pro Trp Ala His Arg Thr Val Ile Thr Arg Arg Leu Leu  
65 70 75 80

Gly Leu Glu Asn Val Ile Ser Leu Gly Leu Thr Gly Pro Thr His Asp  
85 90 95

Val	Arg	Ser	Trp	Thr	Phe	Asp	Leu	Asp	Pro	Asn	His	Leu	Asp	Pro	Val
			100					105					110		

Leu Gln Ile Pro Arg Leu Gln Asp Ala Tyr Phe Asn Arg Phe Pro Asp

[illegible]



	115					120					125				
Tyr	Pro 130	Arg	Gly	Ile	Thr	Val 135	Pro	Ala	Leu	Val	Glu 140	Glu	Ser	Ser	Lys
Lys 145	Val	Val	Thr	Asn	Asp 150	Tyr	Pro	Ser	Ile	Thr 155	Ile	Asp	Phe	Asn	Leu 160
Glu	Trp	Lys	Gln	Phe 165	His	Arg	Glu	Gly	Ala 170	Pro	Asn	Leu	Tyr	Pro 175	Ala
Glu	Leu	Arg	Glu 180	Glu	Met	Ala	Pro	Val 185	Met	Lys	Arg	Ile	Phe 190	Thr	Glu
Val	Asn	Asn 195	Gly	Val	Tyr	Arg	Thr 200	Gly	Phe	Ala	Gly	Ser 205	Gln	Glu	Ala
His	Asn 210	Glu	Ala	Tyr	Lys	Arg 215	Leu	Trp	Val	Ala	Leu 220	Asp	Trp	Leu	Glu
Asp 225	Arg	Leu	Ser	Thr	Arg 230	Arg	Tyr	Leu	Met	Gly 235	Asp	His	Ile	Thr	Glu 240
Ala	Asp	Ile	Arg	Leu 245	Tyr	Pro	Thr	Leu	Val 250	Arg	Phe	Asp	Ala	Val 255	Tyr
His	Gly	His	Phe 260	Lys	Cys	Gly	Arg	Asn 265	Lys	Ile	Thr	Glu	Met 270	Pro	Asn
Leu	Trp	Gly 275	Tyr	Leu	Arg	Asp	Leu 280	Phe	Gln	Thr	Pro	Gly 285	Phe	Gly	Asp
Thr	Thr 290	Asp	Phe	Thr	Glu	Ile 295	Lys	Gln	His	Tyr	Tyr 300	Ile	Thr	His	Ala
Glu 305	Ile	Asn	Pro	Thr	Arg 310	Ile	Val	Pro	Val	Gly 315	Pro	Asp	Leu	Ser	Gly 320
Phe	Ala	Thr	Pro	His 325	Gly	Arg	Glu	Lys	Leu 330	Gly	Gly	Ser	Pro	Phe 335	Ala
Glu	Gly	Val	Thr 340	Leu	Pro	Gly	Pro	Ile 345	Pro	Ala	Gly	Glu	Glu 350	Val	Lys
Asn	Pro	Glu 355	Pro	Phe	Gln	Lys									

```
<210> 741
<211> 1227
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(1204)  
<223> RXA00800
```

<400> 741  
gactccgcag ggatggccta caagtacggt cacggactta atttctagat tgtaggtagt 60



[illegible]



Asn Ser Ser Gly Leu Gly Gly Glu Gly Asp Ala Ser Glu Val Val Ala  
 230 235 240 245  
 aag gtt cgt gag ctc acc gat ggt ttc ggc acc gat gtc tcc atc gat 883  
 Lys Val Arg Glu Leu Thr Asp Gly Phe Gly Thr Asp Val Ser Ile Asp  
 250 255 260  
 gcg gta ggc atc atg ccg acc tgg cag cag gcg ttt tac tcc cgt gac 931  
 Ala Val Gly Ile Met Pro Thr Trp Gln Gln Ala Phe Tyr Ser Arg Asp  
 265 270 275  
 cat gca ggc cgc atg gtg atg gtg ggc gtt cca aac ctg acg tct cgc 979  
 His Ala Gly Arg Met Val Met Val Gly Val Pro Asn Leu Thr Ser Arg  
 280 285 290  
 gta gat gtt cct gcg att gat ttt tac ggt cgc ggt gga tcc gtg cgc 1027  
 Val Asp Val Pro Ala Ile Asp Phe Tyr Gly Arg Gly Gly Ser Val Arg  
 295 300 305  
 cct gca tgg tac ggc gac tgc ctg cct gag cgt gat ttc cca act tat 1075  
 Pro Ala Trp Tyr Gly Asp Cys Leu Pro Glu Arg Asp Phe Pro Thr Tyr  
 310 315 320 325  
 gtg gat ctg cac ctg cag ggt cgt ttc cca ctg gat aag ttt gtt tct 1123  
 Val Asp Leu His Leu Gln Gly Arg Phe Pro Leu Asp Lys Phe Val Ser  
 330 335 340  
 gag cgt att ggt ctt gat gat gtt gaa gag gct ttc aac acc atg aag 1171  
 Glu Arg Ile Gly Leu Asp Asp Val Glu Glu Ala Phe Asn Thr Met Lys  
 345 350 355  
 gct ggc gac gtg ctg cgt tct gtg gtg gag atc taaatggctc acgacggatt 1224  
 Ala Gly Asp Val Leu Arg Ser Val Val Glu Ile  
 360 365  
 gcg 1227  
 <210> 742  
 <211> 368  
 <212> PRT  
 <213> Corynebacterium glutamicum  
 <400> 742  
 Met Ser Thr Val Val Pro Gly Ile Val Ala Leu Ser Lys Gly Ala Pro  
 1 5 10 15  
 Val Glu Lys Val Asn Val Val Val Pro Asp Pro Gly Ala Asn Asp Val  
 20 25 30  
 Ile Val Lys Ile Gln Ala Cys Gly Val Cys His Thr Asp Leu Ala Tyr  
 35 40 45  
 Arg Asp Gly Asp Ile Ser Asp Glu Phe Pro Tyr Leu Leu Gly His Glu  
 50 55 60  
 Ala Ala Gly Ile Val Glu Glu Val Gly Glu Ser Val Thr His Val Glu  
 65 70 75 80  
 Val Gly Asp Phe Val Ile Leu Asn Trp Arg Ala Val Cys Gly Glu Cys  
 85 90 95

00602740.062300



Arg Ala Cys Lys Lys Gly Glu Pro Lys Tyr Cys Phe Asn Thr His Asn  
 100 105 110  
 Ala Ser Lys Lys Met Thr Leu Glu Asp Gly Thr Glu Leu Ser Pro Ala  
 115 120 125  
 Leu Gly Ile Gly Ala Phe Leu Glu Lys Thr Leu Val His Glu Gly Gln  
 130 135 140  
 Cys Thr Lys Val Asn Pro Glu Glu Asp Pro Ala Ala Ala Gly Leu Leu  
 145 150 155 160  
 Gly Cys Gly Ile Met Ala Gly Leu Gly Ala Ala Val Asn Thr Gly Asp  
 165 170 175  
 Ile Lys Arg Gly Glu Ser Val Ala Val Phe Gly Leu Gly Gly Val Gly  
 180 185 190  
 Met Ala Ala Ile Ala Gly Ala Lys Ile Ala Gly Ala Ser Lys Ile Ile  
 195 200 205  
 Ala Val Asp Ile Asp Glu Lys Lys Leu Glu Trp Ala Lys Glu Phe Gly  
 210 215 220  
 Ala Thr His Thr Ile Asn Ser Ser Gly Leu Gly Gly Glu Gly Asp Ala  
 225 230 235 240  
 Ser Glu Val Val Ala Lys Val Arg Glu Leu Thr Asp Gly Phe Gly Thr  
 245 250 255  
 Asp Val Ser Ile Asp Ala Val Gly Ile Met Pro Thr Trp Gln Gln Ala  
 260 265 270  
 Phe Tyr Ser Arg Asp His Ala Gly Arg Met Val Met Val Gly Val Pro  
 275 280 285  
 Asn Leu Thr Ser Arg Val Asp Val Pro Ala Ile Asp Phe Tyr Gly Arg  
 290 295 300  
 Gly Gly Ser Val Arg Pro Ala Trp Tyr Gly Asp Cys Leu Pro Glu Arg  
 305 310 315 320  
 Asp Phe Pro Thr Tyr Val Asp Leu His Leu Gln Gly Arg Phe Pro Leu  
 325 330 335  
 Asp Lys Phe Val Ser Glu Arg Ile Gly Leu Asp Asp Val Glu Glu Ala  
 340 345 350  
 Phe Asn Thr Met Lys Ala Gly Asp Val Leu Arg Ser Val Val Glu Ile  
 355 360 365

&lt;210&gt; 743

&lt;211&gt; 1011

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

002290.0420960



<400> 743

[illegible]



```
<210> 744
<211> 296
<212> PRT
<213> Corynebacterium glutamicum
```

```

<400> 744
Met Met Glu Thr Asn Pro Gln Thr Pro Glu Gly Asn Ser Met Ala Lys
  1          5          10
Pro Ser Ala Lys Lys Val Lys Asn Arg Arg Lys Val Arg Arg Thr Val
          20          25          30
Ala Gly Ala Leu Ala Leu Thr Ile Gly Leu Ser Gly Ala Gly Ile Leu
          35          40          45
Ala Thr Ala Ile Thr Pro Asp Ala Gln Val Ala Thr Ala Gln Arg Asp
          50          55          60
Asp Gln Ala Leu Ile Ser Glu Gly Lys Asp Leu Tyr Asp Val Ala Cys
  65          70          75          80
Ile Thr Cys His Gly Val Asn Leu Gln Gly Val Glu Asp Arg Gly Pro
          85          90          95
Ser Leu Val Gly Val Gly Glu Gly Ala Val Tyr Phe Gln Val His Ser
          100          105          110
Gly Arg Met Pro Ile Leu Arg Asn Glu Ala Gln Ala Glu Arg Lys Ala
          115          120          125
Pro Arg Tyr Thr Glu Ala Gln Thr Leu Ala Ile Ala Ala Tyr Val Ala
          130          135          140

```



Ala Met Trp Ile Gly Ser Arg Ser  
290 295

aagatcatgc tcatcgaagc cggcgcccga agatggcagt tggctggcat qqgtccttat 60

tcc act gcc ctg ttg gtt tcc gca tcc ctt gct gta tcc gtg ctc qca 307



```
<210> 746
<211> 134
<212> PRT
<213> Corynebacterium glutamicum
```

<210>	747
<211>	504
<212>	DNA

<210>	747
<211>	504
<212>	DNA



&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(481)

&lt;223&gt; RXN02036

&lt;400&gt; 747

```

ctaaaatgga aggcaatgga taccgcgccgc atgaacctcc gccaatggaa aatcctcggt 60
gccctcatct ctgctgcagt ggcggctctc ggagggtggt gtg cat att cct ttt 115
                               Val His Ile Pro Phe
                               1           5

ggg cac ctc gcc gac acc gtc tcc tgg gac tgc ggg gga ggc agc tgc 163
Gly His Leu Ala Asp Thr Val Ser Trp Asp Cys Gly Gly Gly Ser Cys
                10                15                20

gcc acc aac gat ttg gta tcc ctg ttc atg ccg gcc gcc ttc atg agt 211
Ala Thr Asn Asp Leu Val Ser Leu Phe Met Pro Ala Ala Phe Met Ser
                25                30                35

acc ctc gcc gcc tgc gta ttt ggc gcg tgg gcc ata ggt ttg atc gct 259
Thr Leu Ala Ala Cys Val Phe Gly Ala Trp Ala Ile Gly Leu Ile Ala
                40                45                50

ccc gca cta ttc atc gcg gtg act gcc tgg gca ttt cgc tcc ggc gtg 307
Pro Ala Leu Phe Ile Ala Val Thr Ala Trp Ala Phe Arg Ser Gly Val
                55                60                65

cag gct gcg att gcc gac ggc tac acg tcc gcg act tcc gtc ggc ttc 355
Gln Ala Ala Ile Ala Asp Gly Tyr Thr Ser Ala Thr Ser Val Gly Phe
                70                75                80                85

gaa atg act gtc tcg ctc att ctt ttc atc atc gca ggt ctg tgc ttt 403
Glu Met Thr Val Ser Leu Ile Leu Phe Ile Ile Ala Gly Leu Cys Phe
                90                95                100

ctg ggc tgg atc ccc atg ttc atc aac aac cgc caa gtc gcg cgc aag 451
Leu Gly Trp Ile Pro Met Phe Ile Asn Asn Arg Gln Val Ala Arg Lys
                105                110                115

gtc cgc gag agg gct gcg ggc ttg agc aat taggctctcg cttttcgacg 501
Val Arg Glu Arg Ala Ala Gly Leu Ser Asn
                120                125

ttt 504

```

&lt;210&gt; 748

&lt;211&gt; 127

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 748

```

Val His Ile Pro Phe Gly His Leu Ala Asp Thr Val Ser Trp Asp Cys
  1           5           10           15

Gly Gly Gly Ser Cys Ala Thr Asn Asp Leu Val Ser Leu Phe Met Pro
    20           25           30

```

09602740-062300



```
<210> 749
<211> 882
<212> DNA
<213> Corynebacterium glutamicum
```

<400> 749																
tctgaacttt tccgcatcga cccagatgag gtttaccctcg acgacgacgc cacctgcgaa																60
ttcaaccccat ggccgtatcc tgcgcgattt taggagataa atg tct aat caa tta																115
Met Ser Asn Gln Leu																5
ccc gat cac gtc cgc gac gcc ttc caa gta ggt gcg gga cct gcc gaa																163
Pro Asp His Val Arg Asp Ala Phe Gln Val Gly Ala Gly Pro Ala Glu																20
10 15																
caa ctc ggt caa gct tgg gac ttc gga ttc cgc gtc ggc aac act gtg																211
Gln Leu Gly Gln Ala Trp Asp Phe Gly Phe Arg Val Gly Asn Thr Val																35
25 30																
ttc gcc aaa gtg acg gcg ccg gaa gtg tcg ggc tgg tcg tcg aaa acc																259
Phe Ala Lys Val Thr Ala Pro Glu Val Ser Gly Trp Ser Ser Lys Thr																50
40 45																
cgc gaa acc ctg aaa cca gaa ggc gtg cgc gtc gta cga ccg atc cgc																307
Arg Glu Thr Leu Lys Pro Glu Gly Val Arg Val Val Arg Pro Ile Arg																65
55 60																
tcc acc gac ggc cga ttt gtg gtt gcg ggg tgg cgc gca tcg gtg ttc																355
Ser Thr Asp Gly Arg Phe Val Val Ala Gly Trp Arg Ala Ser Val Phe																85
70 75																
tct acg gga acg atc agc aag cga gtc gat gag acg gtc gtt gcg ggt																403
Ser Thr Gly Thr Ile Ser Lys Arg Val Asp Glu Thr Val Val Ala Gly																100
90 95																
ctt cgt ttg gca gat gca tta gtg gat acg cat gca ccg gaa cct gtg																451

	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2423	2424	2425	2426	2427	2428	2429	2430	2431	2432	2
--	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	---



Leu Arg Leu Ala Asp Ala Leu Val Asp Thr His Ala Pro Glu Pro Val  
 105 110 115  
 gac aat gtg ttt aac cgt gct gat gtg cag gcc tgg gaa gag cag ccc 499  
 Asp Asn Val Phe Asn Arg Ala Asp Val Gln Ala Trp Glu Glu Gln Pro  
 120 125 130  
 ggt cga atc ggt gaa ttg ttg gag ccg att aat cgc gtg aac cag gtt 547  
 Gly Arg Ile Gly Glu Leu Leu Glu Pro Ile Asn Arg Val Asn Gln Val  
 135 140 145  
 ggt cat gcg gat atg ttg gcg aca acg ctg tat gcg gga act cag cca 595  
 Gly His Ala Asp Met Leu Ala Thr Thr Leu Tyr Ala Gly Thr Gln Pro  
 150 155 160 165  
 cct gca gtg acg gat ttg gtg cca gtg ctg cgt ccg cat ggt ttc act 643  
 Pro Ala Val Thr Asp Leu Val Pro Val Leu Arg Pro His Gly Phe Thr  
 170 175 180  
 gcg gca ttg gtg atc gtt gat ggg ttg ctg ctg ggt gcg gtt gat gag 691  
 Ala Ala Leu Val Ile Val Asp Gly Leu Leu Leu Gly Ala Val Asp Glu  
 185 190 195  
 gga att ctg cgg agg ttt tcg cat ttg ccg gaa att gag cag ctg gtt 739  
 Gly Ile Leu Arg Arg Phe Ser His Leu Pro Glu Ile Glu Gln Leu Val  
 200 205 210  
 ttg agg gca ttt ttg ttc cgt cga aac ttg cag gag ttc tct gag aac 787  
 Leu Arg Ala Phe Leu Phe Arg Arg Asn Leu Gln Glu Phe Ser Glu Asn  
 215 220 225  
 aac gat ccg aat gtt att tcg aac cta aac agg gtg gaa tcg aca ctc 835  
 Asn Asp Pro Asn Val Ile Ser Asn Leu Asn Arg Val Glu Ser Thr Leu  
 230 235 240 245  
 gtg tcg tat gtt tct gac aag att tgaggatatgt cggaatacaa acc 882  
 Val Ser Tyr Val Ser Asp Lys Ile  
 250

&lt;210&gt; 750

&lt;211&gt; 253

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 750

Met Ser Asn Gln Leu Pro Asp His Val Arg Asp Ala Phe Gln Val Gly  
 1 5 10 15  
 Ala Gly Pro Ala Glu Gln Leu Gly Gln Ala Trp Asp Phe Gly Phe Arg  
 20 25 30  
 Val Gly Asn Thr Val Phe Ala Lys Val Thr Ala Pro Glu Val Ser Gly  
 35 40 45  
 Trp Ser Ser Lys Thr Arg Glu Thr Leu Lys Pro Glu Gly Val Arg Val  
 50 55 60  
 Val Arg Pro Ile Arg Ser Thr Asp Gly Arg Phe Val Val Ala Gly Trp  
 65 70 75 80

002290"0420960



Arg	Ala	Ser	Val	Phe 85	Ser	Thr	Gly	Thr	Ile 90	Ser	Lys	Arg	Val	Asp 95	Glu
Thr	Val	Val	Ala 100	Gly	Leu	Arg	Leu	Ala 105	Asp	Ala	Leu	Val	Asp 110	Thr	His
Ala	Pro	Glu 115	Pro	Val	Asp	Asn	Val 120	Phe	Asn	Arg	Ala	Asp 125	Val	Gln	Ala
Trp	Glu 130	Glu	Gln	Pro	Gly	Arg 135	Ile	Gly	Glu	Leu	Leu 140	Glu	Pro	Ile	Asn
Arg 145	Val	Asn	Gln	Val	Gly 150	His	Ala	Asp	Met	Leu 155	Ala	Thr	Thr	Leu	Tyr 160
Ala	Gly	Thr	Gln	Pro 165	Pro	Ala	Val	Thr	Asp 170	Leu	Val	Pro	Val	Leu 175	Arg
Pro	His	Gly	Phe 180	Thr	Ala	Ala	Leu	Val 185	Ile	Val	Asp	Gly	Leu 190	Leu	Leu
Gly	Ala	Val 195	Asp	Glu	Gly	Ile	Leu 200	Arg	Arg	Phe	Ser	His 205	Leu	Pro	Glu
Ile 210	Glu	Gln	Leu	Val	Leu	Arg 215	Ala	Phe	Leu	Phe	Arg 220	Arg	Asn	Leu	Gln
Glu 225	Phe	Ser	Glu	Asn	Asn 230	Asp	Pro	Asn	Val	Ile 235	Ser	Asn	Leu	Asn	Arg 240
Val	Glu	Ser	Thr	Leu 245	Val	Ser	Tyr	Val	Ser 250	Asp	Lys	Ile			

```
<210> 751
<211> 1059
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(1036)  
<223> RXN02206
```

```
<400> 751
ggcaggatct gctgctgcgg ctaggagggt tatctcttca ttcacccgat ctaccgtact 60
```

accttatgac ctcagtagtg tgggtgggcgt gaaacagcga atg gtc ggt tca agt 115  
Met Val Gly Ser Ser  
1 5

ggt ttg cgg gta tcc agg ctc ggt ttg ggc acc tca aca tgg ggc tcg 163  
Gly Leu Arg Val Ser Arg Leu Gly Leu Gly Thr Ser Thr Trp Gly Ser  
10 15 20

ggc acc gag ctg gct gag gca ggc gat atc ttt aag gcg ttc atc aat 211  
Gly Thr Glu Leu Ala Glu Ala Gly Asp Ile Phe Lys Ala Phe Ile Asn  
25 30 35

tct ggt ggc acg ctt atc gac gtc tcc ccc aac tac acc acc ggc gtc 259  
Ser Gly Gly Thr Leu Ile Asp Val Ser Pro Asn Tyr Thr Thr Gly Val



40					45					50							
gcg	gaa	gaa	atg	ctc	ggc	acg	atg	ttg	gat	gcg	gaa	gtc	tct	cgt	tcg	307	
Ala	Glu	Glu	Met	Leu	Gly	Thr	Met	Leu	Asp	Ala	Glu	Val	Ser	Arg	Ser		
55					60					65							
gct	gtc	gtc	att	tcc	tcc	agc	gca	ggg	gtc	aac	ccc	gct	ctg	ccg	ctc	355	
Ala	Val	Val	Ile	Ser	Ser	Ser	Ala	Gly	Val	Asn	Pro	Ala	Leu	Pro	Leu		
70					75					80					85		
ggc	cga	cgt	gtg	gat	tgc	tcc	cgc	cgc	aat	ttg	att	gcc	caa	tta	gat	403	
Gly	Arg	Arg	Val	Asp	Cys	Ser	Arg	Arg	Asn	Leu	Ile	Ala	Gln	Leu	Asp		
90					95					100							
gtc	acc	ctg	cgg	gca	tta	aac	act	gac	tat	ttg	gat	ttg	tgg	tct	gtg	451	
Val	Thr	Leu	Arg	Ala	Leu	Asn	Thr	Asp	Tyr	Leu	Asp	Leu	Trp	Ser	Val		
105					110					115							
ggc	tat	tgg	gat	gag	ggc	acc	cca	ccg	cat	gag	gtg	gcc	gat	act	ttg	499	
Gly	Tyr	Trp	Asp	Glu	Gly	Thr	Pro	Pro	His	Glu	Val	Ala	Asp	Thr	Leu		
120					125					130							
gat	tac	gcc	gtg	cgc	acc	ggc	cga	gtc	cga	tat	gcc	ggg	gtc	cga	gga	547	
Asp	Tyr	Ala	Val	Arg	Thr	Gly	Arg	Val	Arg	Tyr	Ala	Gly	Val	Arg	Gly		
135					140					145							
tat	tcc	ggg	tgg	cag	tta	gcg	gtc	acc	cac	gct	gca	tcc	aat	cat	gca	595	
Tyr	Ser	Gly	Trp	Gln	Leu	Ala	Val	Thr	His	Ala	Ala	Ser	Asn	His	Ala		
150					155					160					165		
gcg	gcc	tcc	gcc	cgc	ccc	gtg	gtc	gtt	gca	caa	aat	gaa	tac	agc	ctg	643	
Ala	Ala	Ser	Ala	Arg	Pro	Val	Val	Val	Ala	Gln	Asn	Glu	Tyr	Ser	Leu		
170					175					180							
ctg	gaa	cgc	cgc	gca	gaa	caa	gaa	ctc	ctc	cct	gcc	acc	caa	cac	cta	691	
Leu	Glu	Arg	Arg	Ala	Glu	Gln	Glu	Leu	Leu	Pro	Ala	Thr	Gln	His	Leu		
185					190					195							
ggg	gtc	gga	ttc	ttt	gct	ggc	gct	ccg	ctg	ggg	caa	ggc	gtg	ctg	act	739	
Gly	Val	Gly	Phe	Phe	Ala	Gly	Ala	Pro	Leu	Gly	Gln	Gly	Val	Leu	Thr		
200					205					210							
gct	aaa	tac	cgc	tcc	gaa	att	ccc	cat	gat	tcc	aga	gct	gca	tcc	aca	787	
Ala	Lys	Tyr	Arg	Ser	Glu	Ile	Pro	His	Asp	Ser	Arg	Ala	Ala	Ser	Thr		
215					220					225							
gga	cgc	gac	gca	gaa	gtc	caa	agc	tac	cta	gat	aat	cga	ggc	cgc	atc	835	
Gly	Arg	Asp	Ala	Glu	Val	Gln	Ser	Tyr	Leu	Asp	Asn	Arg	Gly	Arg	Ile		
230					235					240					245		
att	gtc	gat	gct	ctt	gat	act	gca	gcc	aaa	gga	tta	ggc	att	agc	ccc	883	
Ile	Val	Asp	Ala	Leu	Asp	Thr	Ala	Ala	Lys	Gly	Leu	Gly	Ile	Ser	Pro		
250					255					260							
gct	gtc	aca	gcc	acc	acc	tgg	gtg	cgt	gat	cgt	ccc	gga	gtg	aca	gct	931	
Ala	Val	Thr	Ala	Thr	Thr	Trp	Val	Arg	Asp	Arg	Pro	Gly	Val	Thr	Ala		
265					270					275							
gtc	atc	gtg	ggc	gct	cgc	aca	cat	gaa	cag	ctg	tca	cat	ctt	ctc	aag	979	
Val	Ile	Val	Gly	Ala	Arg	Thr	His	Glu	Gln	Leu	Ser	His	Leu	Leu	Lys		
280					285					290							

09602740-062300



gcg gaa tcg gtg act ttg cca aca cca atc aca caa gcc ctt gat gat 1027  
 Ala Glu Ser Val Thr Leu Pro Thr Pro Ile Thr Gln Ala Leu Asp Asp  
 295 300 305

gtc tcc ctg tgacttggtc caattacatt cac 1059  
 Val Ser Leu  
 310

<210> 752

<211> 312

<212> PRT

<213> Corynebacterium glutamicum

<400> 752

Met Val Gly Ser Ser Gly Leu Arg Val Ser Arg Leu Gly Leu Gly Thr  
 1 5 10 15

Ser Thr Trp Gly Ser Gly Thr Glu Leu Ala Glu Ala Gly Asp Ile Phe  
 20 25 30

Lys Ala Phe Ile Asn Ser Gly Gly Thr Leu Ile Asp Val Ser Pro Asn  
 35 40 45

Tyr Thr Thr Gly Val Ala Glu Glu Met Leu Gly Thr Met Leu Asp Ala  
 50 55 60

Glu Val Ser Arg Ser Ala Val Val Ile Ser Ser Ser Ala Gly Val Asn  
 65 70 75 80

Pro Ala Leu Pro Leu Gly Arg Arg Val Asp Cys Ser Arg Arg Asn Leu  
 85 90 95

Ile Ala Gln Leu Asp Val Thr Leu Arg Ala Leu Asn Thr Asp Tyr Leu  
 100 105 110

Asp Leu Trp Ser Val Gly Tyr Trp Asp Glu Gly Thr Pro Pro His Glu  
 115 120 125

Val Ala Asp Thr Leu Asp Tyr Ala Val Arg Thr Gly Arg Val Arg Tyr  
 130 135 140

Ala Gly Val Arg Gly Tyr Ser Gly Trp Gln Leu Ala Val Thr His Ala  
 145 150 155 160

Ala Ser Asn His Ala Ala Ala Ser Ala Arg Pro Val Val Val Ala Gln  
 165 170 175

Asn Glu Tyr Ser Leu Leu Glu Arg Arg Ala Glu Gln Glu Leu Leu Pro  
 180 185 190

Ala Thr Gln His Leu Gly Val Gly Phe Phe Ala Gly Ala Pro Leu Gly  
 195 200 205

Gln Gly Val Leu Thr Ala Lys Tyr Arg Ser Glu Ile Pro His Asp Ser  
 210 215 220

Arg Ala Ala Ser Thr Gly Arg Asp Ala Glu Val Gln Ser Tyr Leu Asp  
 225 230 235 240

09602740-062300



```
<210> 753
<211> 747
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(724)
<223> RXN02554
```

<400> 753																
gcttttgaag tgtgtcgcgt gtgcggactg aaatagtttc cgcttcaact tggttgctaa																60
ggataggctc cataaaaaata accaaaggcg gaaaattttca atg tca cac act aag																115
Met Ser His Thr Lys																5
cca tcc att gcc atc ctc ggt gct ggc cga gtg ggt tct tca ctt gcc																163
Pro Ser Ile Ala Ile Leu Gly Ala Gly Arg Val Gly Ser Ser Leu Ala																20
agg tca gcg gtc gcc gca ggc tat gag gta aag gtt gct ggt tca ggt																211
Arg Ser Ala Val Ala Ala Gly Tyr Glu Val Lys Val Ala Gly Ser Gly																35
gct gtg gac aaa atc gct ctt acc gct gag atc ctt atg ccc ggc gcg																259
Ala Val Asp Lys Ile Ala Leu Thr Ala Glu Ile Leu Met Pro Gly Ala																50
gtt cca agc act gct gac cag gct gta aag gat gca gat att gtg ttc																307
Val Pro Ser Thr Ala Asp Gln Ala Val Lys Asp Ala Asp Ile Val Phe																65
ttg gct gtt ccc ctg cat aaa ttc cgc agt gtc aat cca gcc act tta																355
Leu Ala Val Pro Leu His Lys Phe Arg Ser Val Asn Pro Ala Thr Leu																85
gag ggc aag atc gtt att gac acg atg aac cac tgg gtt ccg gtc aat																403
Glu Gly Lys Ile Val Ile Asp Thr Met Asn His Trp Val Pro Val Asn																100
ggt gag ttg gag gaa att gat cag gat ccg cgc agc act tcg gag att																451
Gly Glu Leu Glu Glu Ile Asp Gln Asp Pro Arg Ser Thr Ser Glu Ile																115

[illegible]



att ggt tat cac gag att gag cag gat gcg ggt acc ggg cgt gcg att 547  
Ile Gly Tyr His Glu Ile Glu Gln Asp Ala Gly Thr Gly Arg Ala Ile  
135 140 145

gcg tat gcc acg gat gat gtg gat gca ggt gcc cag gtt gca cag cta 595  
Ala Tyr Ala Thr Asp Asp Val Asp Ala Gly Ala Gln Val Ala Gln Leu  
150 155 160 165

att aag agt ttt ggg ttt gtt cct tta aat att ggc gca ttg gaa aac 643  
Ile Lys Ser Phe Gly Phe Val Pro Leu Asn Ile Gly Ala Leu Glu Asn  
170 175 180

ggc cgt att ctg gaa cct ggc caa gaa gct ttc ggc gcg cac ctt aat 691  
Gly Arg Ile Leu Glu Pro Gly Gln Glu Ala Phe Gly Ala His Leu Asn  
185 190 195

aaa gat tgc cgc cta gaa ctt gtt aat cag cgg tagtacctcg atcttcagcc 744  
Lys Asp Ser Arg Leu Glu Leu Val Asn Gln Arg  
200 205

aac 747

<210> 754

<211> 208

&lt;212&gt; PRT

<213> Corynebacterium glutamicum

<400> 754

Met Ser His Thr Lys Pro Ser Ile Ala Ile Leu Gly Ala Gly Arg Val  
1 5 10 15

Gly Ser Ser Leu Ala Arg Ser Ala Val Ala Ala Gly Tyr Glu Val Lys  
20 25 30

Val Ala Gly Ser Gly Ala Val Asp Lys Ile Ala Leu Thr Ala Glu Ile  
35 40 45

Leu Met Pro Gly Ala Val Pro Ser Thr Ala Asp Gln Ala Val Lys Asp  
50 55 60

Ala Asp Ile Val Phe Leu Ala Val Pro Leu His Lys Phe Arg Ser Val  
65 70 75 80

Asn Pro Ala Thr Leu Glu Gly Lys Ile Val Ile Asp Thr Met Asn His  
85 90 95

Trp Val Pro Val Asn Gly Glu Leu Glu Glu Ile Asp Gln Asp Pro Arg  
100 105 110

Ser Thr Ser Glu Ile Ile Ala Glu Phe Phe Ala Gly Ser Thr Met Val  
115 120 125

Lys Ser Phe Asn His Ile Gly Tyr His Glu Ile Glu Gln Asp Ala Gly  
130 135 140

Thr Gly Arg Ala Ile Ala Tyr Ala Thr Asp Asp Val Asp Ala Gly Ala

[illegible]



<400> 755																	
ttacagcgag	tttttcagac	gtccatcgca	ccgtgcacaa	caacatttca	ggtgcacggc	60											
ccgaacacgg	gagagaacgc	tgagcgttac	aacactgtcc	atg	aag	ggc	gaa	ttc								115	
				Met	Lys	Gly	Glu	Phe								5	
				1													
cac	gcc	ccc	gat	ttg	gac	aaa	gaa	ttt	ttc	ccg	ggg	cac	gta	acc	gat	163	
His	Ala	Pro	Asp	Leu	Asp	Lys	Glu	Phe	Phe	Pro	Gly	His	Val	Thr	Asp		
				10											15	20	
agt	ggt	gaa	gtc	gtg	aac	atg	ctg	ttc	acc	gat	ttc	gct	aat	ggt	tgg	211	
Ser	Gly	Glu	Val	Val	Asn	Met	Leu	Phe	Thr	Asp	Phe	Ala	Asn	Gly	Trp		
			25											30	35		
ttc	gca	atg	gac	cgc	atc	gta	ttg	atc	cgt	ctt	ctt	atg	acg	gca	gtc	259	
Phe	Ala	Met	Asp	Arg	Ile	Val	Leu	Ile	Arg	Leu	Leu	Met	Thr	Ala	Val		
		40											45	50			
gtt	gtg	gtc	ttc	ttc	ctt	tgg	gct	atg	cgc	aag	cca	aag	ctt	gtt	ccg	307	
Val	Val	Val	Phe	Phe	Leu	Trp	Ala	Met	Arg	Lys	Pro	Lys	Leu	Val	Pro		
		55											60	65			
cat	ggc	gtc	cag	aat	ttt	gca	gag	tac	gca	ctc	gat	ttc	gtt	ggt	att	355	
His	Gly	Val	Gln	Asn	Phe	Ala	Glu	Tyr	Ala	Leu	Asp	Phe	Val	Gly	Ile		
		70											75	80	85		
cac	atc	gct	gaa	gac	atc	ctc	gga	aag	aag	aaa	ggt	cgt	cgg	ttc	ctg	403	
His	Ile	Ala	Glu	Asp	Ile	Leu	Gly	Lys	Lys	Lys	Gly	Arg	Arg	Phe	Leu		
				90											95	100	
ccg	atc	ctg	gcc	acc	atc	ttc	ttc	gcg	gct	ctg	ttg	atg	aac	ctt	gca	451	
Pro	Ile	Leu	Ala	Thr	Ile	Phe	Phe	Ala	Ala	Leu	Leu	Met	Asn	Leu	Ala		
			105											110	115		
acg	atc	atc	ccg	gga	cta	aac	atc	tcc	tcc	aac	tca	cgt	att	gca	ttc	499	

[illegible]



[illegible]

```
<210> 756
<211> 270
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 756																
Met	Lys	Gly	Glu	Phe	His	Ala	Pro	Asp	Leu	Asp	Lys	Glu	Phe	Phe	Pro	
1				5					10					15		
Gly	His	Val	Thr	Asp	Ser	Gly	Glu	Val	Val	Asn	Met	Leu	Phe	Thr	Asp	
			20					25					30			
Phe	Ala	Asn	Gly	Trp	Phe	Ala	Met	Asp	Arg	Ile	Val	Leu	Ile	Arg	Leu	
		35					40					45				
Leu	Met	Thr	Ala	Val	Val	Val	Val	Phe	Phe	Leu	Trp	Ala	Met	Arg	Lys	
	50					55					60					
Pro	Lys	Leu	Val	Pro	His	Gly	Val	Gln	Asn	Phe	Ala	Glu	Tyr	Ala	Leu	

**SECRET**



```

<400> 757
ttacagcgag tttttcagac gtccatcgca ccgtgcacaa caacatttca ggtgcacggc 60

ccgaacacgg gagagaacgc tgagcggttac aacactgtcc  atg  aag  ggc  gaa  ttc      115
                                         Met  Lys  Gly  Glu  Phe
                                         1      5

cac  gcc  ccc  gat  ttg  gac  aaa  gaa  ttt  ttc  ccg  ggg  cac  gta  acc  gat      163
His  Ala  Pro  Asp  Leu  Asp  Lys  Glu  Phe  Phe  Pro  Gly  His  Val  Thr  Asp
                        10                        15                        20

agt  ggt  gaa  gtc  gtg  aac  atg  ctg  ttc  acc  gat  ttc  gct  aat  ggt  tgg      211

```



<210> 758

[illegible]



<400> 758

<210> 759

<211> 1764

<212> DNA

<213> Corynebacterium glutamicum

<220>

&lt;221&gt; CDS

**SECRET**



<223> RXA01201

tctgggcaaac tctgagcgtct gcgqggcaagc ttcgcataaa gacacgacga attagacaac 60

atc tcc tcc gat gag atc cgt agc gcg att gcg aac tac acc tcg agc 163  
Ile Ser Ser Asp Glu Ile Arg Ser Ala Ile Ala Asn Tyr Thr Ser Ser  
10 15 20

tac	tcc	gcg	gag	gcc	tcc	cgt	gag	gag	gtc	ggc	gtg	gtt	att	tcg	gcc	211
Tyr	Ser	Ala	Glu	Ala	Ser	Arg	Glu	Glu	Val	Gly	Val	Val	Ile	Ser	Ala	
		25					30						35			

gct gac ggt atc gcc cag gtt tcg ggc ctc ccg tca gta atg gcg aat 259  
Ala Asp Gly Ile Ala Gln Val Ser Gly Leu Pro Ser Val Met Ala Asn  
40 45 50

gag ctc ctc gaa ttc ccg ggc ggc gtc atc ggc gtc gca cag aac ctt 307  
Glu Leu Leu Glu Phe Pro Gly Gly Val Ile Gly Val Ala Gln Asn Leu  
55 60 65

gaa gct gac cga gtc ggc gtc gtg gtc ctg ggt aac tac gag cta ctt 355  
Glu Ala Asp Arg Val Gly Val Val Val Leu Gly Asn Tyr Glu Leu Leu  
70 75 80 85

aaa gaa ggc gac caa gtt cgt cgt act gga gac gtt ctg tct atc cca 403  
Lys Glu Gly Asp Gln Val Arg Arg Thr Gly Asp Val Leu Ser Ile Pro  
90 95 100

gtc ggc gag gca ttc ctt ggc cgc gtt atc aac ccc ctt ggc cag cca 451  
Val Gly Glu Ala Phe Leu Gly Arg Val Ile Asn Pro Leu Gly Gln Pro  
105 110 115

att gac ggc ctg ggc gaa att gca tcc gaa gag gac cgc gtc ctc gag 499  
Ile Asp Gly Leu Gly Glu Ile Ala Ser Glu Glu Asp Arg Val Leu Glu  
120 125 130

ctt cag gca cca acc gtg ctt gag cgc cag cct gtc gag gag cct ttg 547  
 Leu Gln Ala Pro Thr Val Leu Glu Arg Gln Pro Val Glu Glu Pro Leu  
 135 140 145

gca acc ggc atc aag gct atc gat gca atg acc cca atc ggc cgc ggt 595  
Ala Thr Gly Ile Lys Ala Ile Asp Ala Met Thr Pro Ile Gly Arg Gly  
150 155 160 165

cag cgt cag ctg atc att ggt gac cgt aag act ggc aag acc gca gtc 643  
Gln Arg Gln Leu Ile Ile Gly Asp Arg Lys Thr Gly Lys Thr Ala Val  
170 175 180

tgt	gtc	gat	acc	atc	ctt	aac	cag	aag	gcc	aac	tgg	gag	acc	ggc	gac	691
Cys	Val	Asp	Thr	Ile	Leu	Asn	Gln	Lys	Ala	Asn	Trp	Glu	Thr	Gly	Asp	
			185					190					195			

aag acc aag cag gtt cgc tgc atc tac gtc gca atc ggt cag aag ggc 739  
Lys Thr Lys Gln Val Arg Cys Ile Tyr Val Ala Ile Gly Gln Lys Gly  
200 205 210

[illegible]







0960740-062300



[illegible]



09620 : 0740003900

09620 : 0740003900

09620 : 0740003900

09620 : 0740003900







ctg acc tcc acc tct cgt att ctc gag cca gca atc gtt ggt gag cgt 1219  
 Leu Thr Ser Thr Ser Arg Ile Leu Glu Pro Ala Ile Val Gly Glu Arg  
 360 365 370  
 cac tac gag gtt tct cag cgt gtc atc ggc att ctg cag aag aac aag 1267  
 His Tyr Glu Val Ser Gln Arg Val Ile Gly Ile Leu Gln Lys Asn Lys  
 375 380 385  
 gaa ctt cag gac atc atc gcc atc ctt ggt atg gac gag ctt tct gaa 1315  
 Glu Leu Gln Asp Ile Ile Ala Ile Leu Gly Met Asp Glu Leu Ser Glu  
 390 395 400 405  
 gag gac aag atc acc gtt gca cgt gcg cgt cgc atc gag cgc ttc ctg 1363  
 Glu Asp Lys Ile Thr Val Ala Arg Ala Arg Arg Ile Glu Arg Phe Leu  
 410 415 420  
 ggt cag aac ttc ttc gtt gca gag aag ttc acc ggt ctt cct ggc tcc 1411  
 Gly Gln Asn Phe Phe Val Ala Glu Lys Phe Thr Gly Leu Pro Gly Ser  
 425 430 435  
 tac gtg cca ctg acc gac acc gtc gac gct ttc gag cgt att tgc aac 1459  
 Tyr Val Pro Leu Thr Asp Thr Val Asp Ala Phe Glu Arg Ile Cys Asn  
 440 445 450  
 ggc gac ttc gac cac tac cca gag cag gct ttc aac ggc ctc ggt ggt 1507  
 Gly Asp Phe Asp His Tyr Pro Glu Gln Ala Phe Asn Gly Leu Gly Gly  
 455 460 465  
 ttg gac gat gtc gaa gct gca tac aag aag ctg acc gga aag 1549  
 Leu Asp Asp Val Glu Ala Ala Tyr Lys Lys Leu Thr Gly Lys  
 470 475 480  
 taaggtagag acacatggct gaa 1572

&lt;210&gt; 762

&lt;211&gt; 483

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 762

Met Thr Thr Ala Leu Glu Glu Gln Asn Ala Gln Gln Ala Ala Thr Ala  
 1 5 10 15  
 Gly Arg Val Val Arg Val Ile Gly Ala Val Val Asp Val Glu Phe Pro  
 20 25 30  
 Arg Gly Glu Leu Pro Ala Leu Tyr Asn Ala Leu Thr Val Glu Val Thr  
 35 40 45  
 Leu Glu Ser Val Lys Lys Thr Val Val Leu Glu Val Ala Gln His Leu  
 50 55 60  
 Gly Asp Asn Leu Ile Arg Thr Ile Ala Met Ala Pro Thr Asp Gly Leu  
 65 70 75 80  
 Val Arg Gly Ala Ala Val Thr Asp Thr Ala Arg Pro Ile Ser Val Pro  
 85 90 95  
 Val Gly Asp Val Val Lys Gly His Val Phe Asn Ala Leu Gly Asp Cys  
 100 105 110

09602740-062300







Thr Gly Lys

<213> Corynebacterium glutamicum

<223> FRXA01193

ggt tct cag cgt gtc atc ggc att ctg cag aag aac aag qaa ctt caq 482



Val Ser Gln Arg Val Ile Gly Ile Leu Gln Lys Asn Lys Glu Leu Gln  
 145 150 155  
 gac atc atc gcc atc ctt ggt atg gac gag ctt tct gaa gag gac aag 530  
 Asp Ile Ile Ala Ile Leu Gly Met Asp Glu Leu Ser Glu Glu Asp Lys  
 160 165 170  
 atc acc gtt gca cgt gcg cgt cgc atc gag cgc ttc ctg ggt cag aac 578  
 Ile Thr Val Ala Arg Ala Arg Arg Ile Glu Arg Phe Leu Gly Gln Asn  
 175 180 185  
 ttc ttc gtt gca gag aag ttc acc ggt ctt cct ggc tcc tac gtg cca 626  
 Phe Phe Val Ala Glu Lys Phe Thr Gly Leu Pro Gly Ser Tyr Val Pro  
 190 195 200  
 ctg acc gac acc gtc gac gct ttc gag cgt att tgc aac ggc gac ttc 674  
 Leu Thr Asp Thr Val Asp Ala Phe Glu Arg Ile Cys Asn Gly Asp Phe  
 205 210 215 220  
 gac cac tac cca gag cag gct ttc aac ggc ctc ggt ggt ttg gac gat 722  
 Asp His Tyr Pro Glu Gln Ala Phe Asn Gly Leu Gly Gly Leu Asp Asp  
 225 230 235  
 gtc gaa gct gca tac aag aag ctg acc gga aag taaggtagag acacatggct 775  
 Val Glu Ala Ala Tyr Lys Lys Leu Thr Gly Lys  
 240 245  
 gaa 778  
 <210> 764  
 <211> 247  
 <212> PRT  
 <213> Corynebacterium glutamicum  
 <400> 764  
 Met Arg Val Ala Leu Ser Gly Leu Thr Met Ala Glu Tyr Phe Arg Asp  
 1 5 10 15  
 Val Gln Asn Gln Asp Val Leu Leu Phe Ile Asp Asn Ile Phe Arg Phe  
 20 25 30  
 Thr Gln Ala Gly Ser Glu Val Ser Thr Leu Leu Gly Arg Met Pro Ser  
 35 40 45  
 Ala Val Gly Tyr Gln Pro Thr Leu Ala Asp Glu Met Gly Val Leu Gln  
 50 55 60  
 Glu Arg Ile Thr Ser Thr Lys Gly Arg Ser Ile Thr Ser Leu Gln Ala  
 65 70 75 80  
 Val Tyr Val Pro Ala Asp Asp Tyr Thr Asp Pro Ala Pro Ala Thr Thr  
 85 90 95  
 Phe Ala His Leu Asp Ala Thr Thr Glu Leu Asp Arg Ser Ile Ala Ser  
 100 105 110  
 Lys Gly Ile Tyr Pro Ala Val Asn Pro Leu Thr Ser Thr Ser Arg Ile  
 115 120 125  
 Leu Glu Pro Ala Ile Val Gly Glu Arg His Tyr Glu Val Ser Gln Arg

09602740-062300



```
<210> 765
<211> 739
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(739)
<223> FRXA01203
```

<400> 765																
gtgtggccaa ccaggcacgt caggcacaga tcaccagga aatcacagag attgttggtg																60
gcgcaggcgc gctcgccgac agcggagaaa gtgactaatt atg act aca gct ctt																115
Met Thr Thr Ala Leu																
1 5																
gaa gag cag aac gca cag cag gca gcc act gcc ggc cgt gtc gtg cgt																163
Glu Glu Gln Asn Ala Gln Gln Ala Ala Thr Ala Gly Arg Val Val Arg																
10 15 20																
gtc att ggt gcg gtc gtc gac gtg gag ttt ccc cgc ggc gag ctg cca																211
Val Ile Gly Ala Val Val Asp Val Glu Phe Pro Arg Gly Glu Leu Pro																
25 30 35																
gca ctg tac aac gca ctt act gta gag gta acc ctc gaa tca gtt aag																259
Ala Leu Tyr Asn Ala Leu Thr Val Glu Val Thr Leu Glu Ser Val Lys																
40 45 50																
aag acc gtt gtt ctc gag gtt gct cag cac ctc ggc gac aac ctc atc																307
Lys Thr Val Val Leu Glu Val Ala Gln His Leu Gly Asp Asn Leu Ile																
55 60 65																
cgc acc atc gct atg gca cca acc gac gga ctt gtc cgc ggt gct gct																355
Arg Thr Ile Ala Met Ala Pro Thr Asp Gly Leu Val Arg Gly Ala Ala																
70 75 80 85																



gta acc gat act gca cgc cca att tcc gta cca gtg ggc gat gtt gtt 403  
 Val Thr Asp Thr Ala Arg Pro Ile Ser Val Pro Val Gly Asp Val Val  
 90 95 100

aag ggc cac gta ttc aac gct ttg ggc gac tgc cta gac gac gtt tcc 451  
 Lys Gly His Val Phe Asn Ala Leu Gly Asp Cys Leu Asp Asp Val Ser  
 105 110 115

ctg aac aac aac cca gag atc gag cgt tgg ggc atc cac cgc gag cca 499  
 Leu Asn Asn Asn Pro Glu Ile Glu Arg Trp Gly Ile His Arg Glu Pro  
 120 125 130

cca tca ttc gat cag ctt gag ggt aag acc gag atc ctg gaa aca ggc 547  
 Pro Ser Phe Asp Gln Leu Glu Gly Lys Thr Glu Ile Leu Glu Thr Gly  
 135 140 145

atc aag gtt atc gac ctt ctc acc cct tac gtt aag ggt gga aag atc 595  
 Ile Lys Val Ile Asp Leu Leu Thr Pro Tyr Val Lys Gly Gly Lys Ile  
 150 155 160 165

ggc ctc ttc ggt ggt gca ggt gtg ggt aag acc gtt ctt atc cag gaa 643  
 Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr Val Leu Ile Gln Glu  
 170 175 180

atg atc acc cgt att gca cgt gag ttc tcc ggt act tcc gtg ttc gca 691  
 Met Ile Thr Arg Ile Ala Arg Glu Phe Ser Gly Thr Ser Val Phe Ala  
 185 190 195

ggt gtt ggt aag cgt acc cgt gag ggc acc gac ctc ttc ctc gaa atg 739  
 Gly Val Gly Lys Arg Thr Arg Glu Gly Thr Asp Leu Phe Leu Glu Met  
 200 205 210

<210> 766  
 <211> 213  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 766  
 Met Thr Thr Ala Leu Glu Glu Gln Asn Ala Gln Gln Ala Ala Thr Ala  
 1 5 10 15  
 Gly Arg Val Val Arg Val Ile Gly Ala Val Val Asp Val Glu Phe Pro  
 20 25 30  
 Arg Gly Glu Leu Pro Ala Leu Tyr Asn Ala Leu Thr Val Glu Val Thr  
 35 40 45  
 Leu Glu Ser Val Lys Lys Thr Val Val Leu Glu Val Ala Gln His Leu  
 50 55 60  
 Gly Asp Asn Leu Ile Arg Thr Ile Ala Met Ala Pro Thr Asp Gly Leu  
 65 70 75 80  
 Val Arg Gly Ala Ala Val Thr Asp Thr Ala Arg Pro Ile Ser Val Pro  
 85 90 95  
 Val Gly Asp Val Val Lys Gly His Val Phe Asn Ala Leu Gly Asp Cys  
 100 105 110  
 Leu Asp Asp Val Ser Leu Asn Asn Asn Pro Glu Ile Glu Arg Trp Gly

09602740-062300



<400> 767															
aagtcgcccc gatagcgagc ggaccactcg gtcaactgaa taacccact aaacacttca															60
cagcccgaac acacgggcac cagaaaggga acgacacctc															
Met Asn Glu Ile Ile															115
1 5															
ctg gca cag gac gca acc gag tcc acc atc acc gga ctt ggc gct gtc															163
Leu Ala Gln Asp Ala Thr Glu Ser Thr Ile Thr Gly Leu Gly Ala Val															
10 15 20															
ggc tac ggc atc gca acc atc gga cct ggc ctc ggc atc ggc atc ctg															211
Gly Tyr Gly Ile Ala Thr Ile Gly Pro Gly Leu Gly Ile Gly Ile Leu															
25 30 35															
gtt ggt aag gct ctc gag ggt atg gca cgt cag cct gag atg gct gga															259
Val Gly Lys Ala Leu Glu Gly Met Ala Arg Gln Pro Glu Met Ala Gly															
40 45 50															
cag ctc cgt acc acc atg ttc ctg ggc atc gcc ttc gtt gag gcc ctg															307
Gln Leu Arg Thr Thr Met Phe Leu Gly Ile Ala Phe Val Glu Ala Leu															
55 60 65															
gca ctg atc ggc ctt gtt gct ggc ttc ctg ttc taatcagcta acttaaccga															360
Ala Leu Ile Gly Leu Val Ala Gly Phe Leu Phe															
70 75 80															
aag															363



```

<400> 768
Met Asn Glu Ile Ile Leu Ala Gln Asp Ala Thr Glu Ser Thr Ile Thr
  1             5             10             15

Gly Leu Gly Ala Val Gly Tyr Gly Ile Ala Thr Ile Gly Pro Gly Leu
      20             25             30

Gly Ile Gly Ile Leu Val Gly Lys Ala Leu Glu Gly Met Ala Arg Gln
      35             40             45

Pro Glu Met Ala Gly Gln Leu Arg Thr Thr Met Phe Leu Gly Ile Ala
  50             55             60

Phe Val Glu Ala Leu Ala Leu Ile Gly Leu Val Ala Gly Phe Leu Phe
  65             70             75             80

```

```
<220>
<221> CDS
<222> (101)..(280)
<223> FRXA02821
```

```
<210> 770
<211> 60
```

[illegible]



<213> Corynebacterium glutamicum

Val Gly Tyr Gly Ile Ala Thr Ile Gly Pro Gly Leu Gly Ile Gly Ile  
1 5 10 15

Leu Val Gly Lys Ala Leu Glu Gly Met Ala Arg Gln Pro Glu Met Ala  
20 25 30

Gly Gln Leu Arg Thr Thr Met Phe Leu Gly Ile Ala Phe Val Glu Ala  
35 40 45

Leu Ala Leu Ile Gly Leu Val Ala Gly Phe Leu Phe  
50 55 60

<213> Corynebacterium glutamicum

<223> RXA01200

ggc Gly 1	tgt Cys	ctt Leu	cgg Arg	tgg Trp 5	aaa Lys	agt Ser	gag Glu	cca Pro	tct Ser 10	gtt Val	ctc Leu	gaa Glu	gtc Val	ctc Leu 15	aag Lys	48
gac Asp	gcc Ala	gca Ala	gag Glu 20	cag Gln	acc Thr	tgg Trp	tcc Ser	act Thr 25	cca Pro	cgc Arg	gag Glu	ttc Phe	cgc Arg 30	gct Ala	gga Gly	96
cta Leu	gtc Val	caa Gln 35	ctt Leu	ggc Gly	cgt Arg	cgc Arg	gcc Ala 40	ctt Leu	ctt Leu	cgc Arg	tct Ser	gcg Ala 45	gag Glu	aaa Lys	cag Gln	144
ggt Gly	cag Gln 50	ctt Leu	ggt Gly	cag Gln	gtg Val	gaa Glu 55	gat Asp	gaa Glu	ctg Leu	ttc Phe	cga Arg 60	ctc Leu	agc Ser	cga Arg	atc Ile	192
ctg Leu 65	gat Asp	cgc Arg	gaa Glu	agc Ser	aag Lys 70	ctg Leu	act Thr	cag Gln	ctt Leu	ctt Leu 75	tca Ser	gat Asp	cgc Arg	act Thr 80	cag Gln	240
gaa Glu	att Ile	ggc Gly	ggt Gly	cga Arg 85	cgt Arg	gac Asp	ctc Leu	ctg Leu	gct Ala 90	aag Lys	gtg Val	ctc Leu	tac Tyr	ggc Gly 95	aag Lys	288
gta Val	act Thr	gct Ala	gtt Val 100	acc Thr	gaa Glu	gcc Ala	ctc Leu	gca Ala 105	ctg Leu	cag Gln	gct Ala	att Ile	ggt Gly 110	cgc Arg	cct Pro	336
gag Glu	cac His	aac Asn 115	cca Pro	att Ile	gac Asp	gat Asp	atc Ile 120	gca Ala	gct Ala	ttg Leu	gct Ala	ggc Gly 125	gct Ala	gta Val	gca Ala	384
gag	cta	cag	ggt	cgt	tcc	gtt	gca	cat	gtc	gtt	acc	qca	qtt	qaa	ctc	432

**SECRET**



```

<210> 772
<211> 203
<212> PRT
<213> Corynebacterium glutamicum

<400> 772
Gly Cys Leu Arg Trp Lys Ser Glu Pro Ser Val Leu Glu Val Leu Lys
 1           5           10
Asp Ala Ala Glu Gln Thr Trp Ser Thr Pro Arg Glu Phe Arg Ala Gly
      20           25           30
Leu Val Gln Leu Gly Arg Arg Ala Leu Leu Arg Ser Ala Glu Lys Gln
      35           40           45
Gly Gln Leu Gly Gln Val Glu Asp Glu Leu Phe Arg Leu Ser Arg Ile
 50           55           60
Leu Asp Arg Glu Ser Lys Leu Thr Gln Leu Leu Ser Asp Arg Thr Gln
 65           70           75           80
Glu Ile Gly Gly Arg Arg Asp Leu Leu Ala Lys Val Leu Tyr Gly Lys
      85           90           95
Val Thr Ala Val Thr Glu Ala Leu Ala Leu Gln Ala Ile Gly Arg Pro
      100           105           110
Glu His Asn Pro Ile Asp Asp Ile Ala Ala Leu Ala Gly Ala Val Ala
      115           120           125
Glu Leu Gln Gly Arg Ser Val Ala His Val Val Thr Ala Val Glu Leu
      130           135           140
Asn Glu Gly Gln Gln Gln Ala Leu Ala Glu Lys Leu Gly Arg Ile Tyr
145           150           155           160
Gly Arg Ala Met Ser Ile His Ser Glu Val Asp Thr Ser Leu Leu Gly
      165           170           175

```

<400> 772															
Gly 1	Cys	Leu	Arg	Trp 5	Lys	Ser	Glu	Pro	Ser 10	Val	Leu	Glu	Val	Leu 15	Lys
Asp	Ala	Ala	Glu 20	Gln	Thr	Trp	Ser	Thr 25	Pro	Arg	Glu	Phe	Arg 30	Ala	Gly
Leu	Val	Gln 35	Leu	Gly	Arg	Arg	Ala 40	Leu	Leu	Arg	Ser	Ala 45	Glu	Lys	Gln
Gly 50	Gln	Leu	Gly	Gln	Val	Glu 55	Asp	Glu	Leu	Phe	Arg 60	Leu	Ser	Arg	Ile
Leu 65	Asp	Arg	Glu	Ser	Lys 70	Leu	Thr	Gln	Leu	Leu 75	Ser	Asp	Arg	Thr	Gln 80
Glu	Ile	Gly	Gly	Arg 85	Arg	Asp	Leu	Leu	Ala 90	Lys	Val	Leu	Tyr	Gly 95	Lys
Val	Thr	Ala	Val 100	Thr	Glu	Ala	Leu	Ala 105	Leu	Gln	Ala	Ile	Gly 110	Arg	Pro
Glu	His	Asn 115	Pro	Ile	Asp	Asp	Ile 120	Ala	Ala	Leu	Ala	Gly 125	Ala	Val	Ala
Glu 130	Leu	Gln	Gly	Arg	Ser	Val 135	Ala	His	Val	Val	Thr 140	Ala	Val	Glu	Leu
Asn 145	Glu	Gly	Gln	Gln	Gln 150	Ala	Leu	Ala	Glu	Lys 155	Leu	Gly	Arg	Ile	Tyr 160
Gly	Arg	Ala	Met	Ser 165	Ile	His	Ser	Glu	Val 170	Asp	Thr	Ser	Leu	Leu 175	Gly



```
<210> 774
<211> 124
<212> PRT
<213> Corynebacterium glutamicum
```

**090627Z**



<210> 775

<211> 1098

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) .. (1075)

<223> RXA01202

<400> 775

agaaagacca gctcaccgtt tcccgcaagg tcagcaagaa gtaaggcagc gagcctacac 60

taaatgactg tccaagcaac tgaagggagg cgtgtgaacc atg gca aca att cgt 115  
Met Ala Thr Ile Arg  
1 5

gaa ttg cgt gac cga att cgt tcg gtt aac tca acc aag aag atc acc 163  
Glu Leu Arg Asp Arg Ile Arg Ser Val Asn Ser Thr Lys Lys Ile Thr  
10 15 20

aag gct caa gag ctc atc gcc acc tct cgc atc acc aag gca cag ggt 211  
Lys Ala Gln Glu Leu Ile Ala Thr Ser Arg Ile Thr Lys Ala Gln Gly  
25 30 35

cgc gtc gcg gca gct gcg ccg tac gcc gag gaa atc cag cgc gtg ctg 259  
Arg Val Ala Ala Ala Ala Pro Tyr Ala Glu Glu Ile Gln Arg Val Leu  
40 45 50

gag cgc ctc gcg tcg gca agc tcc cta gac cac cca atg ctg cgt gag 307  
Glu Arg Leu Ala Ser Ala Ser Ser Leu Asp His Pro Met Leu Arg Glu  
55 60 65

cgt gaa ggc ggc aag cga gcc gcc gtg ctc gtg gtt act tct gac cgc 355



09602740-062300



1098

<400> 776															
Met 1	Ala	Thr	Ile	Arg 5	Glu	Leu	Arg	Asp	Arg 10	Ile	Arg	Ser	Val	Asn 15	Ser
Thr	Lys	Lys	Ile 20	Thr	Lys	Ala	Gln	Glu 25	Leu	Ile	Ala	Thr	Ser 30	Arg	Ile
Thr	Lys	Ala 35	Gln	Gly	Arg	Val	Ala 40	Ala	Ala	Ala	Pro	Tyr 45	Ala	Glu	Glu
Ile	Gln 50	Arg	Val	Leu	Glu	Arg 55	Leu	Ala	Ser	Ala	Ser 60	Ser	Leu	Asp	His
Pro 65	Met	Leu	Arg	Glu	Arg 70	Glu	Gly	Gly	Lys	Arg 75	Ala	Ala	Val	Leu	Val 80
Val	Thr	Ser	Asp	Arg 85	Gly	Met	Ala	Gly	Gly 90	Tyr	Asn	His	Asn	Val 95	Leu
Lys	Lys	Ala 100	Ala	Glu	Leu	Glu	Lys	Leu 105	Leu	Ala	Glu	Ser	Gly 110	Tyr	Glu
Val	Val	Arg 115	Tyr	Val	Thr	Gly	Lys 120	Lys	Gly	Val	Asp	Tyr 125	Tyr	Lys	Phe
Arg	Ala 130	Glu	Asp	Val	Ala	Gly 135	Thr	Trp	Thr	Gly	Phe 140	Ser	Gln	Asp	Pro
Asp 145	Trp	Ala	Ala	Thr	His 150	Asn	Val	Arg	Arg	His 155	Leu	Ile	Asp	Gly	Phe 160
Thr	Ala	Ser	Ser	Glu 165	Gly	Glu	Ala	Ala 170	Trp	Arg	Glu	Gly	Leu 175	Asn	Leu
Pro	Glu	Gly	Gln 180	Asp	Ile	Gln	Gly	Phe 185	Asp	Gln	Val	His	Val 190	Val	Tyr
Thr	Glu	Phe 195	Ile	Ser	Met	Leu	Thr 200	Gln	Asn	Pro	Val	Val 205	His	Gln	Leu
Leu 210	Pro	Val	Glu	Pro	Val	Ile 215	Glu	Asp	Glu	Ile	Phe 220	Glu	Lys	Gly	Glu
Asp 225	Leu	Leu	Ser	Ser	Ser 230	Gly	Glu	Val	Glu	Pro 235	Asp	Tyr	Glu	Phe	Glu 240
Pro	Asp	Ala	Asp	Thr 245	Leu	Leu	Glu	Ala	Leu 250	Leu	Pro	Gln	Tyr	Val 255	Ser
Arg	Arg	Leu	Phe 260	Ser	Ile	Phe	Leu 265	Glu	Ala	Ala	Ala	Ala	Glu 270	Ser	Ala

**SECRET**



<400> 777																
cttcaatagt caaaaccagc aaactaattt tttaagtttt acgtaactgg ccccaccgct																60
tgtggcaggc cttgcgtttt gacattgaag gacccttttt																
<div>atg cgc act ttt gcc</div> <div>Met Arg Thr Phe Ala</div> <div>1 5</div>																115
gct tat att gcc att gat ggc ctc agc ttt tcc tac ccc aac acc cac																
<div>Ala Tyr Ile Ala Ile Asp Gly Leu Ser Phe Ser Tyr Pro Asn Thr His</div> <div>10 15 20</div>																163
gtt tta agc gat att tcg ctc acc gtt gcc aat ggc gat atc gcc gga																
<div>Val Leu Ser Asp Ile Ser Leu Thr Val Ala Asn Gly Asp Ile Ala Gly</div> <div>25 30 35</div>																211
ctg att ggt gaa aac ggc gca gga aaa tcc acc ctg ctc agc ctc atc																
<div>Leu Ile Gly Glu Asn Gly Ala Gly Lys Ser Thr Leu Leu Ser Leu Ile</div> <div>40 45 50</div>																259
gct ggc gtc atg gaa ccc gac cag ggc agg att tac ctc ccc gaa cgc																
<div>Ala Gly Val Met Glu Pro Asp Gln Gly Arg Ile Tyr Leu Pro Glu Arg</div> <div>55 60 65</div>																307
acc gga ttc atc gcc caa gaa aca gac tta ccg ttt gaa caa ccc gtg																
<div>Thr Gly Phe Ile Ala Gln Glu Thr Asp Leu Pro Phe Glu Gln Pro Val</div> <div>70 75 80 85</div>																355
cag tcg ctt atc gac gcc gcc gtc gcc cca gtg cgc gcg gtc gat gcc																
<div>Gln Ser Leu Ile Asp Ala Ala Val Ala Pro Val Arg Ala Val Asp Ala</div> <div>90 95 100</div>																403
gcg att aca gat ttg tcc acc aag ctt ggc gac gcc tcc ctc agc gcc																
<div>Ala Ile Thr Asp Leu Ser Thr Lys Leu Gly Asp Ala Ser Leu Ser Ala</div> <div>105 110 115</div>																451
gaa gag cag gcg caa gtc gcc aca gat ttc gat gca gcg cta ggc gct																
<div>Glu Glu Gln Ala Gln Val Ala Thr Asp Phe Asp Ala Ala Leu Gly Ala</div>																499

[illegible]



120	125	130	
gca gaa gaa ctc gga ctg tgg gaa tta gat gca cgt att gaa acc atc Ala Glu Glu Leu Gly Leu Trp Glu Leu Asp Ala Arg Ile Glu Thr Ile 135 140 145			547
gtc gcg ggt ctc ggc ctt gcc gag gtg gat cgc agc act ccc att ggt Val Ala Gly Leu Gly Leu Ala Glu Val Asp Arg Ser Thr Pro Ile Gly 150 155 160 165			595
gag ctt tcc ggc ggt cag cgc cgc aga ttc gca ttg gca gcg ctg ctg Glu Leu Ser Gly Gly Gln Arg Arg Arg Phe Ala Leu Ala Ala Leu Leu 170 175 180			643
ttg gaa cca cac gat gct ctg att ttc gat gag ccc acc aac cac ctc Leu Glu Pro His Asp Ala Leu Ile Phe Asp Glu Pro Thr Asn His Leu 185 190 195			691
gac gac aca gcc gta gat ttc ctc atc tcg gag att tcc cgt ttc aaa Asp Asp Thr Ala Val Asp Phe Leu Ile Ser Glu Ile Ser Arg Phe Lys 200 205 210			739
ggt cca gtg ctg atc gcc agc cac gat cgc ttc ttc ctc gac tcc gtc Gly Pro Val Leu Ile Ala Ser His Asp Arg Phe Phe Leu Asp Ser Val 215 220 225			787
tgt acc gag tta atc gac ctc gat cct gca ctt gga cct gag ggc gga Cys Thr Glu Leu Ile Asp Leu Asp Pro Ala Leu Gly Pro Glu Gly Gly 230 235 240 245			835
tcc ggc gaa gaa gta aaa caa gcc gtg tct ttt ggt ggt gga ttt tct Ser Gly Glu Glu Val Lys Gln Ala Val Ser Phe Gly Gly Gly Phe Ser 250 255 260			883
gaa tac atc aaa gaa cgc gag acc cgc cgc acc cgc tgg gct cag ttg Glu Tyr Ile Lys Glu Arg Glu Thr Arg Arg Thr Arg Trp Ala Gln Leu 265 270 275			931
tac acc gca caa gaa acc gag cgg gaa aaa ctc gaa gaa acc acc ggc Tyr Thr Ala Gln Glu Thr Glu Arg Glu Lys Leu Glu Glu Thr Thr Gly 280 285 290			979
acc acc gaa tcg gat att ttc cac agc tcg gtt tcc aaa tcg gaa gct Thr Thr Glu Ser Asp Ile Phe His Ser Ser Val Ser Lys Ser Glu Ala 295 300 305			1027
aaa atc acc gcg aaa ttt tac gca gac cgg gca gct aaa act caa ggc Lys Ile Thr Ala Lys Phe Tyr Ala Asp Arg Ala Ala Lys Thr Gln Gly 310 315 320 325			1075
aac cgc gtc cgc tcc gcc aaa aac cgc ctg aag gaa ttg gaa cgc tat Asn Arg Val Arg Ser Ala Lys Asn Arg Leu Lys Glu Leu Glu Arg Tyr 330 335 340			1123
gaa atc cca gca cct cca aag cca ctg gaa ttc caa ggc atc cca gaa Glu Ile Pro Ala Pro Pro Lys Pro Leu Glu Phe Gln Gly Ile Pro Glu 345 350 355			1171
gcc tcc gga aac ggt cac ggt gaa aca cta gaa gtg cgg gct att gct Ala Ser Gly Asn Gly His Gly Glu Thr Leu Glu Val Arg Ala Ile Ala 360 365 370			1219

0002290" 04220960



<400> 778  
Met Arg Thr Phe Ala Ala Tyr Ile Ala Ile Asp Gly Leu Ser Phe Ser  
1 5 10 15  
Tyr Pro Asn Thr His Val Leu Ser Asp Ile Ser Leu Thr Val Ala Asn  
20 25 30



Gly Asp Ile Ala Gly Leu Ile Gly Glu Asn Gly Ala Gly Lys Ser Thr  
                   35                  40                  45  
 Leu Leu Ser Leu Ile Ala Gly Val Met Glu Pro Asp Gln Gly Arg Ile  
           50                  55                  60  
 Tyr Leu Pro Glu Arg Thr Gly Phe Ile Ala Gln Glu Thr Asp Leu Pro  
       65                  70                  75                  80  
 Phe Glu Gln Pro Val Gln Ser Leu Ile Asp Ala Ala Val Ala Pro Val  
                   85                  90                  95  
 Arg Ala Val Asp Ala Ala Ile Thr Asp Leu Ser Thr Lys Leu Gly Asp  
                  100                 105                 110  
 Ala Ser Leu Ser Ala Glu Glu Gln Ala Gln Val Ala Thr Asp Phe Asp  
          115                 120                 125  
 Ala Ala Leu Gly Ala Ala Glu Glu Leu Gly Leu Trp Glu Leu Asp Ala  
       130                 135                 140  
 Arg Ile Glu Thr Ile Val Ala Gly Leu Gly Leu Ala Glu Val Asp Arg  
   145                 150                 155                 160  
 Ser Thr Pro Ile Gly Glu Leu Ser Gly Gly Gln Arg Arg Arg Phe Ala  
                  165                 170                 175  
 Leu Ala Ala Leu Leu Leu Glu Pro His Asp Ala Leu Ile Phe Asp Glu  
          180                 185                 190  
 Pro Thr Asn His Leu Asp Asp Thr Ala Val Asp Phe Leu Ile Ser Glu  
          195                 200                 205  
 Ile Ser Arg Phe Lys Gly Pro Val Leu Ile Ala Ser His Asp Arg Phe  
       210                 215                 220  
 Phe Leu Asp Ser Val Cys Thr Glu Leu Ile Asp Leu Asp Pro Ala Leu  
   225                 230                 235                 240  
 Gly Pro Glu Gly Gly Ser Gly Glu Glu Val Lys Gln Ala Val Ser Phe  
                  245                 250                 255  
 Gly Gly Gly Phe Ser Glu Tyr Ile Lys Glu Arg Glu Thr Arg Arg Thr  
          260                 265                 270  
 Arg Trp Ala Gln Leu Tyr Thr Ala Gln Glu Thr Glu Arg Glu Lys Leu  
       275                 280                 285  
 Glu Glu Thr Thr Gly Thr Thr Glu Ser Asp Ile Phe His Ser Ser Val  
       290                 295                 300  
 Ser Lys Ser Glu Ala Lys Ile Thr Ala Lys Phe Tyr Ala Asp Arg Ala  
   305                 310                 315                 320  
 Ala Lys Thr Gln Gly Asn Arg Val Arg Ser Ala Lys Asn Arg Leu Lys  
          325                 330                 335  
 Glu Leu Glu Arg Tyr Glu Ile Pro Ala Pro Pro Lys Pro Leu Glu Phe  
          340                 345                 350

002290"0422960







0960240-0604











Arg Val Pro Thr Ser Val Pro Val Thr Trp Asn Ala  
420 425

<213> Corynebacterium glutamicum

<223> RXN00387

ttccgcgccg gcgccaactt cgacggcacc gggctgacca ctttctgctt tgaagcgcac 60

att tcc tac gca gtc ggc gac gac atc caa aac gac cca gaa acc tgg 163  
Ile Ser Tyr Ala Val Gly Asp Asp Ile Gln Asn Asp Pro Glu Thr Trp  
10 15 20

gaa gac tac gaa ctt cgc gtc aac cac cca ctg cgc atc gaa ggc gac 211  
Glu Asp Tyr Glu Leu Arg Val Asn His Pro Leu Arg Ile Glu Gly Asp  
25 30 35

cgc gtc tac ctt cag ggc cac ggc ttc gcc cca aca ttc acc gtg acc 259  
Arg Val Tyr Leu Gln Gly His Gly Phe Ala Pro Thr Phe Thr Val Thr  
40 45 50

tgg cca aat ggc gag acc cgc acc cag acc gtg cag tgg cgc cca gac 307  
 Trp Pro Asn Gly Glu Thr Arg Thr Gln Thr Val Gln Trp Arg Pro Asp  
 55 60 65

gac ccg acc ttc ttc ctg tcc tca ggc gtg gtc cgt ttc gat cca ccc 355  
Asp Pro Thr Phe Phe Leu Ser Ser Gly Val Val Arg Phe Asp Pro Pro  
70 75 80 85

gcc ggc atg tac cca gac ctt tac gag cgc cgc caa aac cag ttg gcc 403  
Ala Gly Met Tyr Pro Asp Leu Tyr Glu Arg Arg Gln Asn Gln Leu Ala  
90 95 100

atc cag gga ctt ttc gca ccg acc gcg gaa tgg gaa ggc gac aac aac 451  
Ile Gln Gly Leu Phe Ala Pro Thr Ala Glu Trp Glu Gly Asp Asn Asn  
105 110 115

gaa ctg ctg acc tcc tcc tac ccg gcg atg cgt gac cca gcc gtg gcg 499  
Glu Leu Leu Thr Ser Ser Tyr Pro Ala Met Arg Asp Pro Ala Val Ala  
120 125 130

atc gat att tac cgc ggc gac aat ggc ctc gat acc ggc atc gga cag 547  
Ile Asp Ile Tyr Arg Gly Asp Asn Gly Leu Asp Thr Gly Ile Gly Gln

[illegible]



<400> 782																
Met	Phe	Arg	Ser	Asn	Ile	Ser	Tyr	Ala	Val	Gly	Asp	Asp	Ile	Gln	Asn	
1				5					10					15		
Asp	Pro	Glu	Thr	Trp	Glu	Asp	Tyr	Glu	Leu	Arg	Val	Asn	His	Pro	Leu	
			20					25					30			
Arg	Ile	Glu	Gly	Asp	Arg	Val	Tyr	Leu	Gln	Gly	His	Gly	Phe	Ala	Pro	
		35					40					45				
Thr	Phe	Thr	Val	Thr	Trp	Pro	Asn	Gly	Glu	Thr	Arg	Thr	Gln	Thr	Val	
	50					55					60					
Gln	Trp	Arg	Pro	Asp	Asp	Pro	Thr	Phe	Phe	Leu	Ser	Ser	Gly	Val	Val	
65					70					75					80	
Arg	Phe	Asp	Pro	Pro	Ala	Gly	Met	Tyr	Pro	Asp	Leu	Tyr	Glu	Arg	Arg	



85																90				95			
Gln	Asn	Gln	Leu 100	Ala	Ile	Gln	Gly	Leu 105	Phe	Ala	Pro	Thr	Ala 110	Glu	Trp								
Glu	Gly	Asp 115	Asn	Asn	Glu	Leu	Leu 120	Thr	Ser	Ser	Tyr	Pro 125	Ala	Met	Arg								
Asp	Pro 130	Ala	Val	Ala	Ile	Asp 135	Ile	Tyr	Arg	Gly	Asp 140	Asn	Gly	Leu	Asp								
Thr 145	Gly	Ile	Gly	Gln	Ser 150	Leu	Phe	Ser	Leu	Asp 155	Ser	Ser	Leu	Met	His 160								
Ser	Gly	Val	Leu	Gln 165	Lys	Ile	Glu	Arg	Val 170	Asn	Leu	Gln	Ile	Gly 175	Asp								
Thr	Val	Thr	Leu 180	Asp	Asp	Gly	Thr	Thr 185	Val	Ser	Phe	Asp	Gly 190	Ala	Ser								
Glu	Phe 195	Ala	Asn	Tyr	Gln	Ile	Ser 200	Arg	Asp	Pro	Thr	Gln 205	Asn	Trp	Val								
Leu 210	Val	Thr	Thr	Val	Ile	Ser 215	Leu	Val	Ser	Leu	Val 220	Gly	Ser	Leu	Met								
Ile 225	Arg	Arg	Arg	Arg	Ile 230	Trp	Val	Arg	Phe	Tyr 235	Pro	Gln	Glu	Asn	Gly 240								
Thr	Thr	Arg	Val	Glu 245	Thr	Gly	Gly	Leu	Ala 250	Arg	Thr	Asp	Arg	Ala 255	Gly								
Trp	Gly	Gly	Glu 260	Tyr	Glu	Lys	Phe	His 265	Arg	Glu	Leu	Leu	Gly 270	Leu	Lys								
Glu	Glu	Asp 275	Glu	Asp	Glu	Glu	Tyr 280	Phe	Asp	His	Asp	Asp 285											